

Supplementary Material

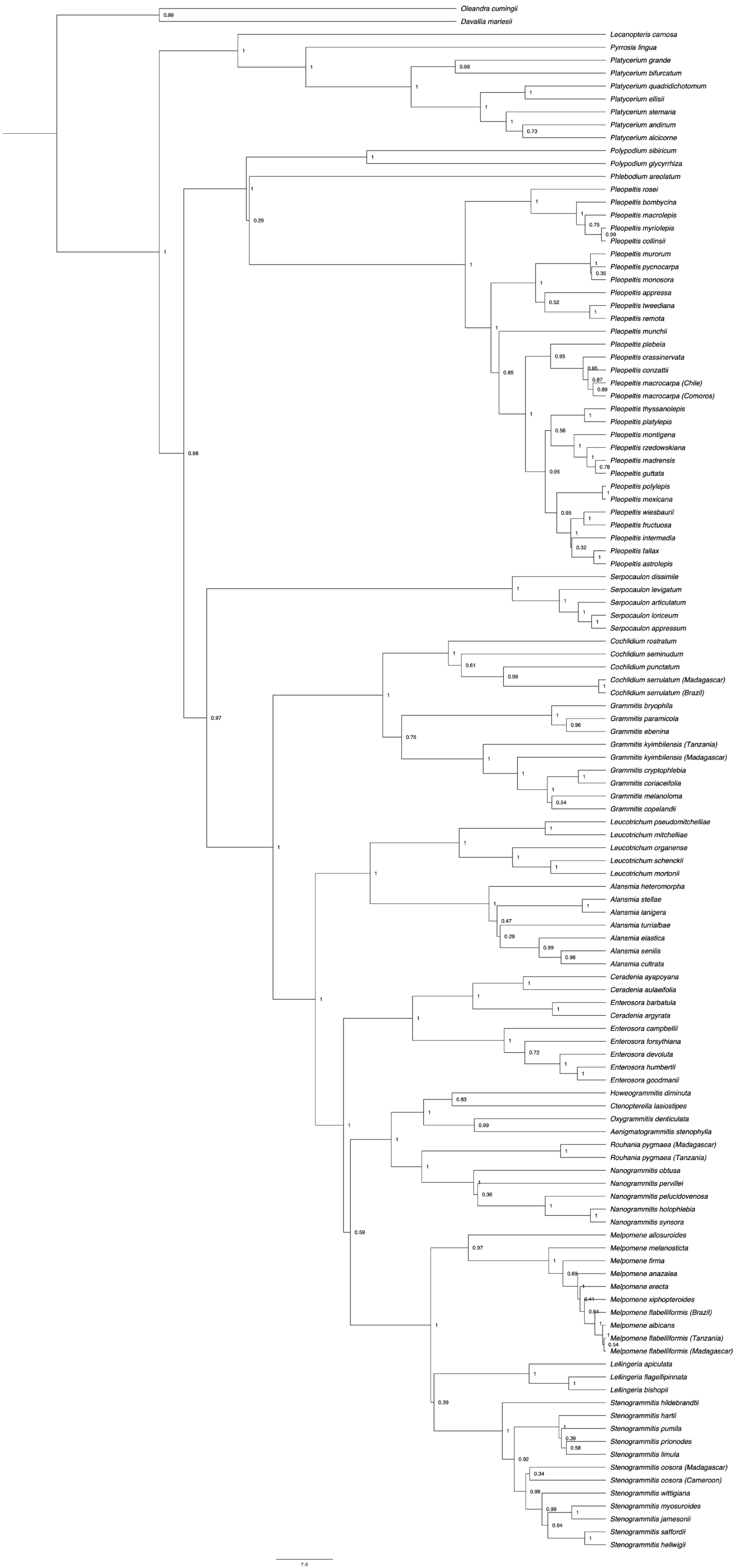


Figure S2. Ultrametric tree representing the phylogenetic reconstruction of Polypodiaceae inferred from Bayesian Inference in BEAST based on combined sequence data from *atpB*, *rbcL*, *rps4-trnS*, and *trnL-trnF*. Node values indicate posterior probabilities (PP). The scale bar represents time (in millions of years) or substitutions per site.