

Fig. S1. Parsimony ancestral character state reconstruction of the character "habit" on the 50% majority rule consensus tree produced by the Bayesian analysis of the combined ITS and plastid datasets. Circle indicate the frequencies of states on the 23,975 trees derived from the Bayesian estimate of phylogeny reconstruction.

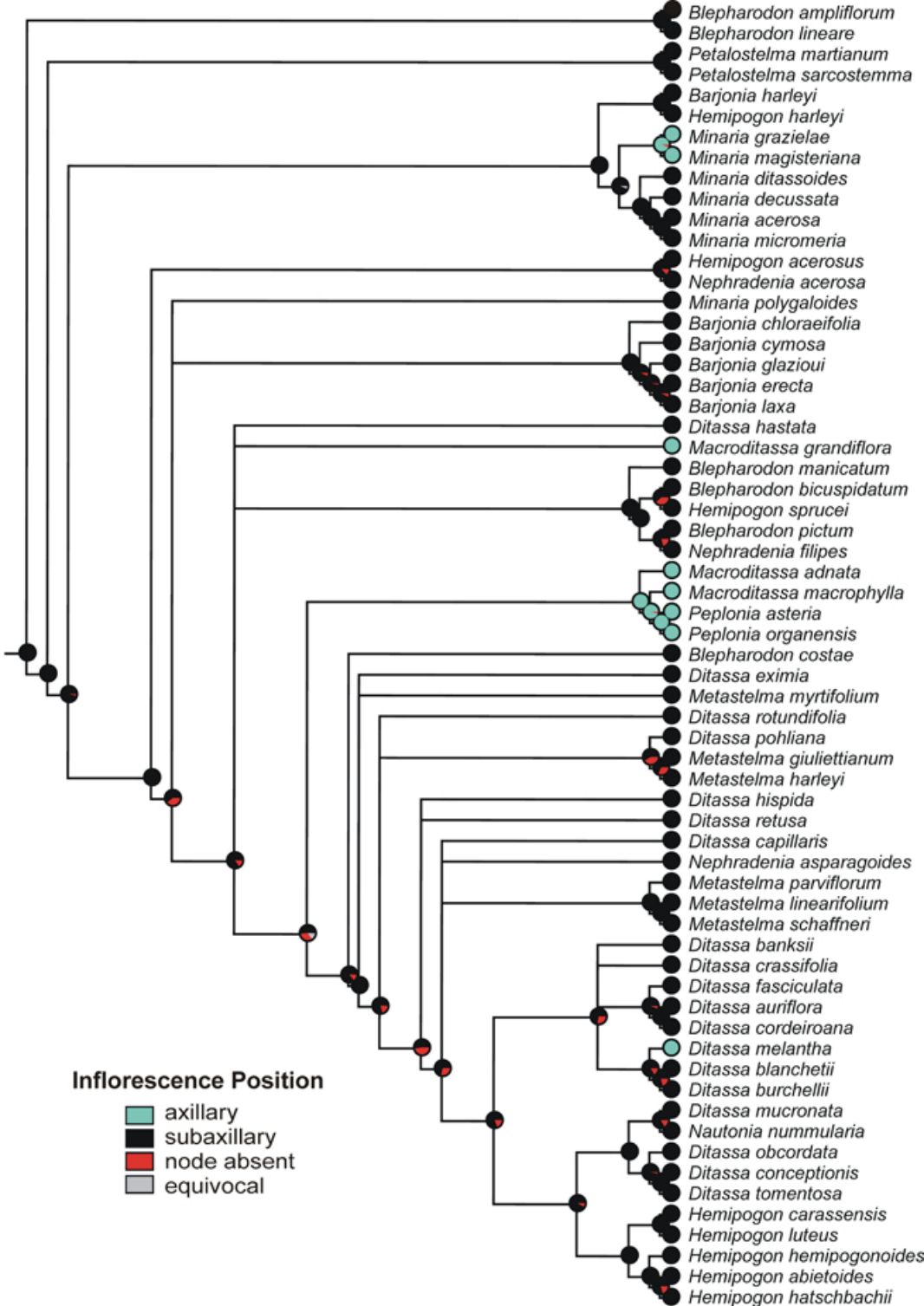


Fig. S2. Parsimony ancestral character state reconstruction of the character "inflorescence position" on the 50% majority rule consensus tree produced by the Bayesian analysis of the combined ITS and plastid datasets. Circles indicate the frequencies of states on the 23,975 trees derived from the Bayesian estimate of phylogeny reconstruction.