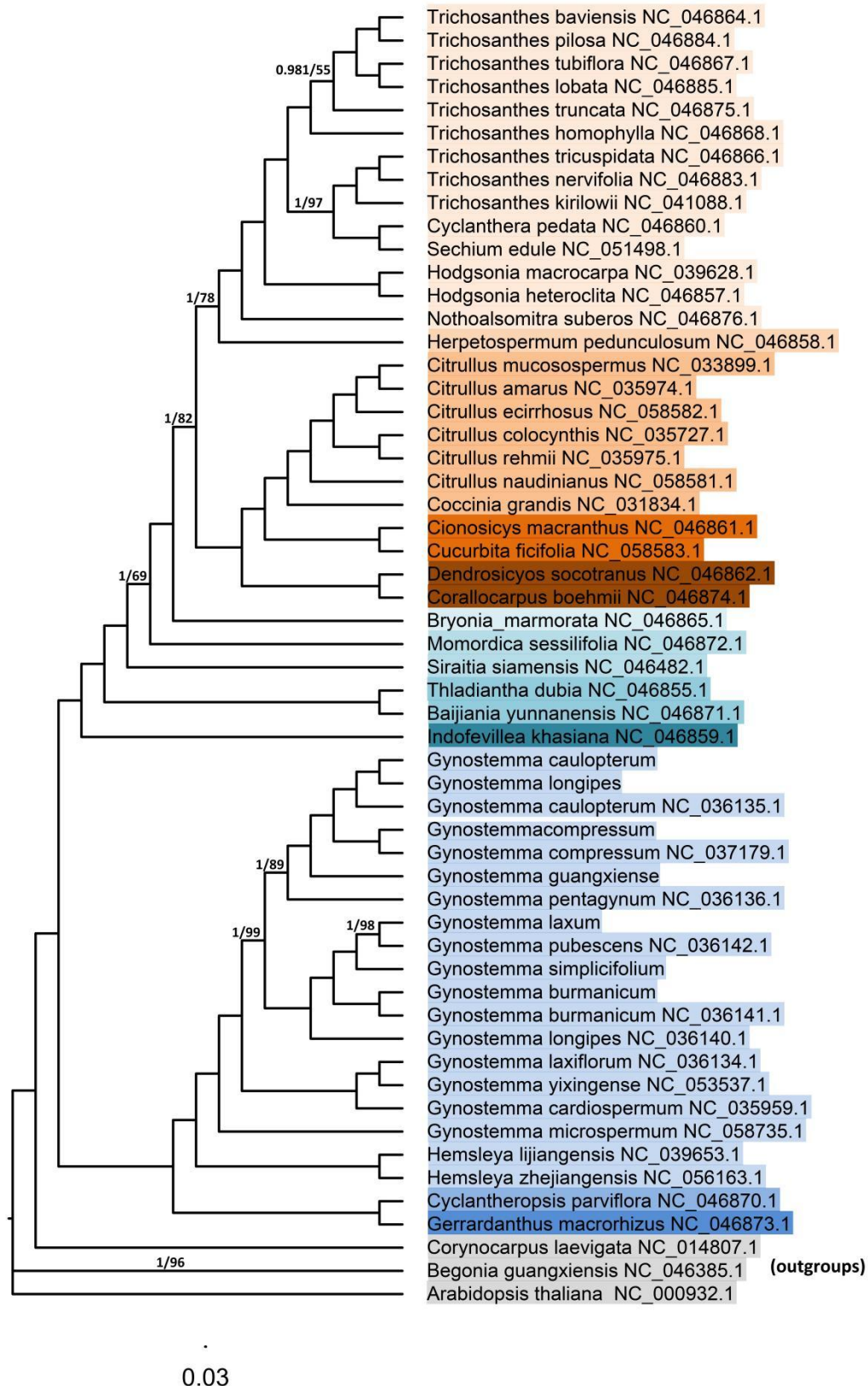


**Figure S1.** MAUVE alignment of chloroplast genomes of 21 individuals of the genus *Gynostemma*. The differently coloured squares represent different types of genes. Black represents transfer RNAs (tRNAs), and green represents tRNAs with introns (rRNAs). Red represents ribosomal RNA, while white represents protein-coding genes.



**Figure S2.** Phylogenetic trees were generated using maximum likelihood (ML) and Bayesian (BI) methods on the basis of 53 *Cucurbitaceae* chloroplast genomic CDS regions. ML trees and BI trees have the same topology. Bayesian posterior probabilities/ML bootstrap values are shown on the nodes and values of 1/100 are unlabelled. Different colours indicate as different tribes according to the APG IV classification system.