SUPPLEMENTAL

FIGURE S1. Majority-rule (50%) consensus tree derived from the BI combined analysis of nuclear (ITS) and plastid (*psbA-trnH*, *trnL-F*) DNA. Posterior Probabilities (PP) support values beside the branches. New species in bolt.

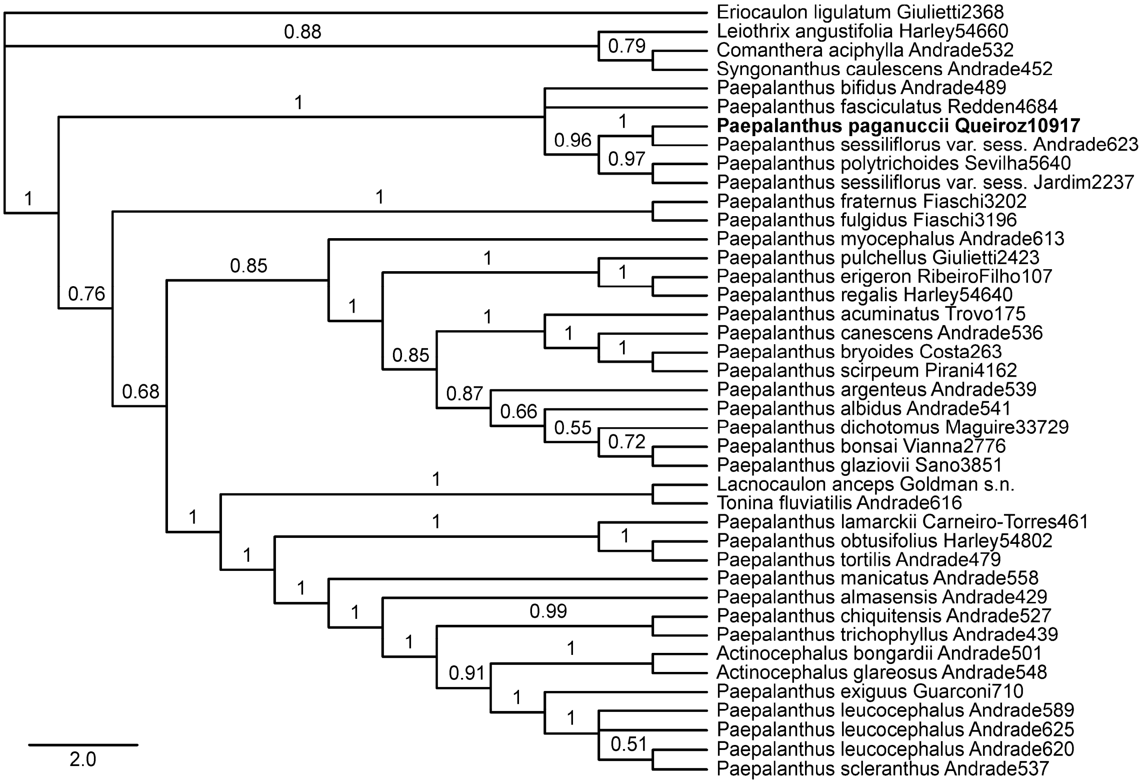

FIGURE S2. Majority-rule (50%) consensus tree from MP combined analysis of nuclear (ITS) and plastid (*psbA-trnH*, *trnL-F*) DNA. Bootstrap (BS) support values beside the branches. New species in bolt.

