Phylogeny and Evolution of the Neotropical Radiation of Lachemilla (Rosaceae):
Uncovering a History of Reticulate Evolution and Implications for Infrageneric
Classification.
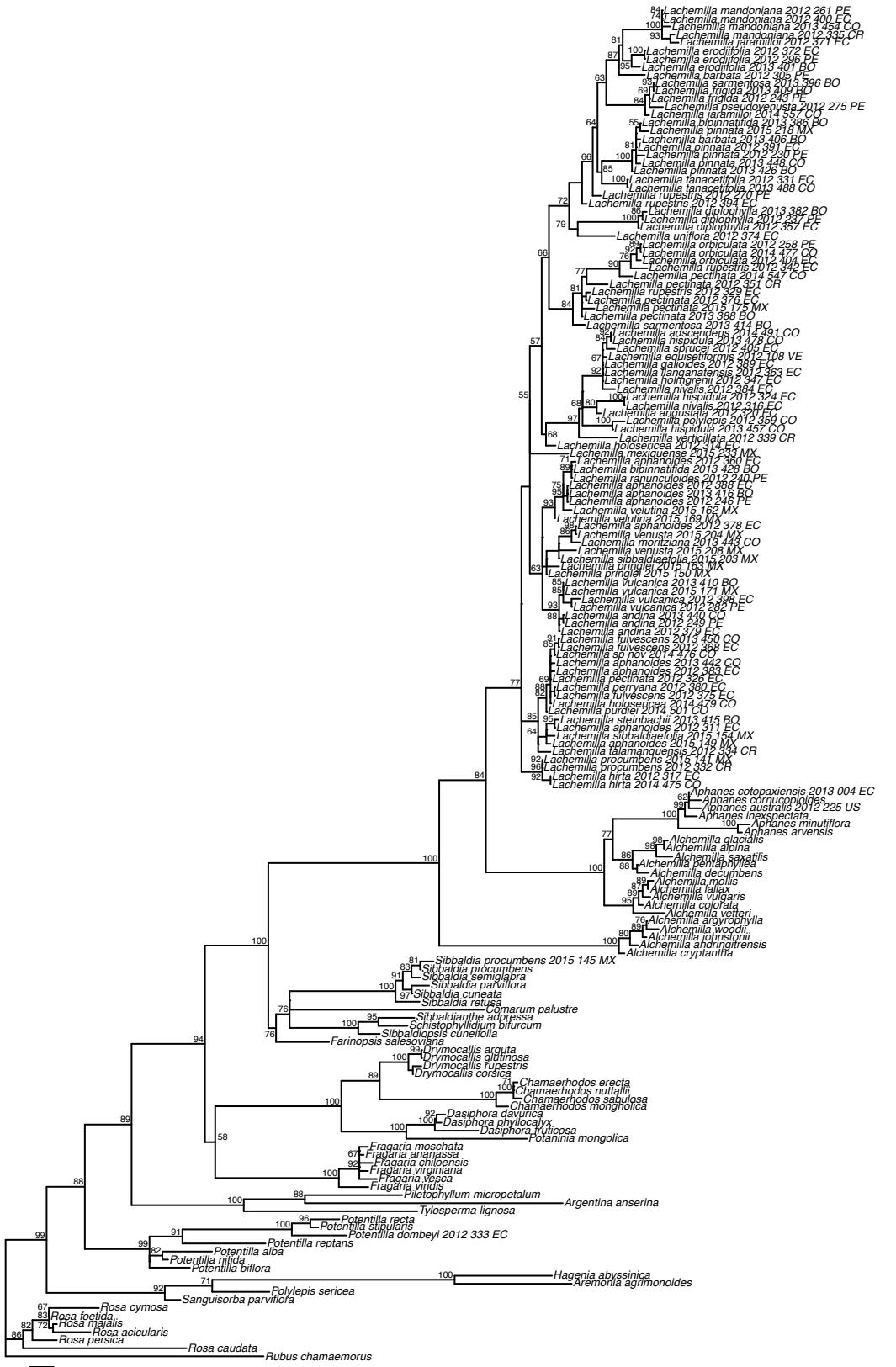

SUPPLEMENTAL FIG. S1. Bayesian 50% majority rule consensus tree of the *trnL-F* chloroplast region. Node labels represent posterior probabilities.
