

Appendix 2. Figures S1-S7. Individual Maximum Likelihood (ML) analyses and Bootstrap support (BS) values of markers ITS1-5.8S-ITS2, 18S, and 26S of the nuclear DNA and markers *rps16*, *trnL-F*, *rbcL* and, *psaB* of the chloroplast DNA.

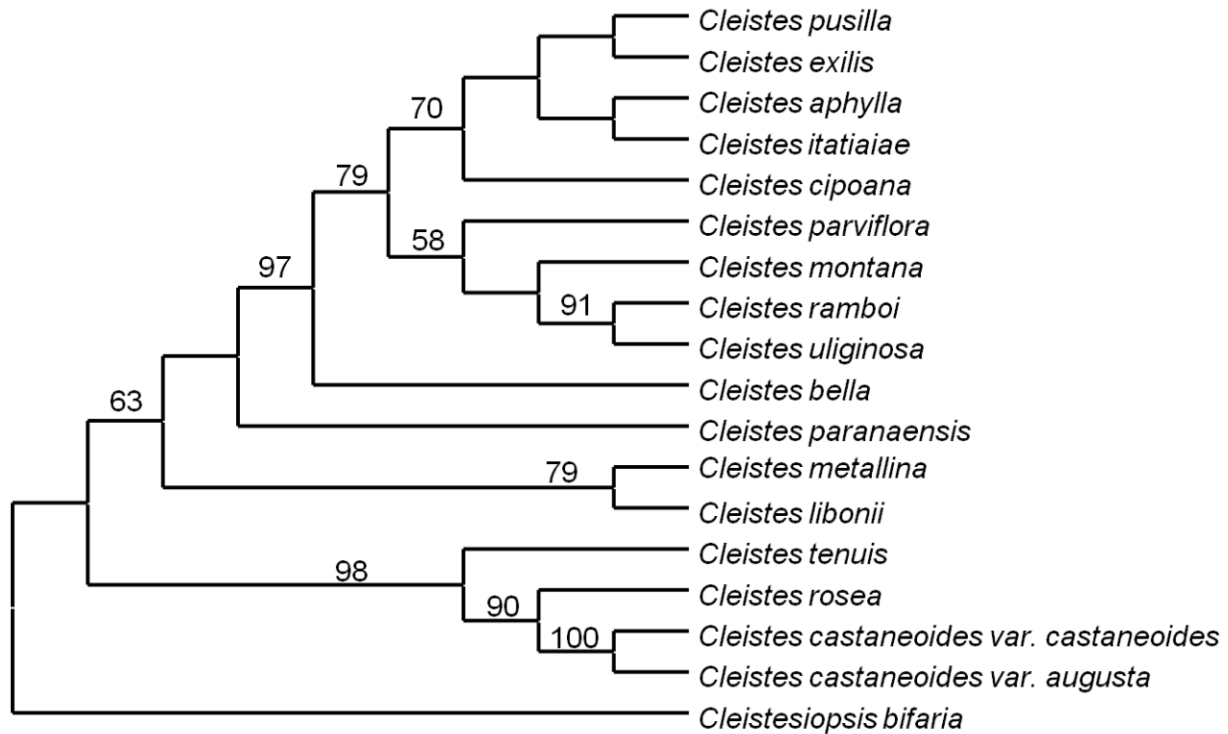


Figure S1. Bootstrap consensus tree based on the maximum likelihood analysis from 18S (nrDNA) sequences of *Cleistes* (Orchidaceae, Vanilloideae). Bootstrap values >50% are given above branches.