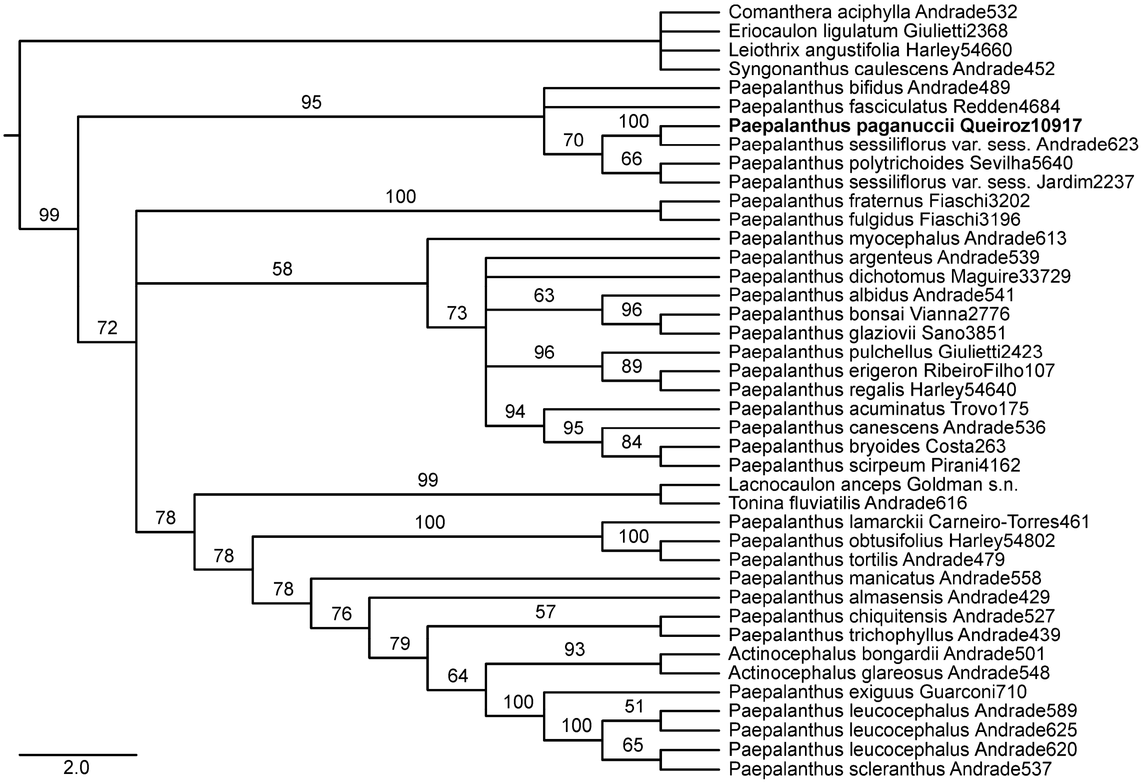

FIGURE S3. ML tree from combined analysis of nuclear (ITS) and plastid (*psbA-trnH*, *trnL-F*) DNA. Bootstrap (BS) support values beside the branches. New species in bolt.