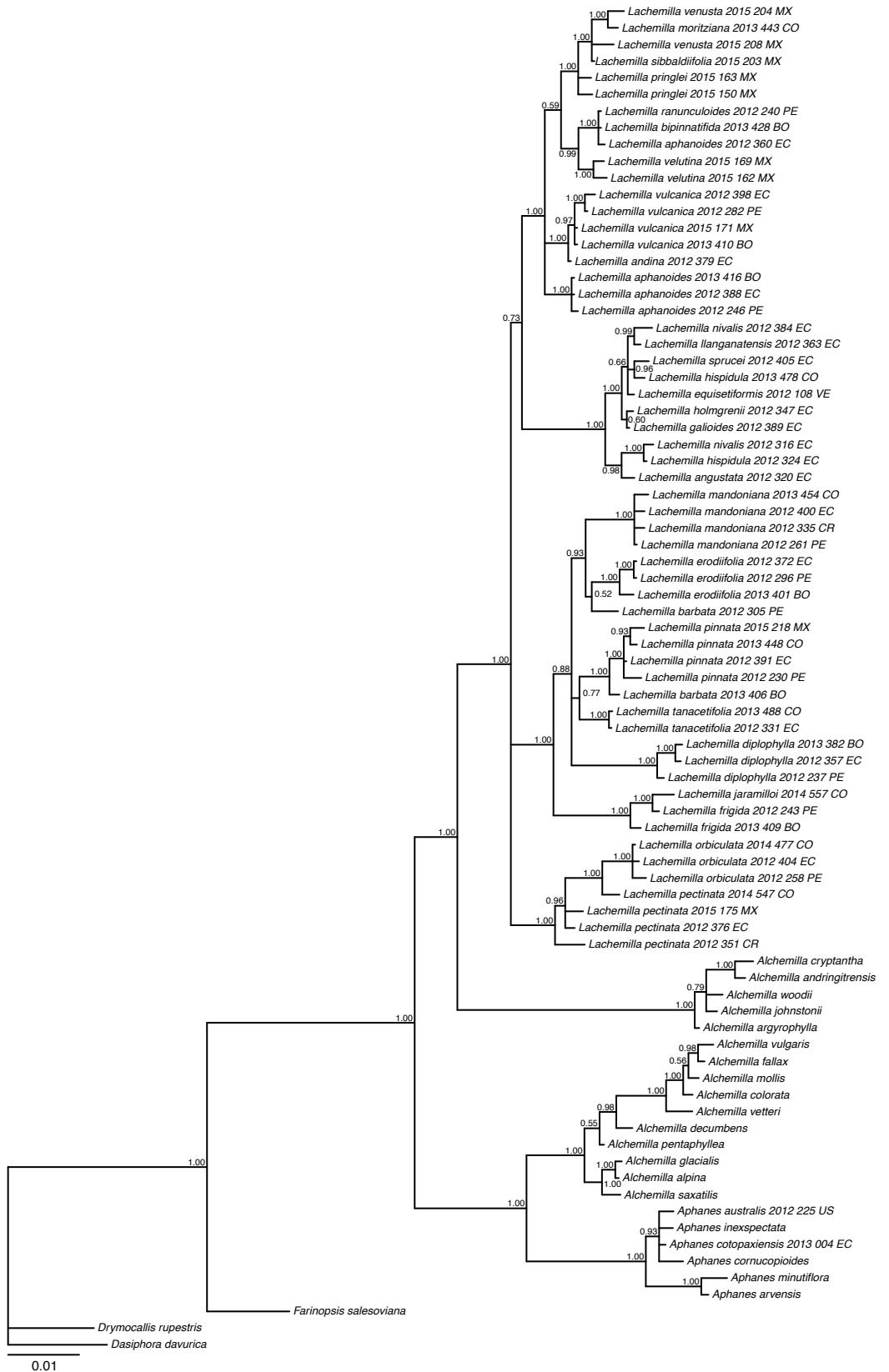
SUPPLEMENTAL FIG. S2. Maximum likelihood tree of the *trnL-F* chloroplast region. Node labels represent bootstrap support values.
