SUPPLEMENTAL Figure 1. Bayesian consensus tree from the analysis of nDNA dataset (first intron of CHS and partial flanking coding regions) of Anthurium. Due to the lack of nDNA sequences for outgroups, the tree was rooted with the earliest diverging lineage within Anthurium (A. flexile – A. clidemioides), as suggested by analyses of cpDNA datasets. Maximum parsimony bootstrap values (MP), maximum likelihood bootstrap values (ML) and Bayesian posterior probabilities (PP) are shown below.
branches in that order. Bootstrap values < 50% are labeled with a dash (–). Support
categories are identified with asterisks above branches, (***) “strongly supported” (MP
and ML > 90%, and PP > 0.95), (**) “highly supported” (one bootstrap value 70–89%,
other bootstrap value > 90%, and PP > 0.95), and (*) “moderately supported” (MP and/or
ML between 70–89% and PP > 0.95). Major clades are identified inside the tree (Clades
A–B) or with bars outside the tree (Clades 1–16).
**SUPPLEMENTAL FIGURE 2.** Bayesian consensus tree from the analysis of the combined cpDNA dataset (*trnG* intron, *trnH*-psbA and *trnC*-ycf6 intergenic spacers) of *Anthurium* and closely related outgroups. Maximum parsimony bootstrap values (MP), maximum likelihood bootstrap values (ML) and Bayesian posterior probabilities (PP) are shown below branches in that order. Bootstrap values < 50% are labeled with a dash (–).
Support categories are identified with asterisks above branches, (***) “strongly supported” (MP and ML > 90%, and PP > 0.95), (**) “highly supported” (one bootstrap value 70–89%, other bootstrap value > 90%, and PP > 0.95), and (*) “moderately supported” (MP and/or ML between 70–89% and PP > 0.95). Major clades are identified inside the tree (Clades A–B) or with bars outside the tree (Clades 1–16).