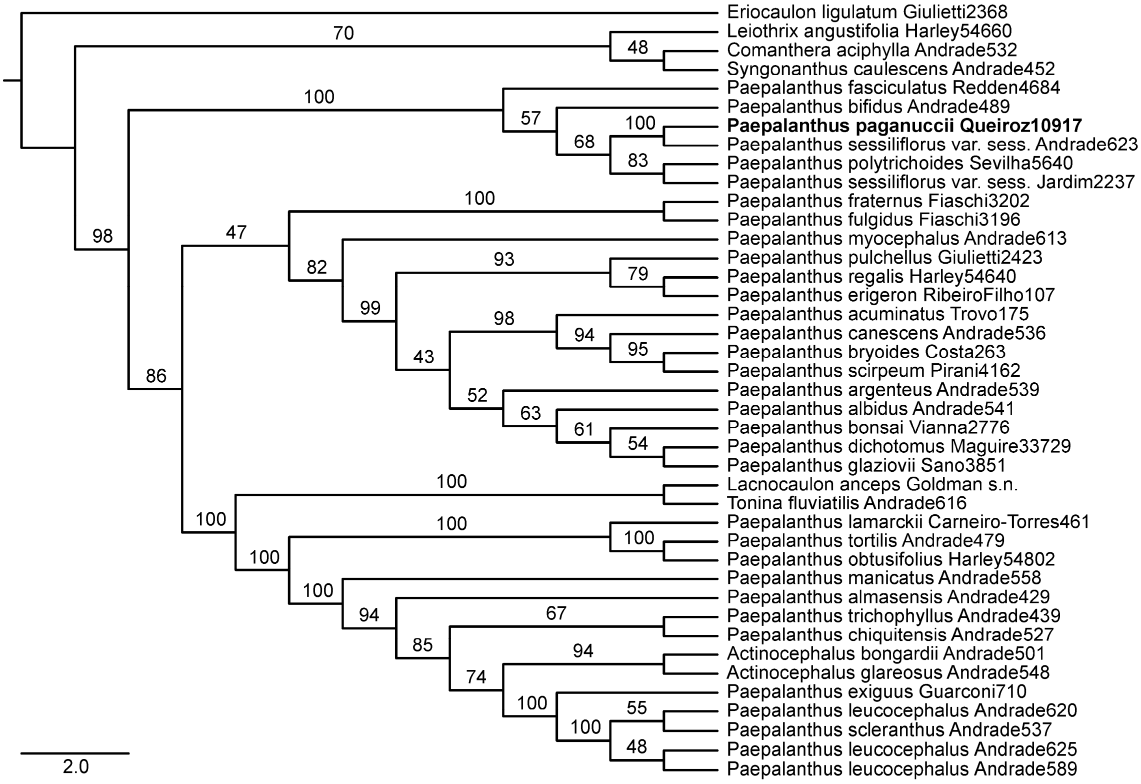

FIGURE S4. Majority-rule (50%) consensus tree derived from the BI analysis of ITS. Posterior Probabilities (PP) support values beside the branches. New species in bolt.

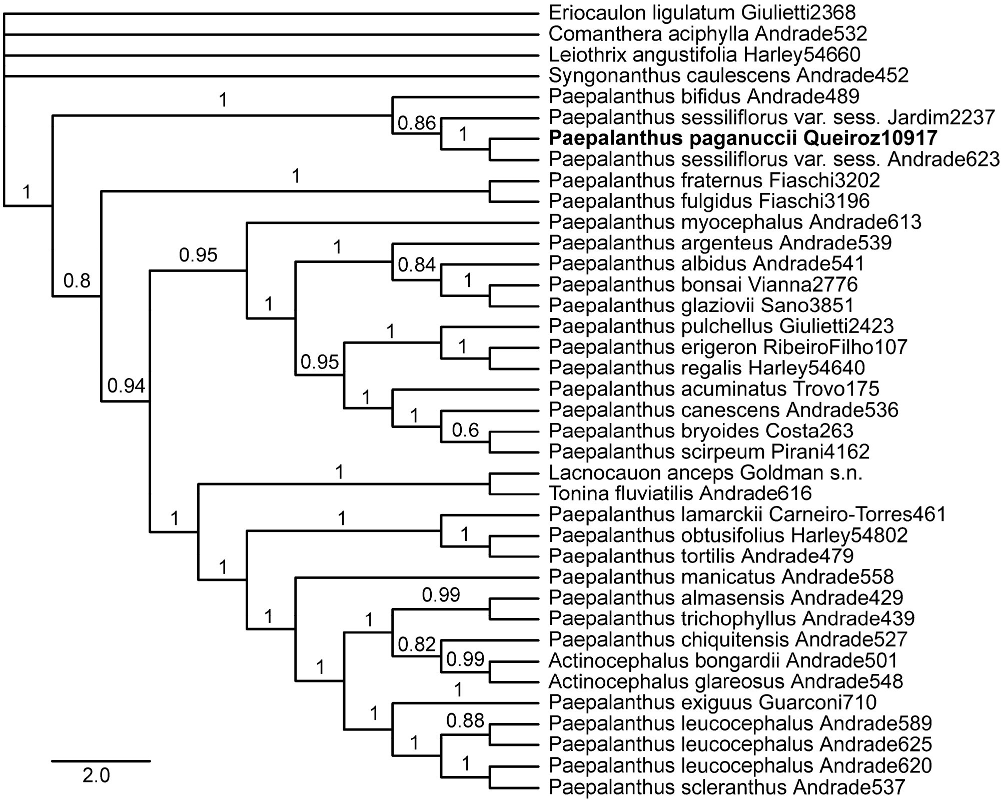

FIGURE S5. Majority-rule (50%) consensus tree from MP analysis of ITS. Bootstrap (BS) support values beside the branches. New species in bolt.