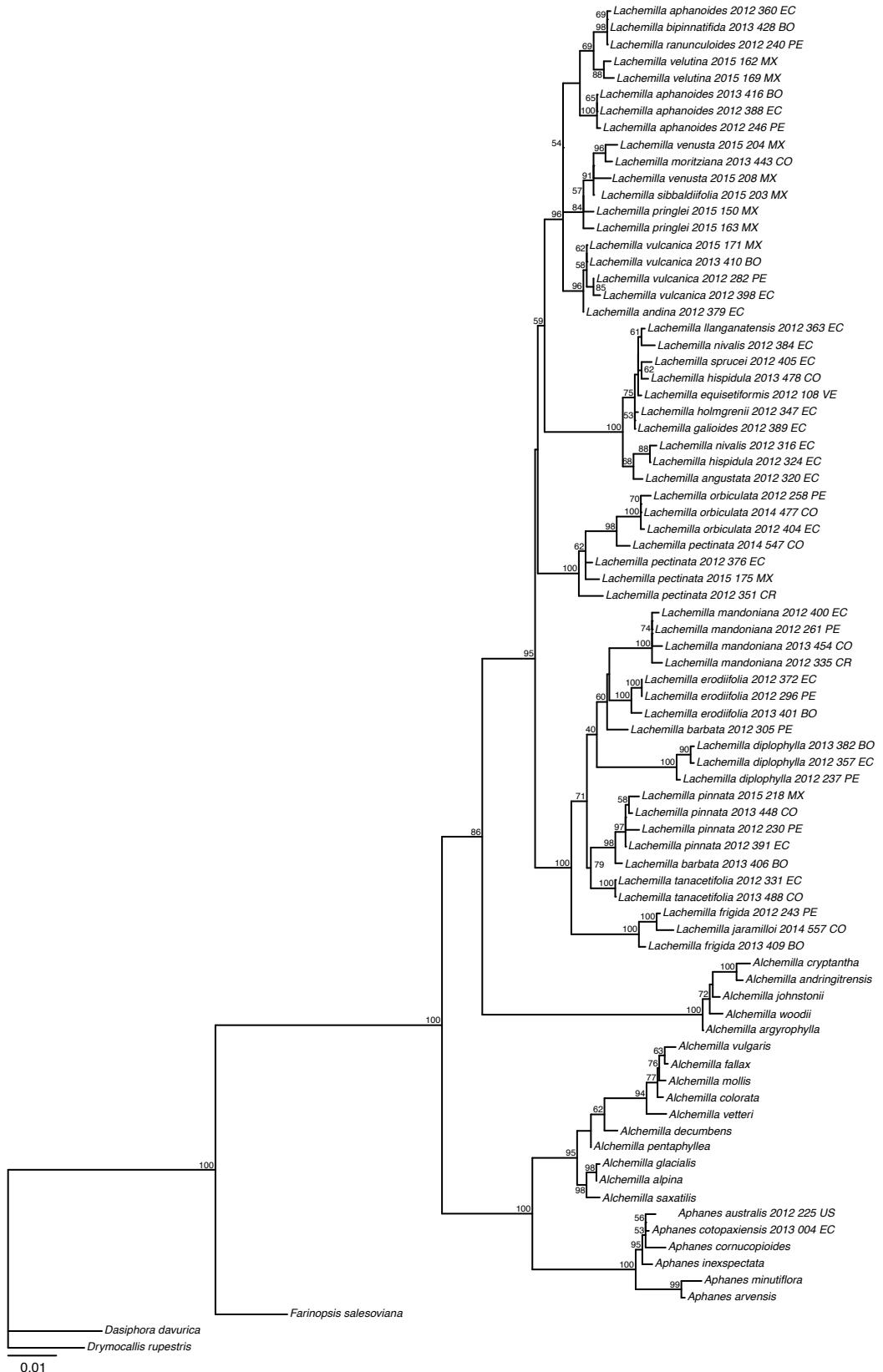
SUPPLEMENTAL FIG. S3. Bayesian 50% majority rule consensus tree of the nuclear ribosomal ITS region. Node labels represent posterior probabilities.