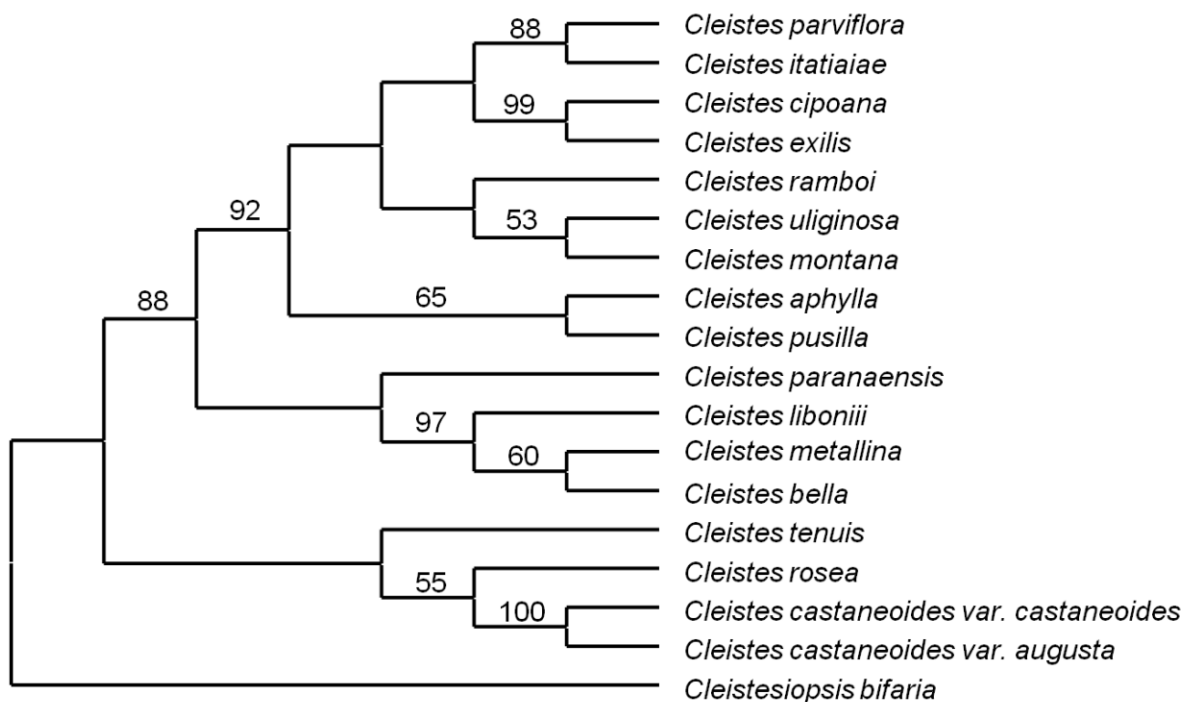


Figure S2. Bootstrap consensus tree based on the maximum likelihood analysis from 26S (nrDNA) sequences of *Cleistes* (Orchidaceae, Vanilloideae). Bootstrap values >50% are given above branches.