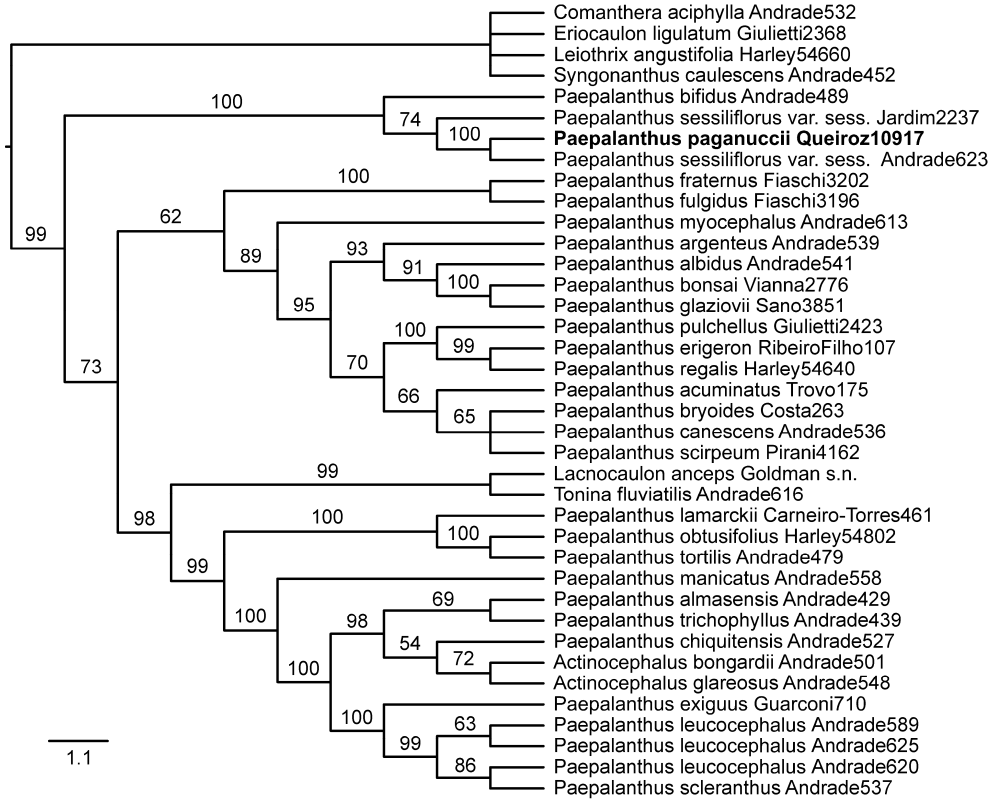

FIGURE S6. ML tree from analysis of ITS. Bootstrap (BS) support values beside the branches. New species in bolt.