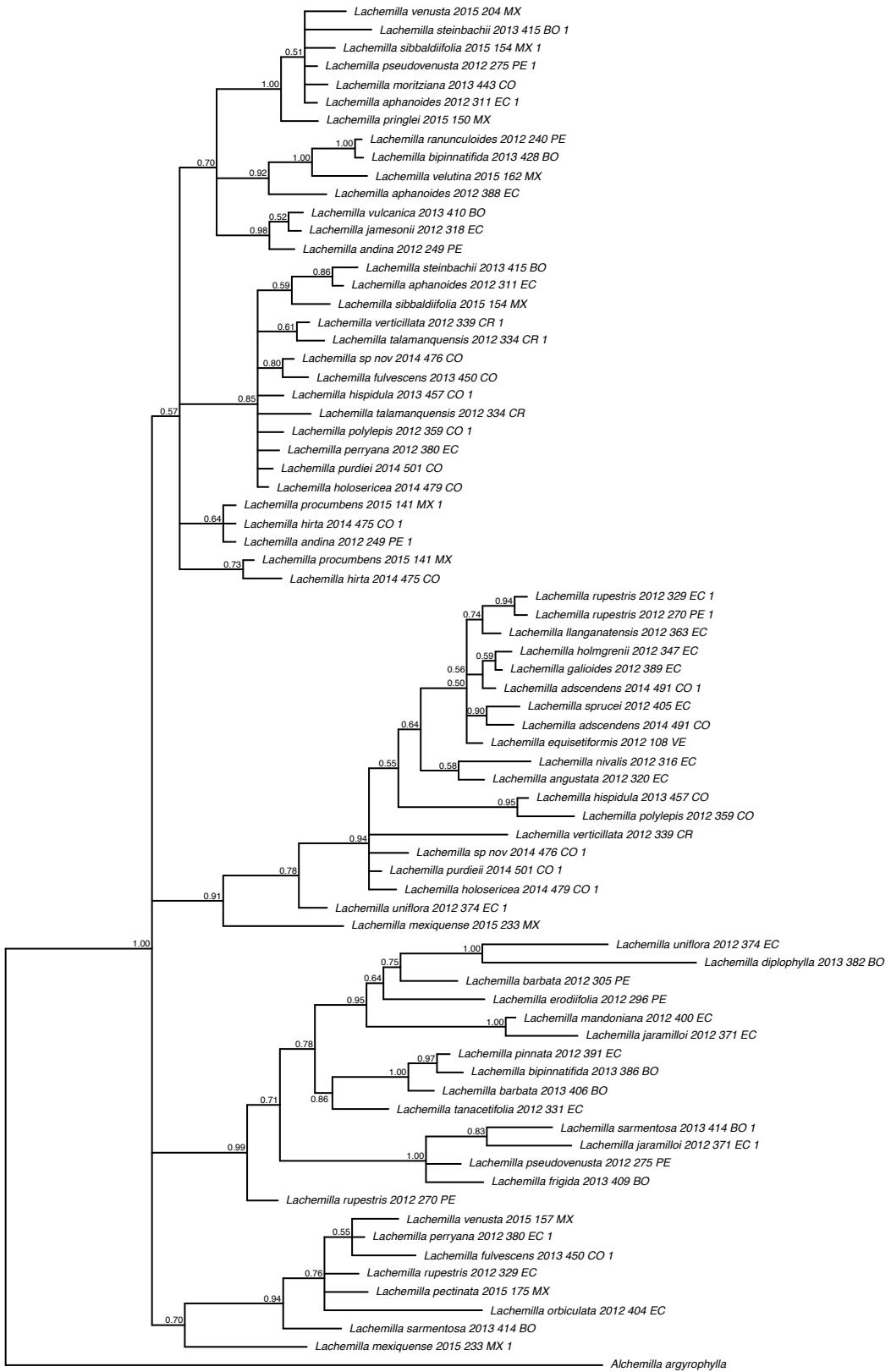
SUPPLEMENTAL FIG. S4. Maximum likelihood tree of the nuclear ribosomal ITS region. Node labels represent bootstrap support values.
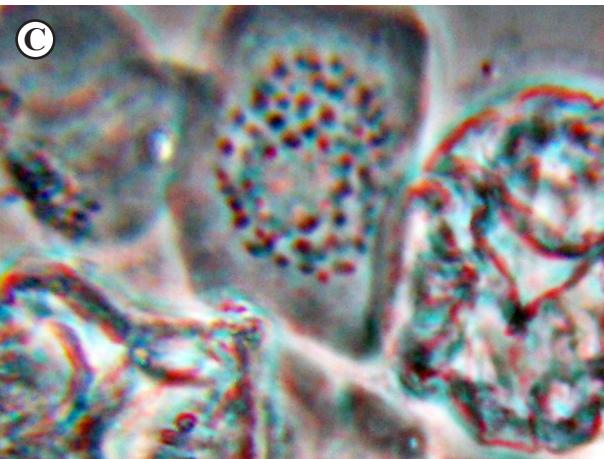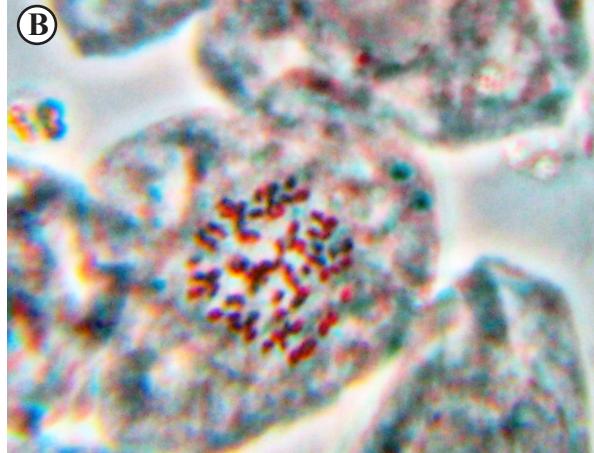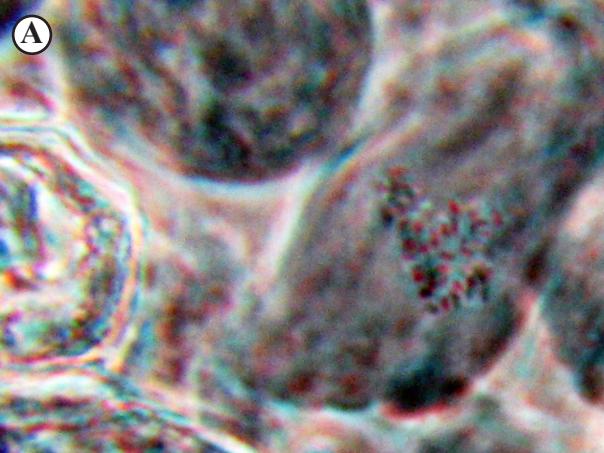
SUPPLEMENTAL FIG. S5. Bayesian 50% majority rule consensus tree of the concatenated *trnL-F* chloroplast and