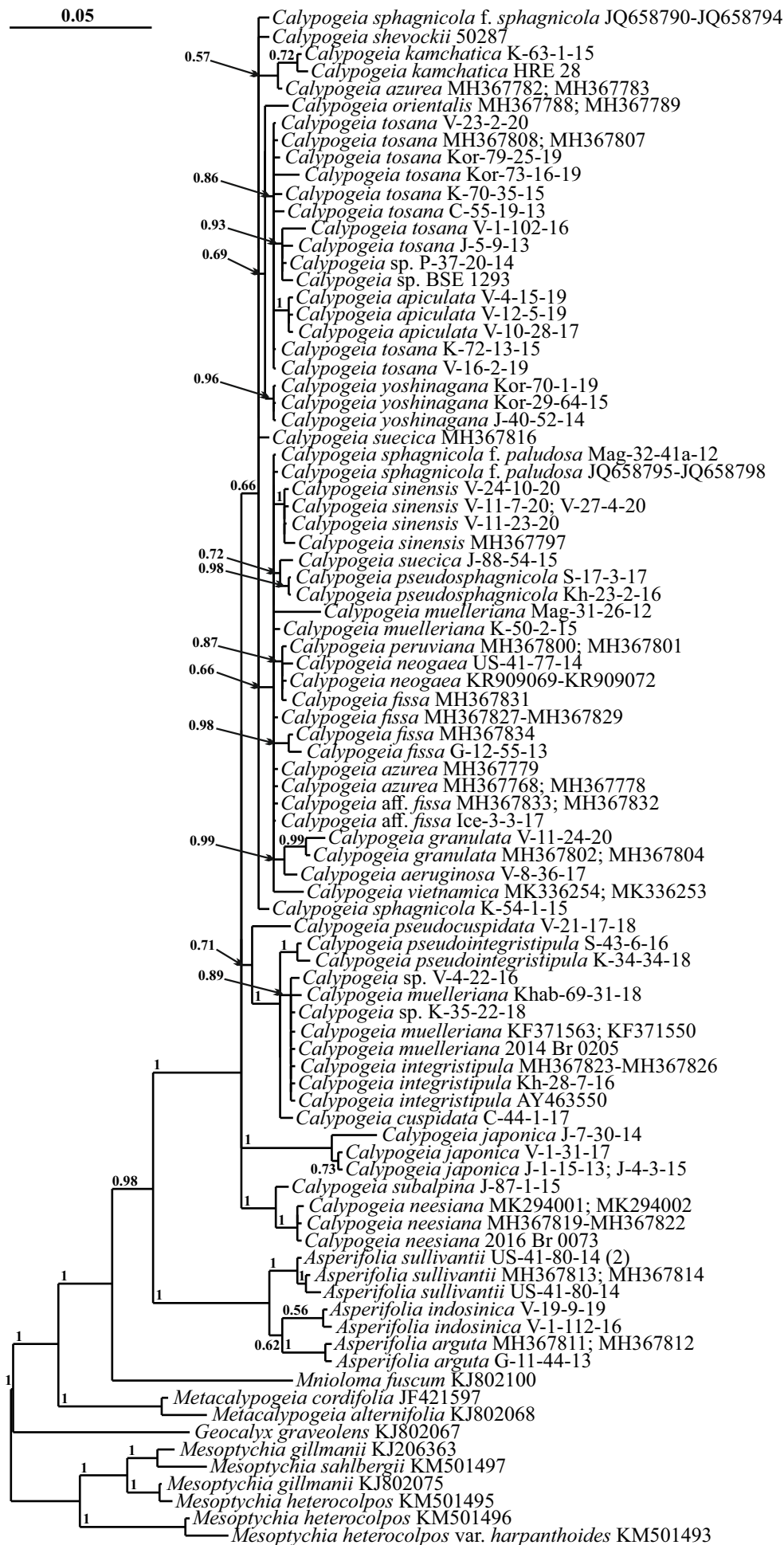
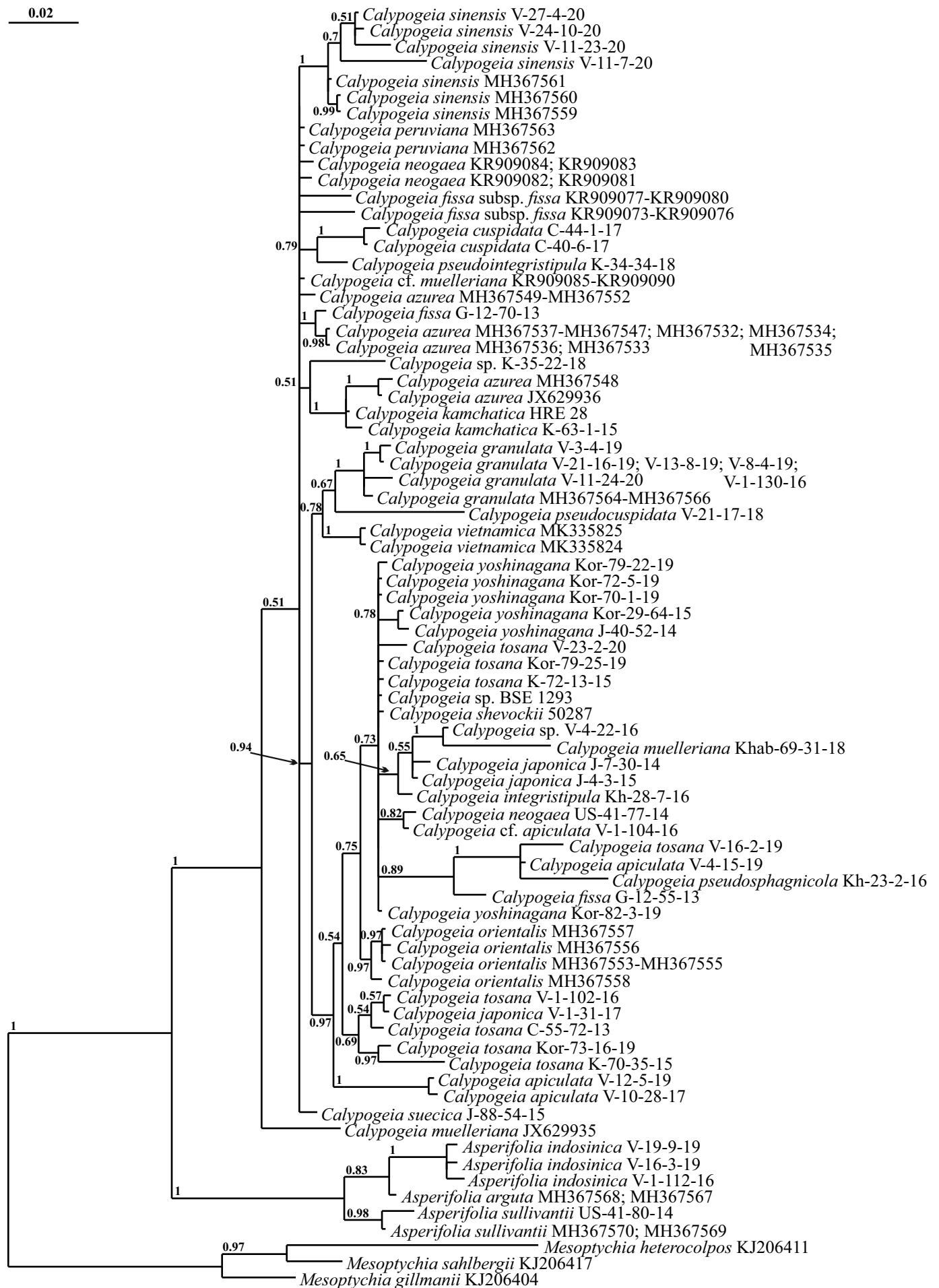


**Figure S1.** Condensed tree obtained in a Bayesian analysis for the genus *Calypogeia* and related taxa based on *trnG*-intron. The values of Bayesian posterior probabilities more than 0.50 are indicated. Scale bar corresponds to a number of nucleotide substitutions per site.



**Figure S2.** Condensed tree obtained in a Bayesian analysis for the genus *Calypogeia* and related taxa based on *trnL*–F. The values of Bayesian posterior probabilities more than 0.50 are indicated. Scale bar corresponds to a number of nucleotide substitutions per site.



**Figure S3.** Condensed tree obtained in a Bayesian analysis for the genus *Calypogeia* and related taxa based on ITS 2. The values of Bayesian posterior probabilities more than 0.50 are indicated. Scale bar corresponds to a number of nucleotide substitutions per site.