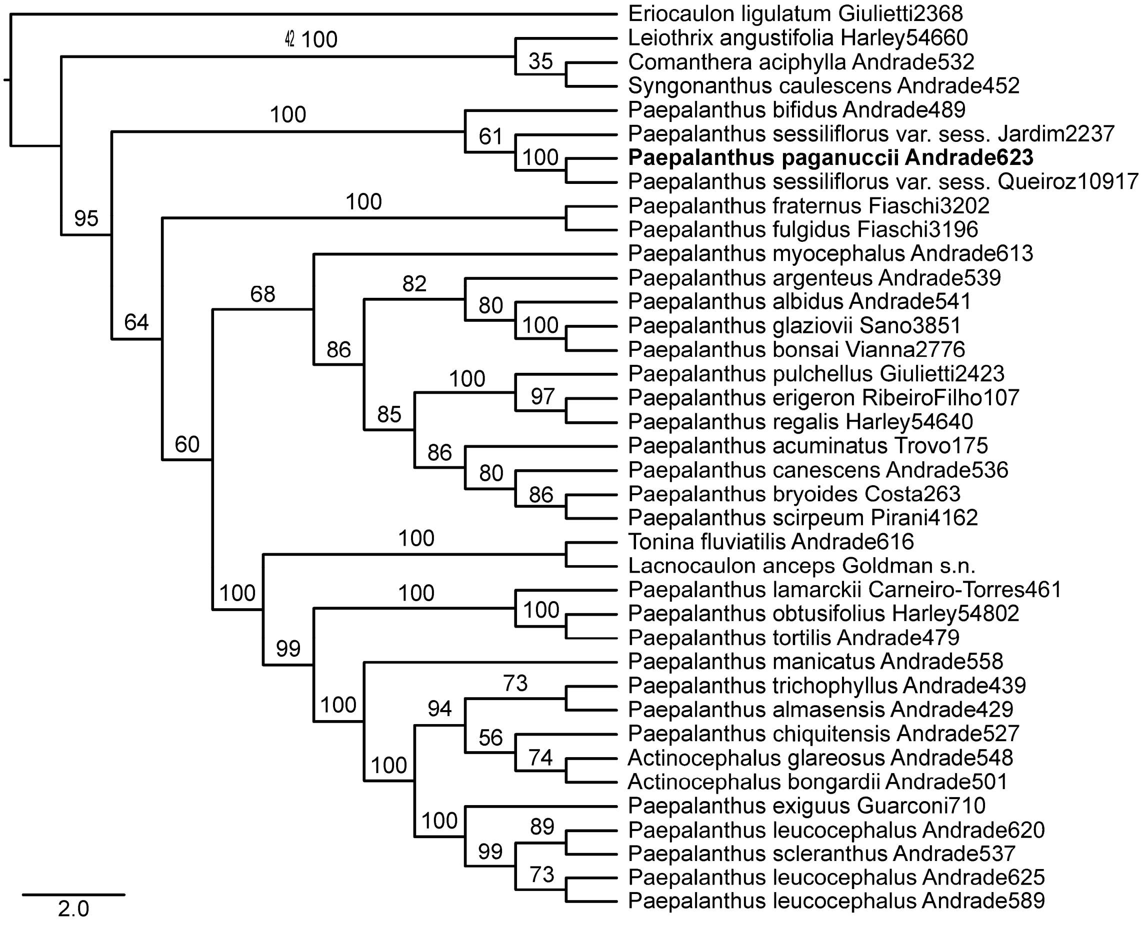

FIGURE S7. Majority-rule (50%) consensus tree derived from the BI analysis of *psbA-trnH* and *trnL-F*. Posterior Probabilities (PP) support values beside the branches. New species in bolt.