nuclear ribosomal ITS regions after removing outlier samples identified by PACo analyses. Node labels represent posterior probabilities.
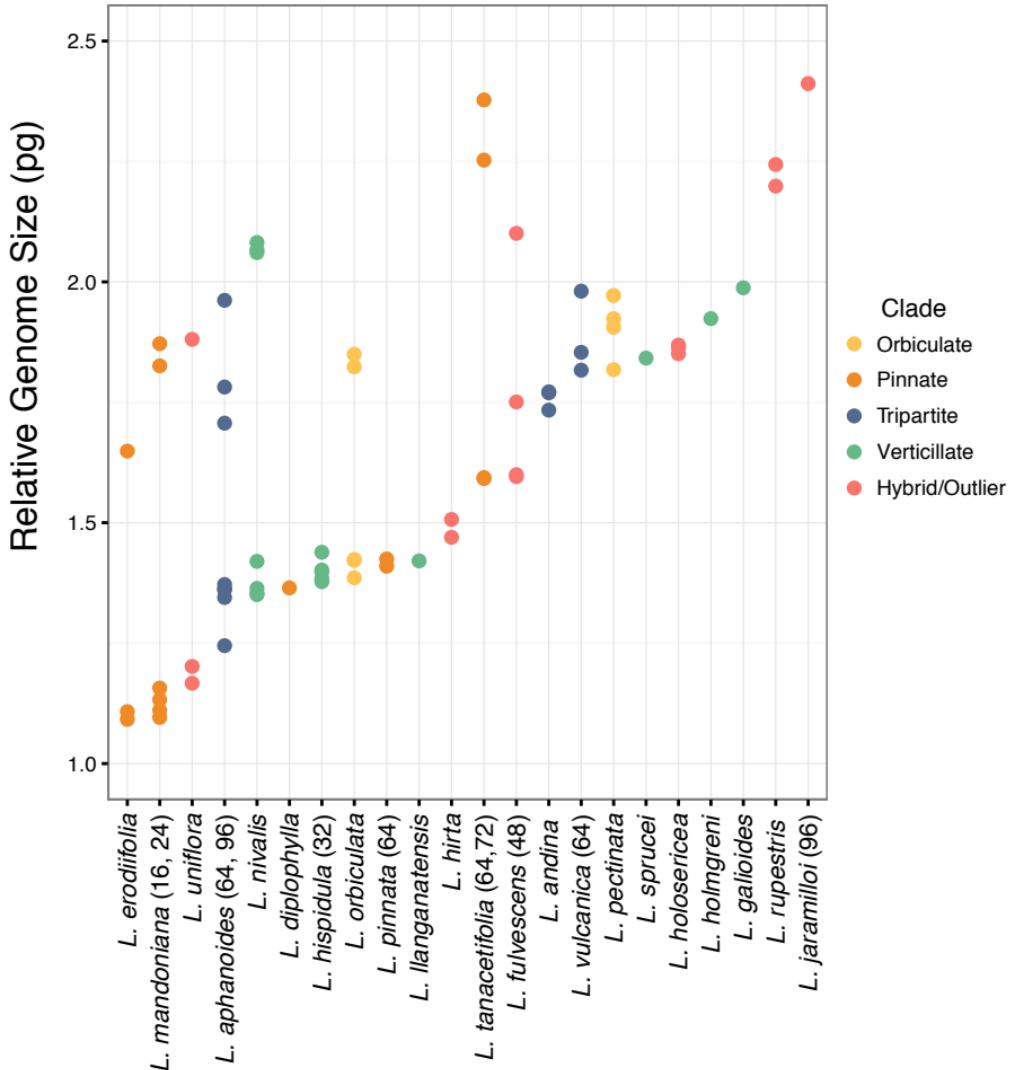
SUPPLEMENTAL FIG. S6. Maximum likelihood tree of the concatenated *trnL-F* chloroplast and nuclear ribosomal ITS regions after removing outlier samples identified by PACo analyses. Node labels represent bootstrap support values.
