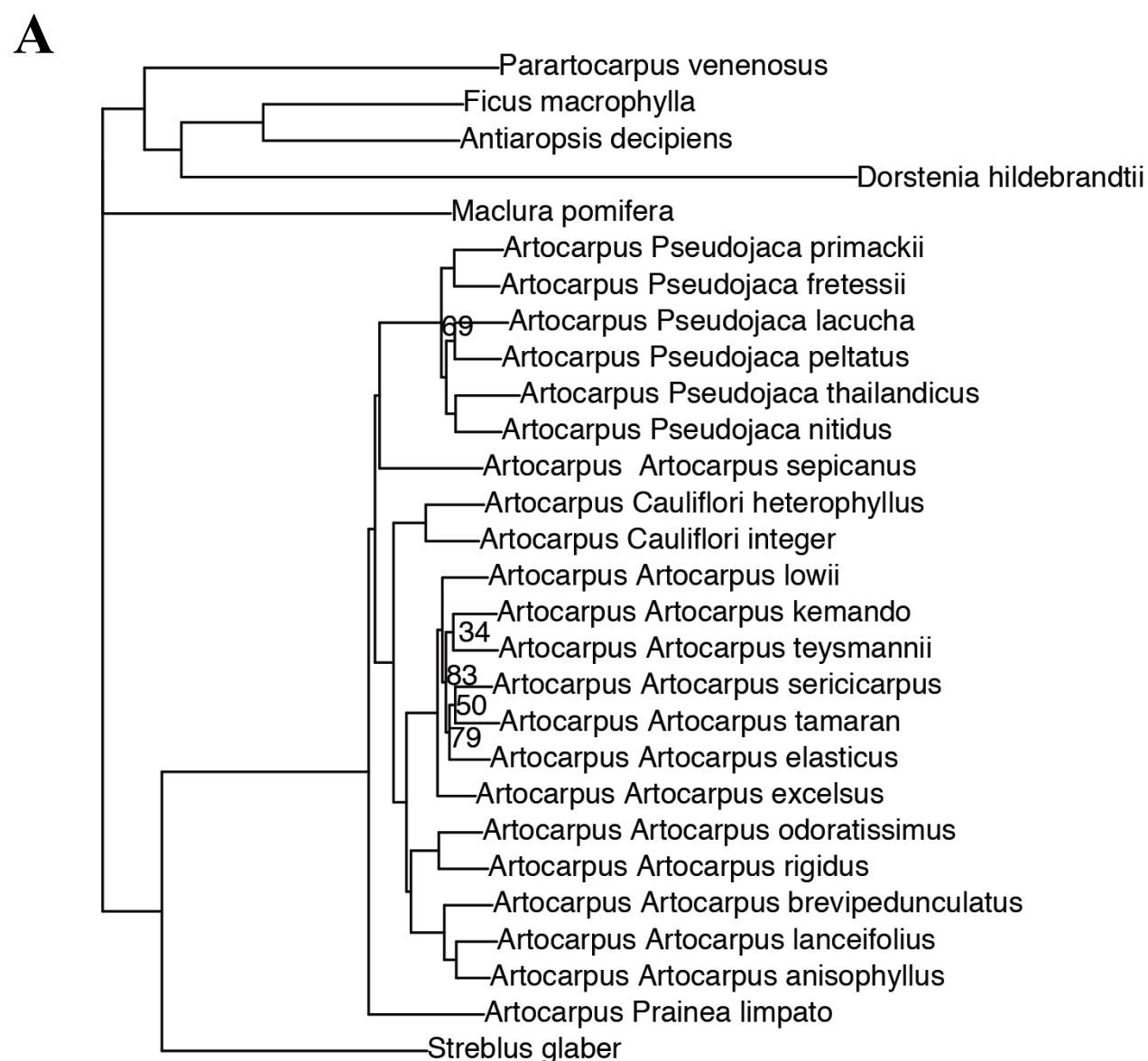


APPENDIX S8. Maximum likelihood phylogeny of *Artocarpus* and other Moraceae constructed from 333 phylogenetic markers recovered from high-throughput sequencing reads by HybPiper. Support values are from 200 fast-bootstrap replicates in RAxML version 8, and nodes without support values have 100% support. (A) Phylogeny reconstructed from coding sequences only. (B) Phylogeny reconstructed from coding sequences and recovered intron sequence. Subgenus-level classifications follow Zerega et al. (2010).



**B**