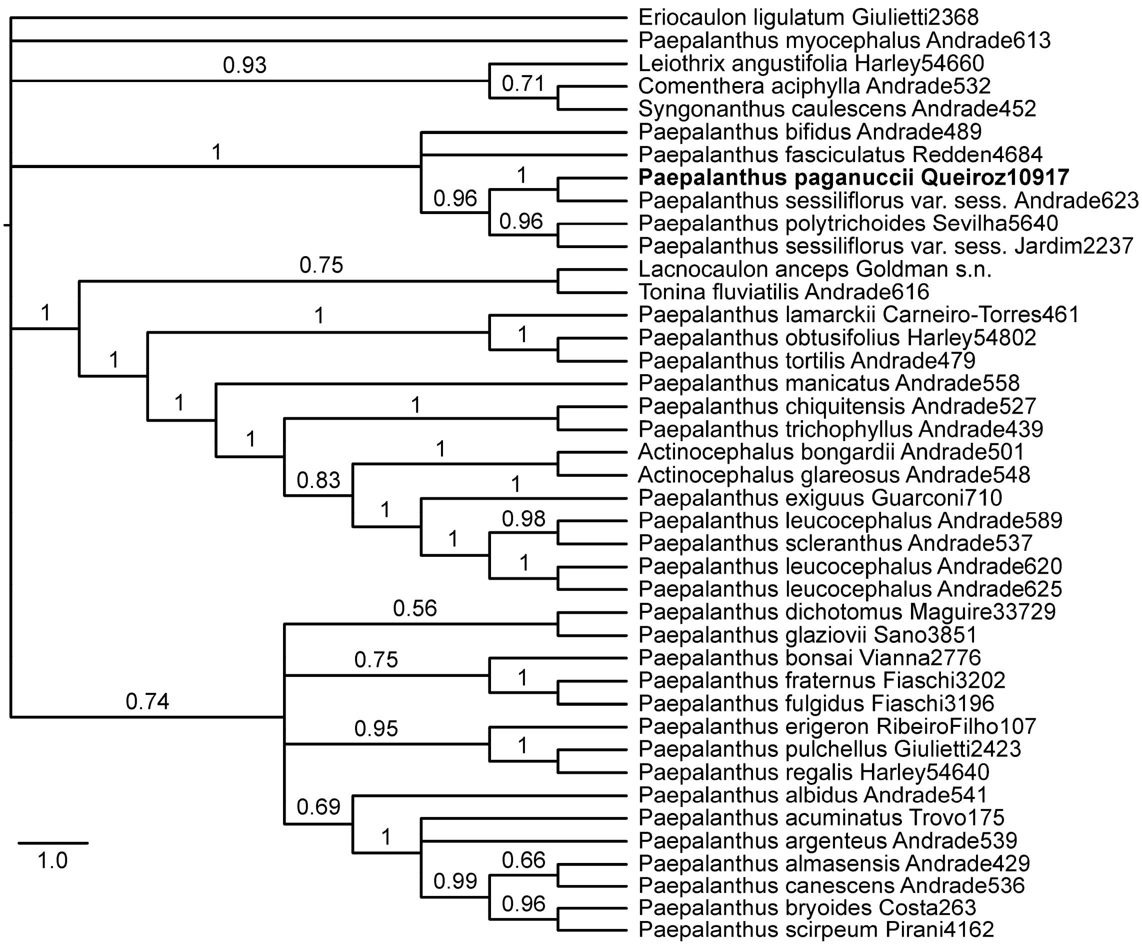

FIGURE S8. Majority-rule (50%) consensus tree from MP analysis of *psbA-trnH* and *trnL-F*. Bootstrap (BS) support values beside the branches. New species in bolt.