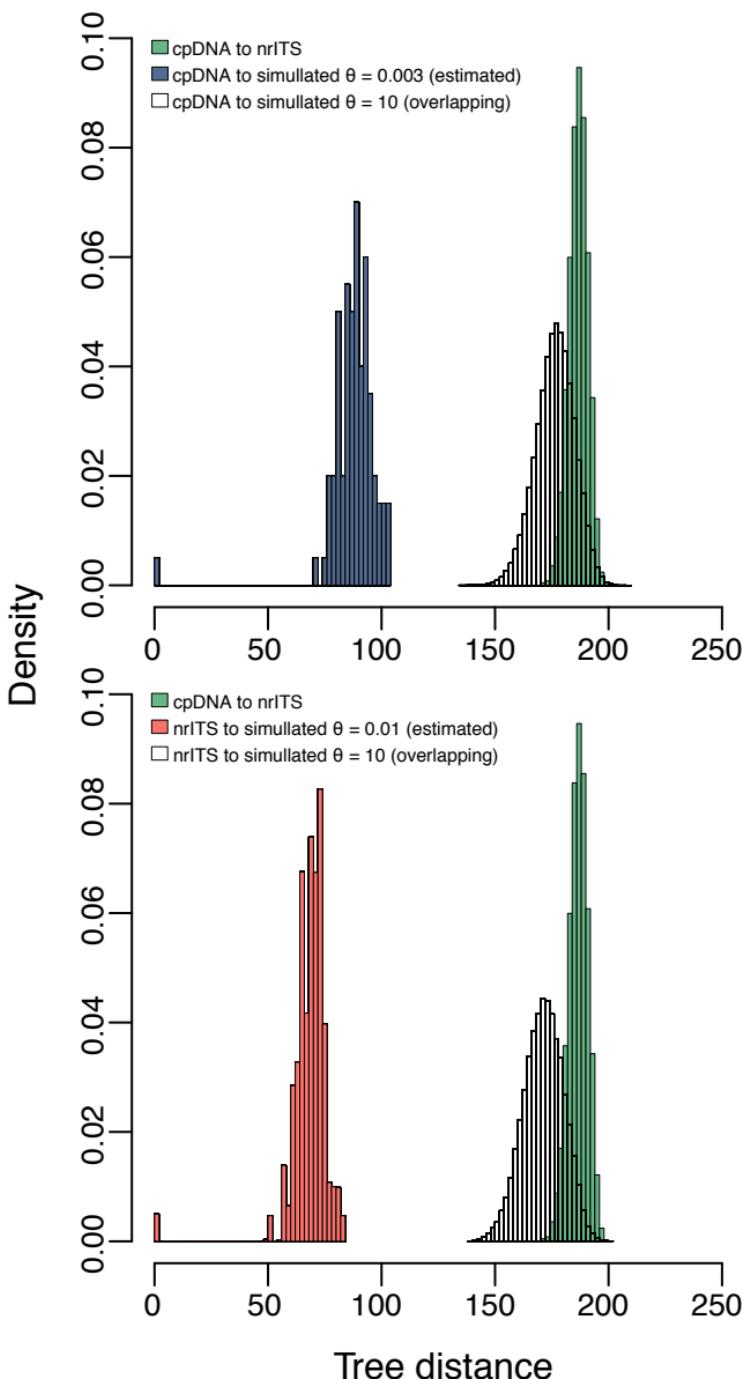
SUPPLEMENTAL FIG. S7. Bayesian 50% majority rule consensus multilabeled tree from the 'Duplicated tree' concatenated matrix of the *trnL-F* chloroplast and nuclear ribosomal ITS regions. Node labels represent posterior probabilities.

