

Figure S1: Phylogenetic trees inferred by the maximum likelihood (ML) approach for (a) sequence data partitioned by genes and (b) un-partitioned sequence data.

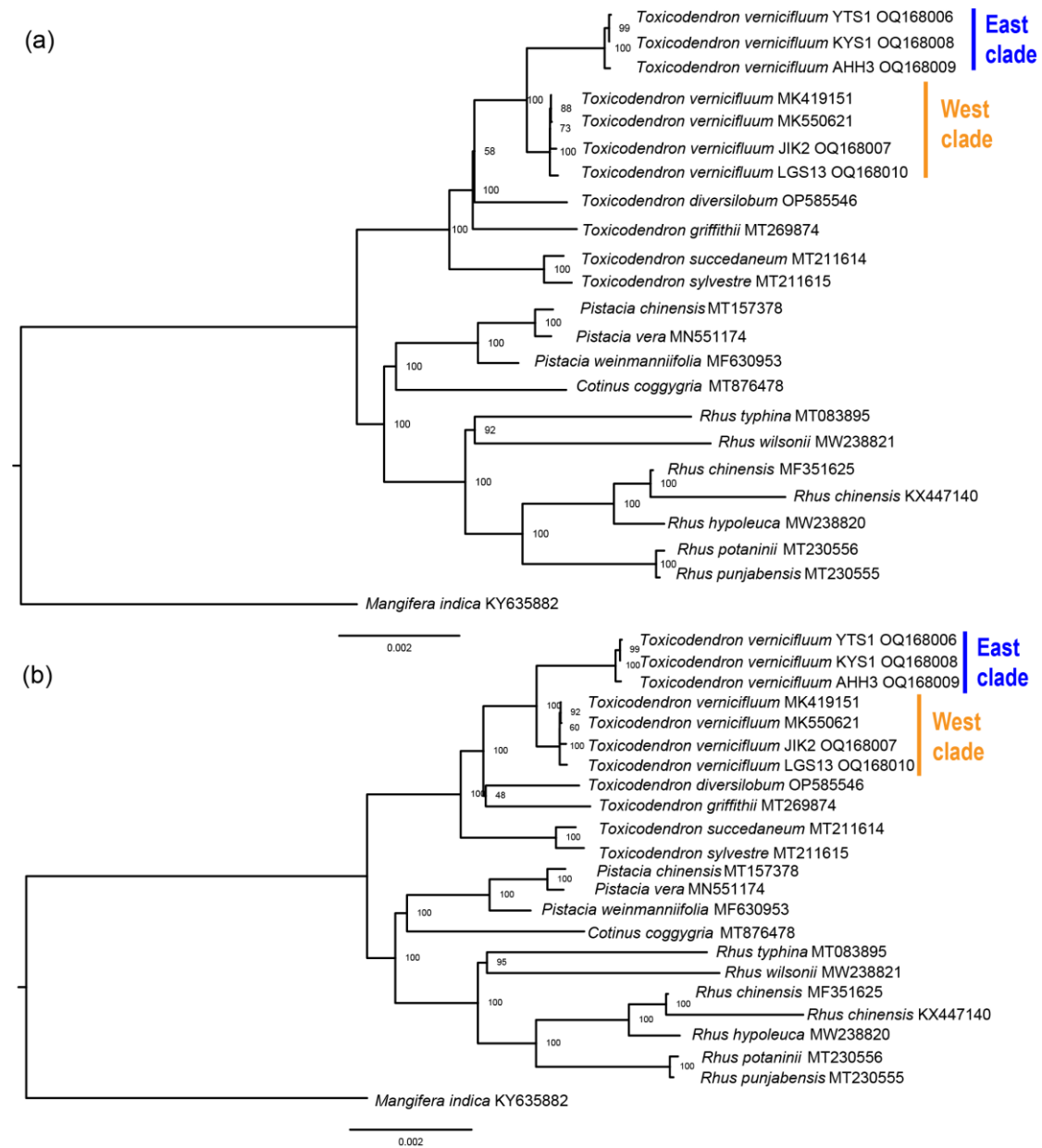


Figure S2: Phylogenetic trees inferred by the Bayesian Inference (BI) approach for (a) sequence data partitioned by genes and (b) un-partitioned sequence data.