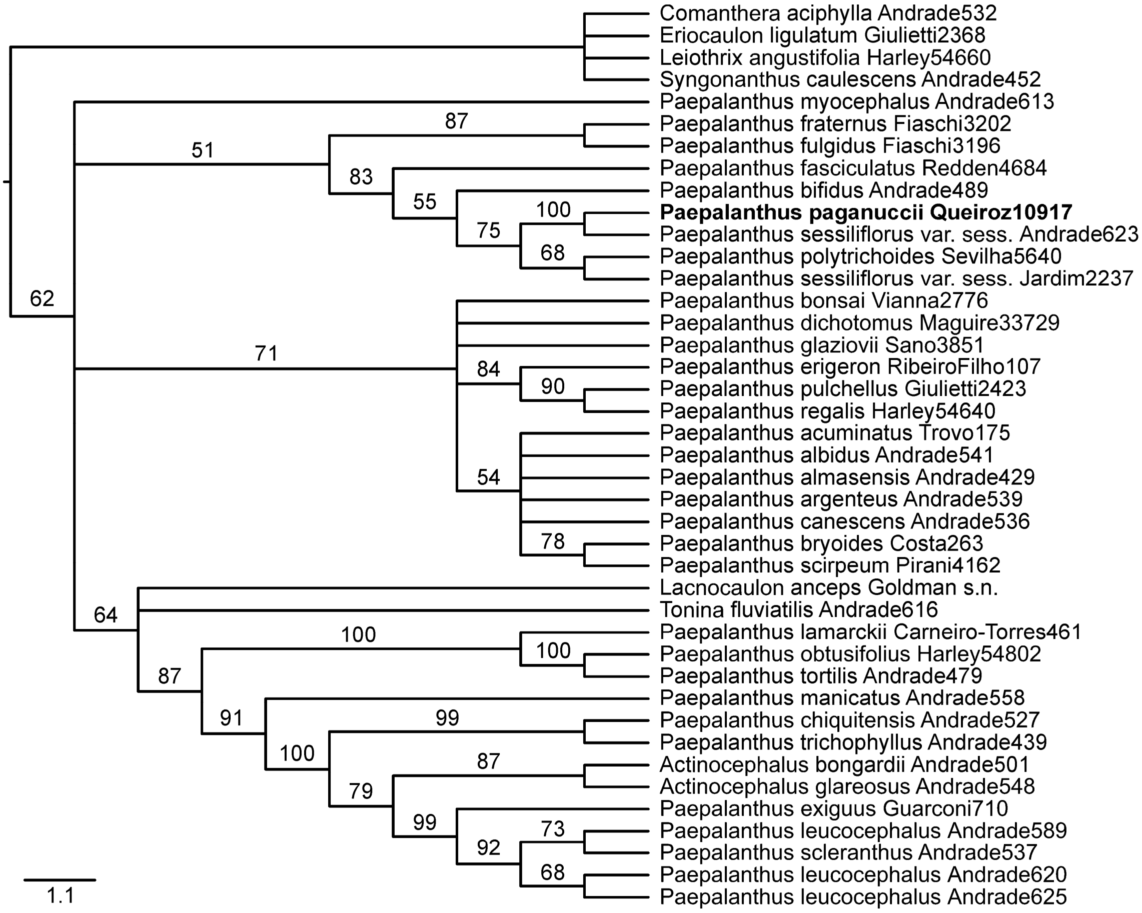

FIGURE S9. ML tree from analysis of *psbA-trnH* and *trnL-F*. Bootstrap (BS) support values beside the branches. New species in bolt.

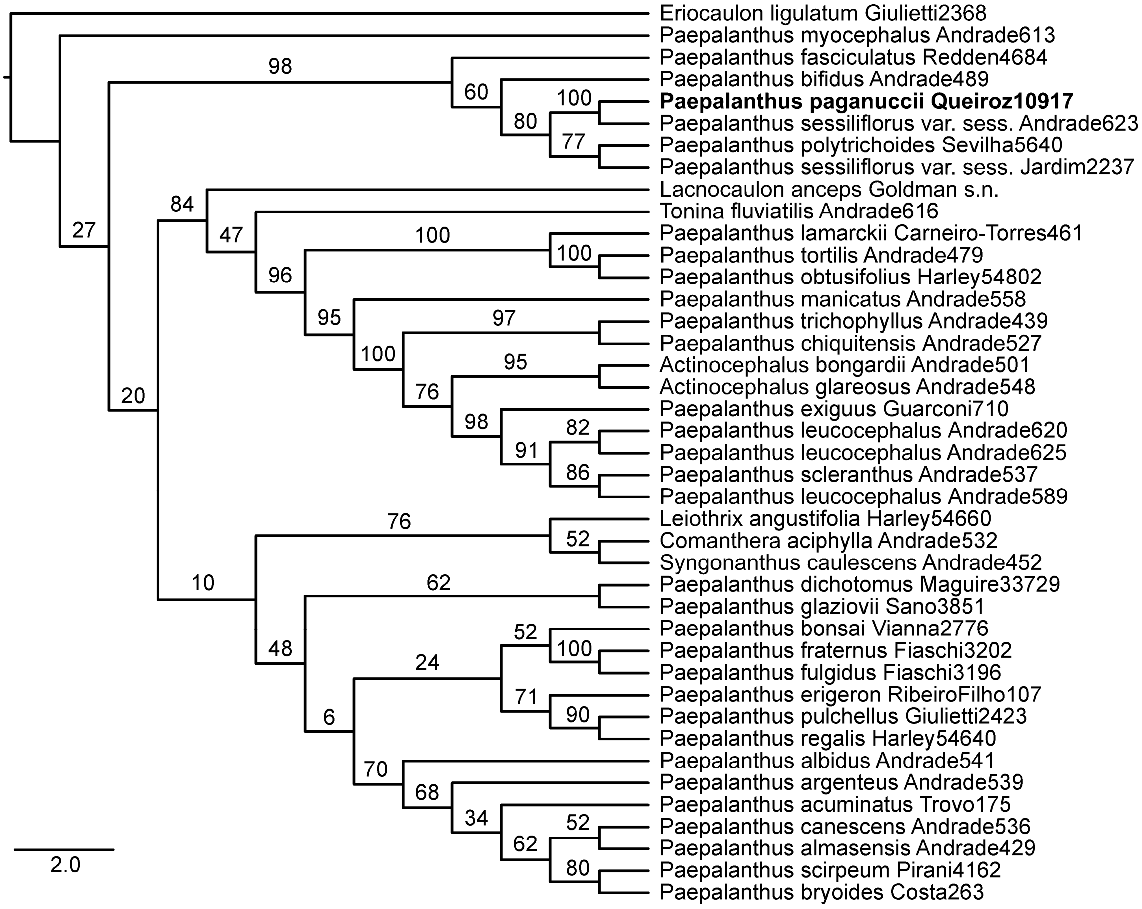

FIGURE S10. Result of ancestral character reconstruction for scape, over the 50% majority-rule consensus tree from IB. Circles indicate the frequency of states. New species in bolt.