SUPPLEMENTAL FIG. S8. Examples of somatic metaphases in *Lachemilla*. A. *L. fulvescens* (*2n* = 48), B. *L. vulcanica* (*2n* = 64), C. *L. tanacetifolia* (*2n* = 72), D. *L. jaramilloi* (*2n* = 96).
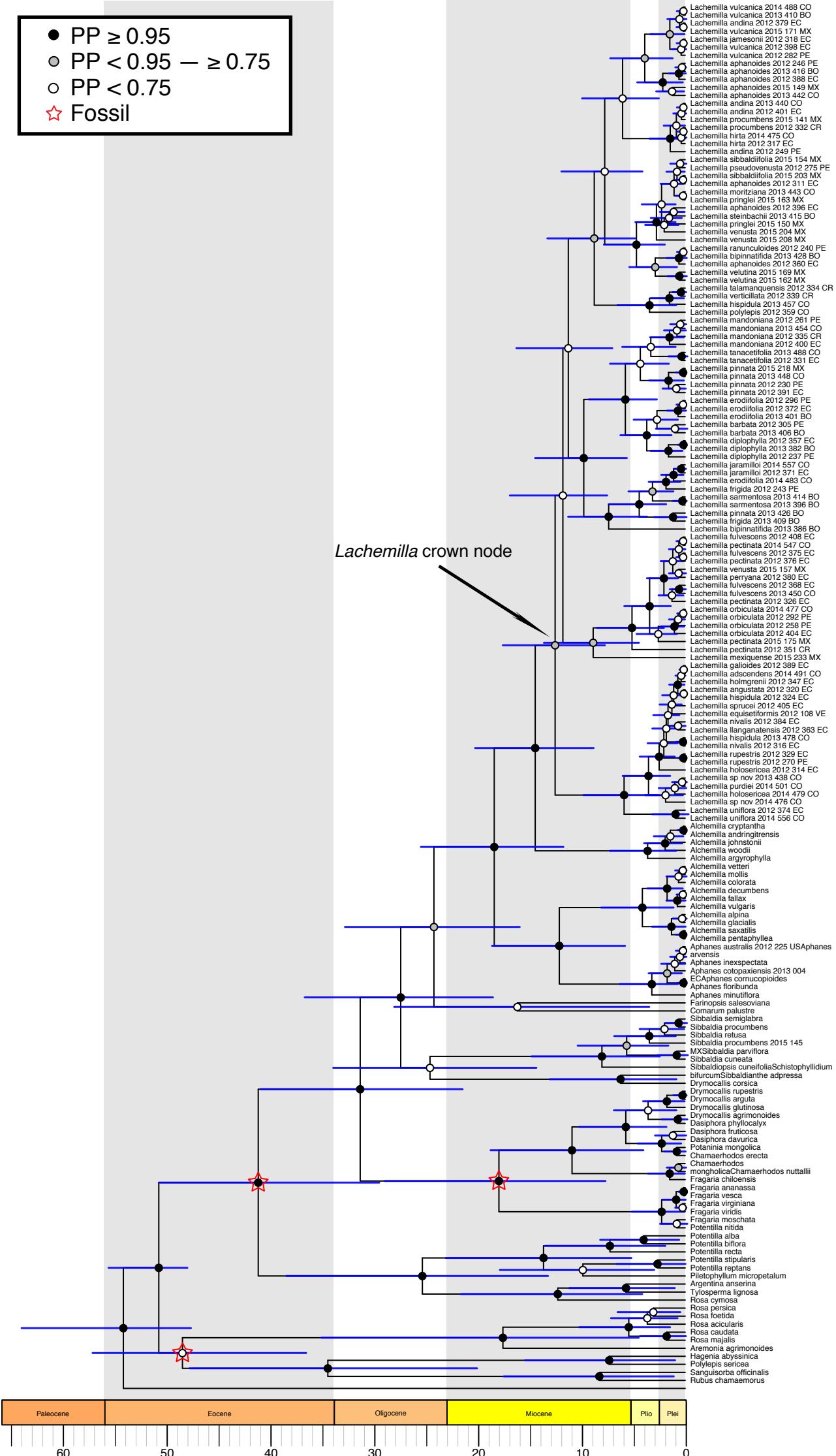
SUPPLEMENTAL FIG. S9. Relative genome sizes in various species of *Lachemilla*. Numbers next to species names are the known chromosome numbers for species with formal chromosome counts.

SUPPLEMENTAL FIG. S10. Observed and simulated tree distances. Distances simulated using cpDNA (top) and nrITS (bottom) time-calibrated trees with the estimated and overlapping θ.