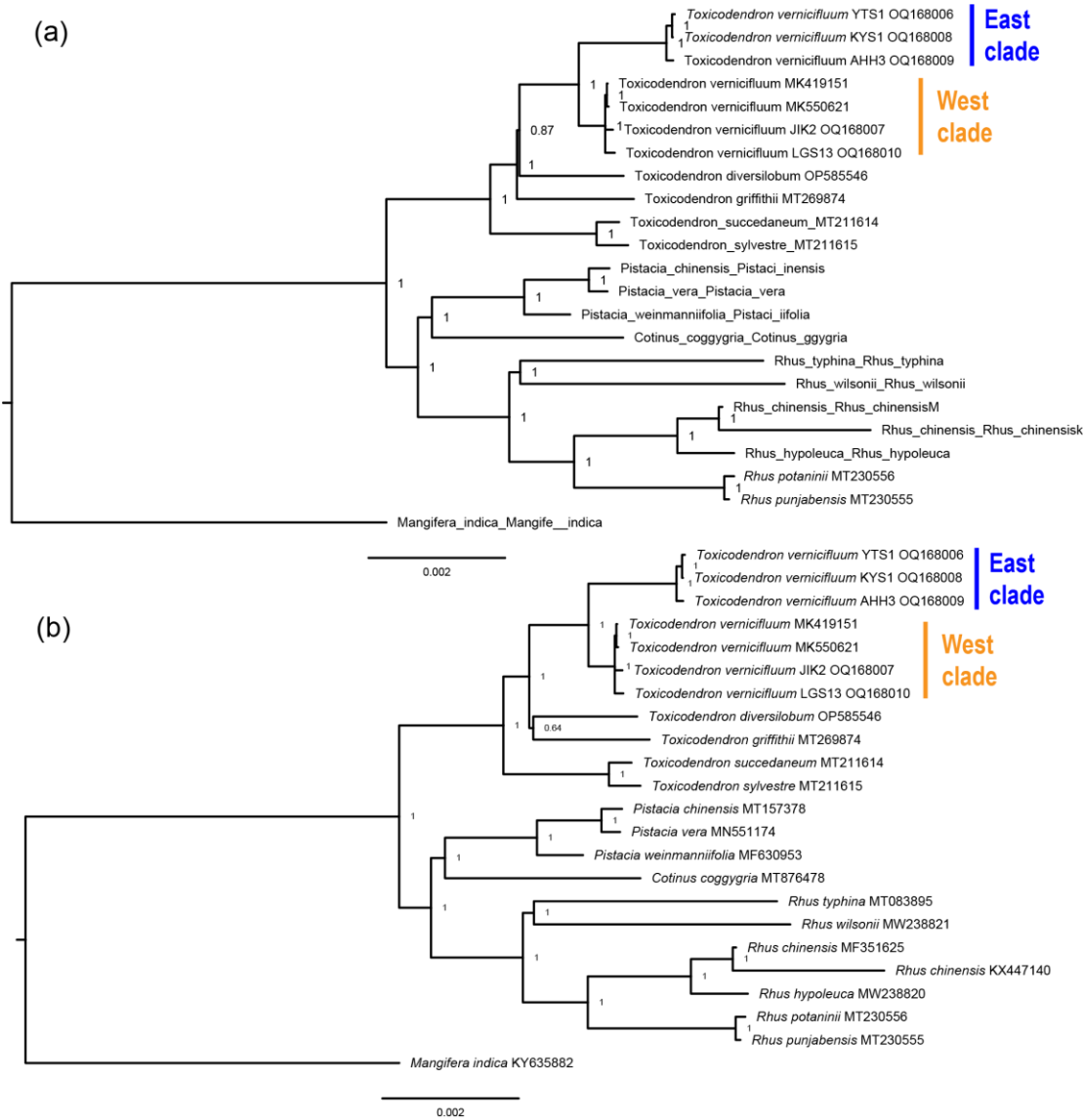


Figure S3: Nucleotide diversity ( $\pi$ ) among the complete chloroplast genome sequences of 11 accessions of *Toxicodendron*.