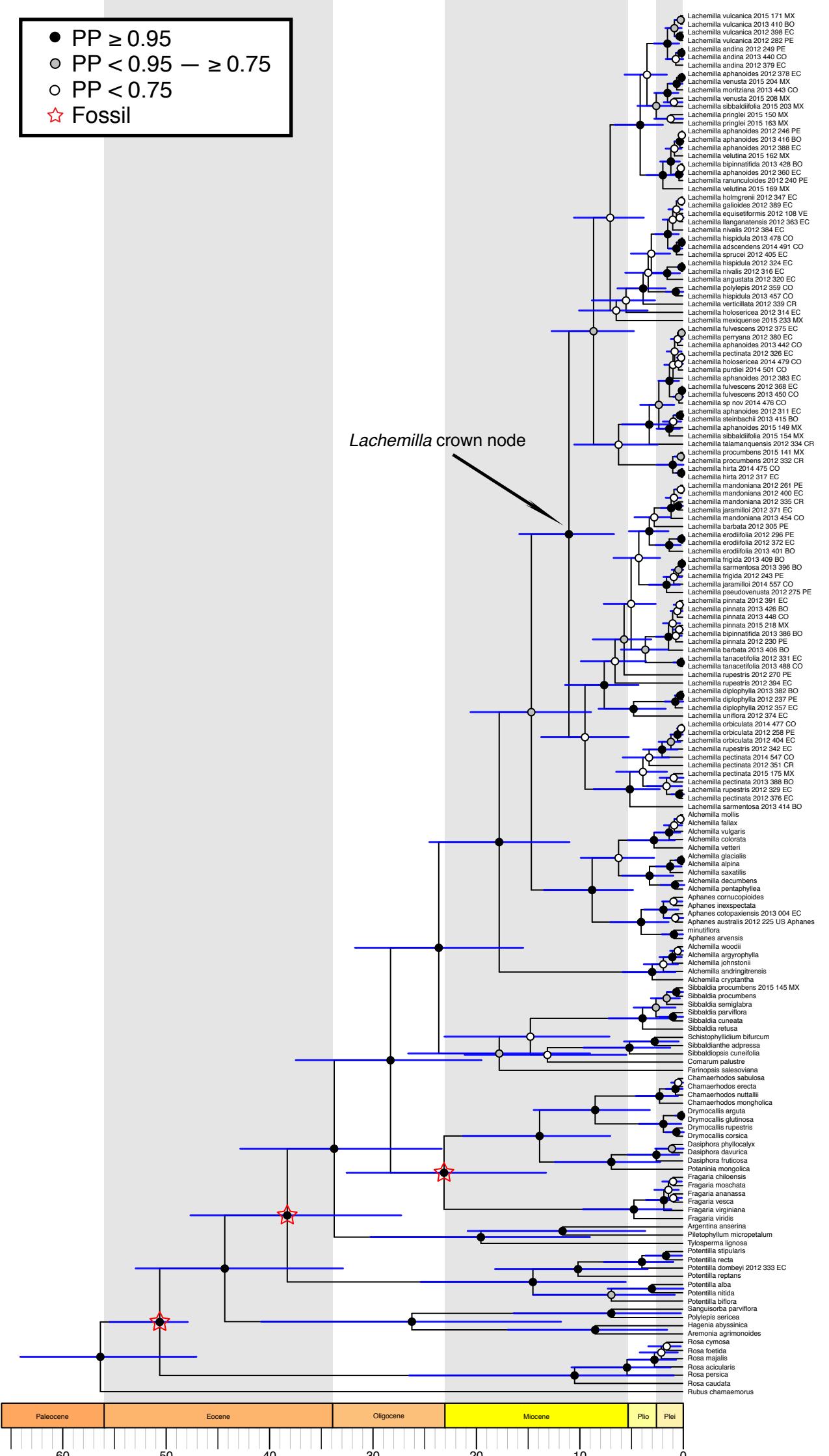
SUPPLEMENTAL FIG. S11. Maximum clade credibility chronogram of the trnL-F chloroplast region. Node labels represent median divergence time estimates, blue bars are the 95% highest posterior density (HPD) intervals and red stars denote fossil placements. Dots in the branches represent posterior probability values.

SUPPLEMENTAL FIG. S12. Maximum clade credibility chronogram of the nuclear ribosomal ITS region. Node labels represent median divergence time estimates, bars are the 95% highest posterior density (HPD) intervals and red stars denote fossil placements. Dots in the branches represent posterior probability values.