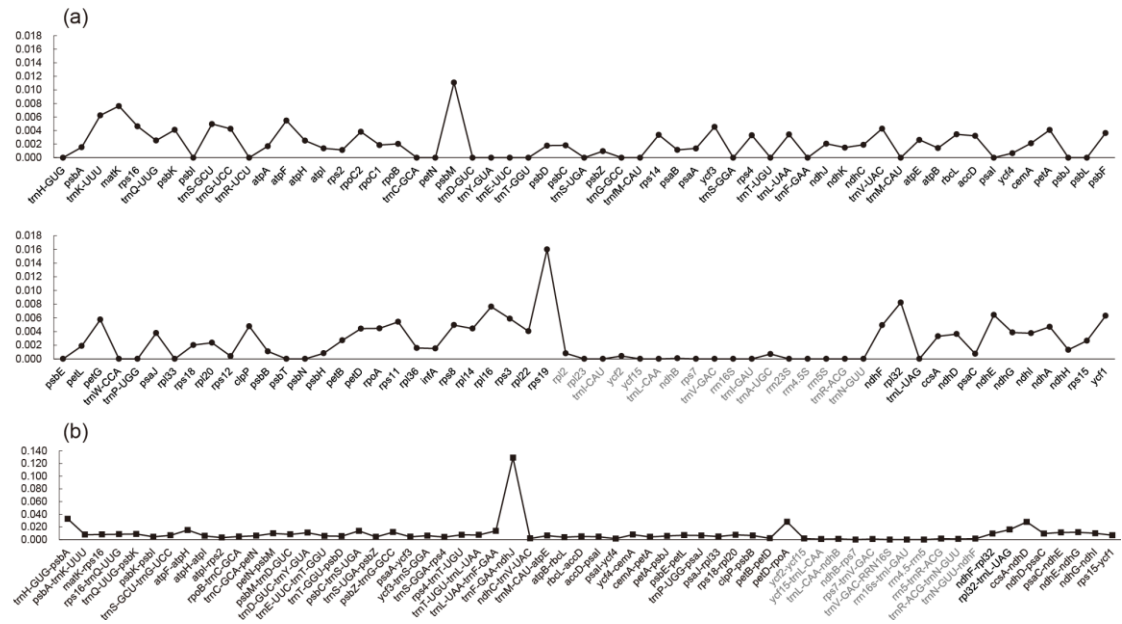


Figure S4: Nucleotide diversity ( $\pi$ ) among the complete chloroplast genome sequences of 22 accessions of the tribe Rhoeae.

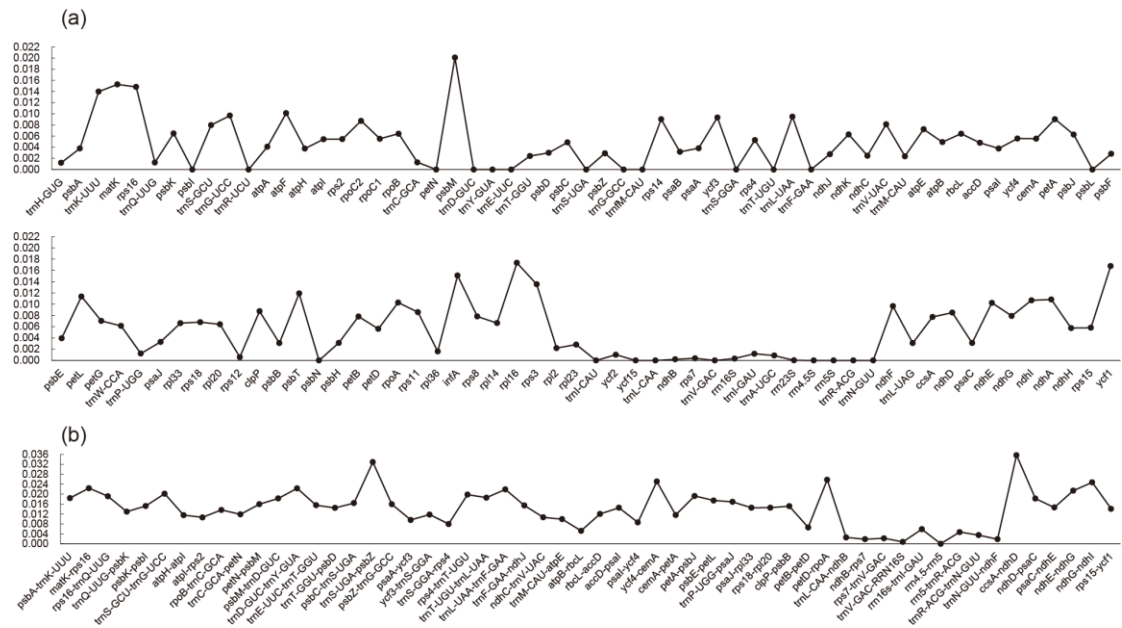


Figure S5: Gene map and MAUVE alignment of six chloroplast genomes of *Toxicodendron vernicifluum*.

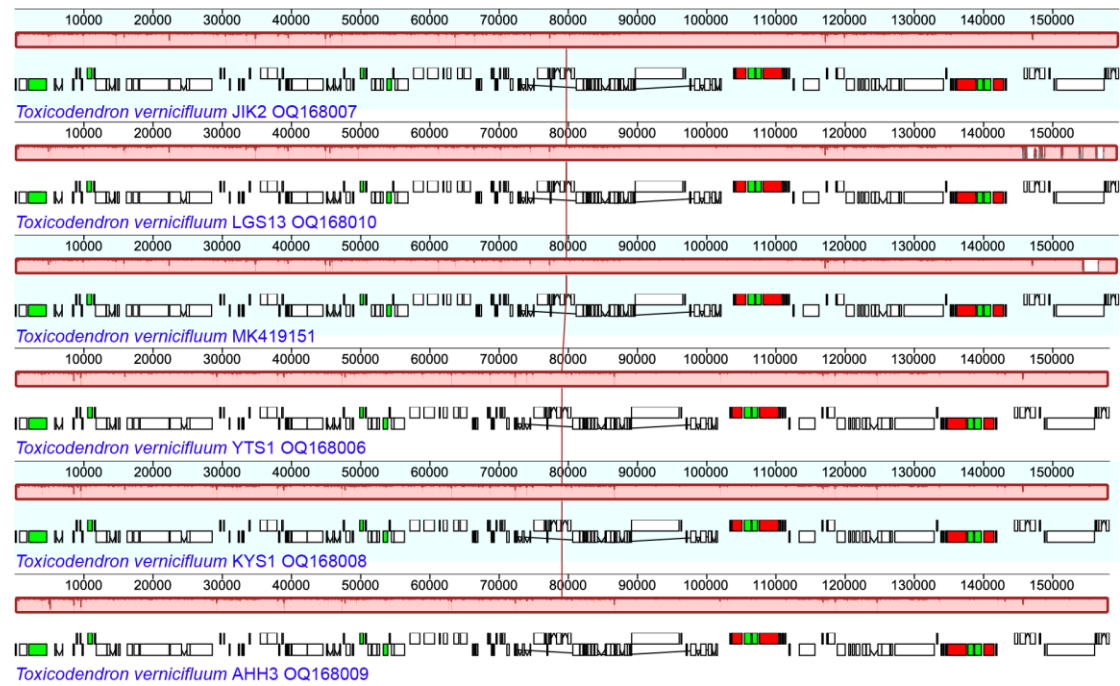


Figure S6: Gene map and MAUVE alignment of five chloroplast genomes of *Toxicodendron*.

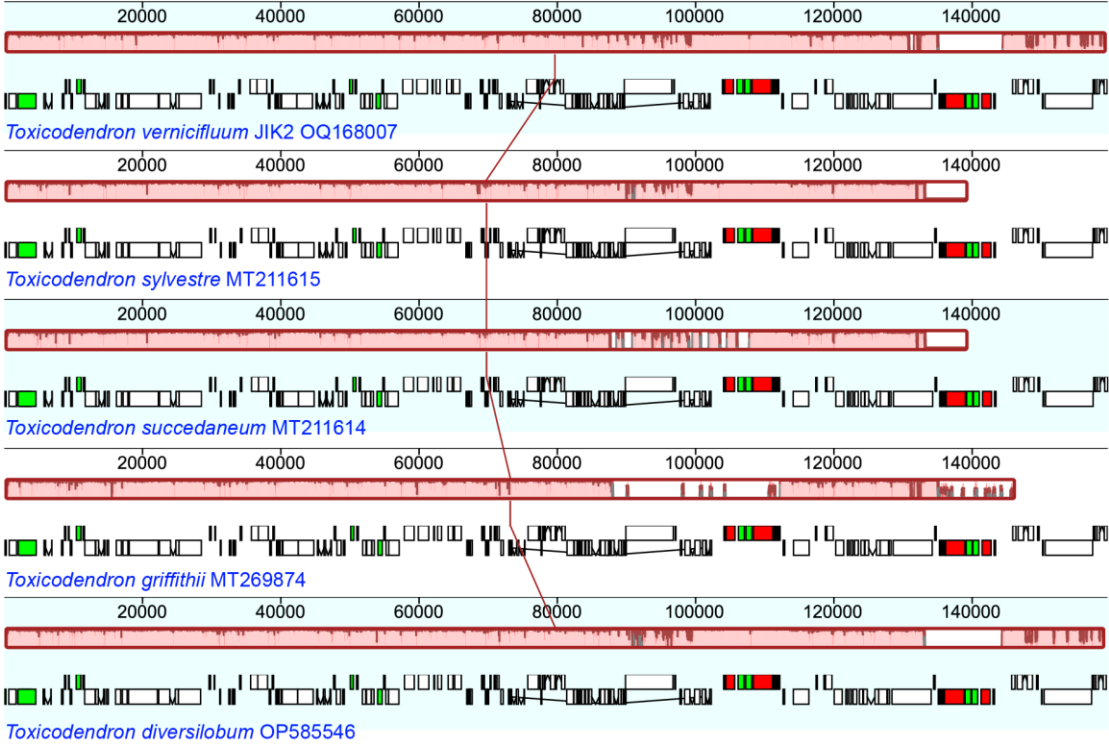


Figure S7: Gene map and MAUVE alignment of six chloroplast genomes of the tribe Rhoeae.