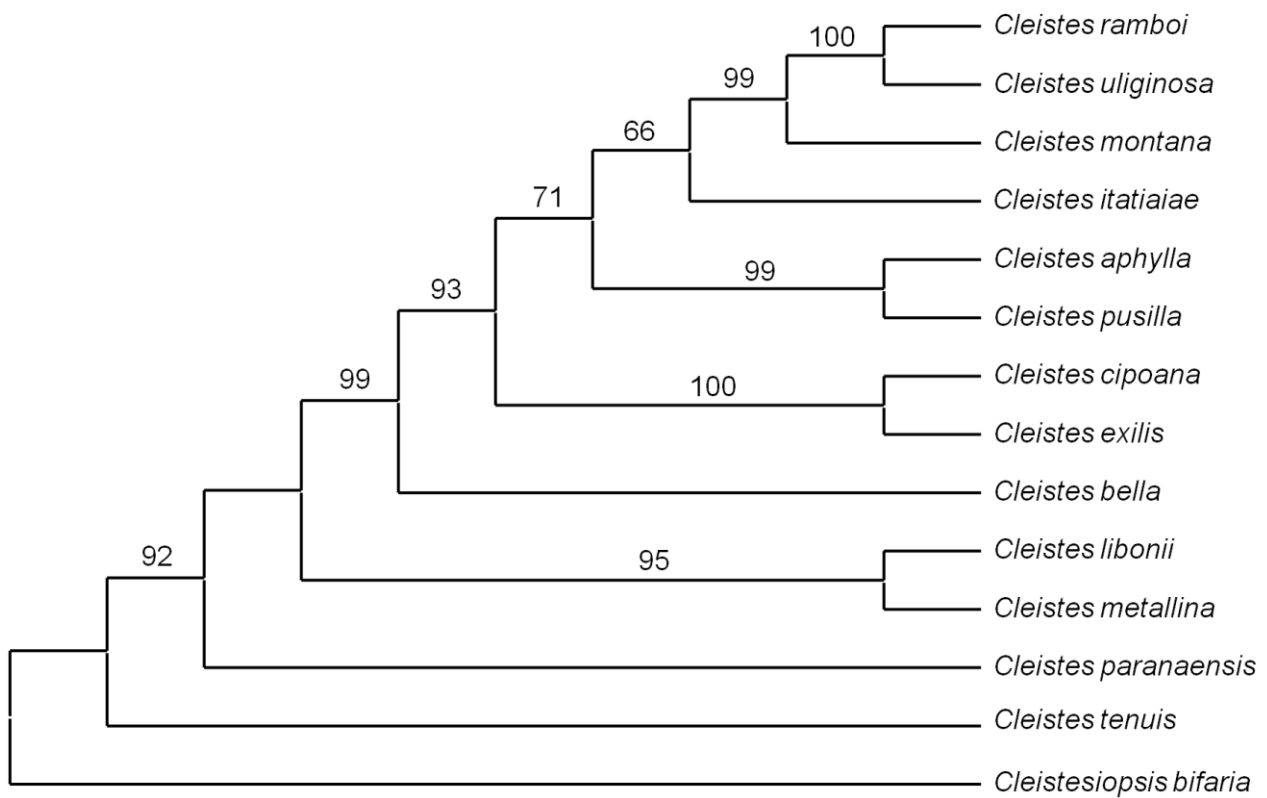


Figure S3. Bootstrap consensus tree based on the maximum likelihood analysis from ITS (nrDNA) sequences of *Cleistes* (Orchidaceae, Vanilloideae). Bootstrap values >50% are given above branches.

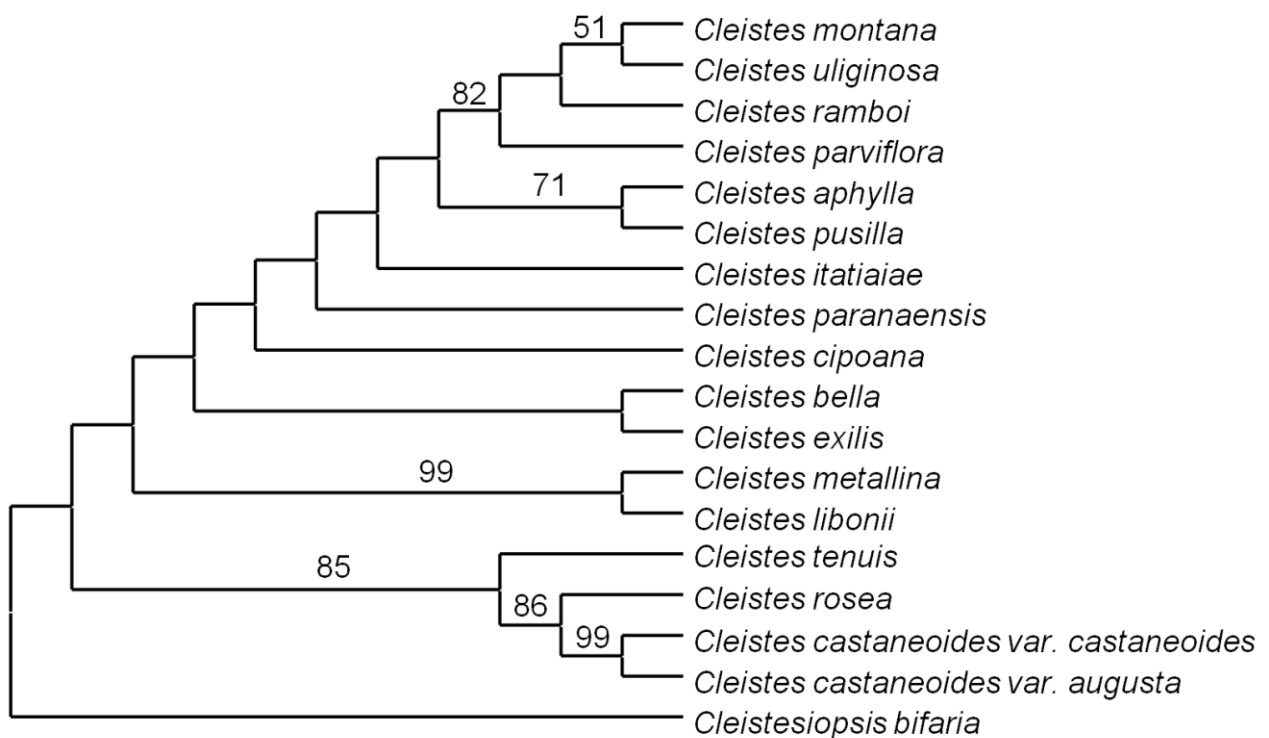


Figure S4. Bootstrap consensus tree based on the maximum likelihood analysis from *psbA* (cpDNA) sequences of *Cleistes* (Orchidaceae, Vanilloideae). Bootstrap values >50% are given above branches.

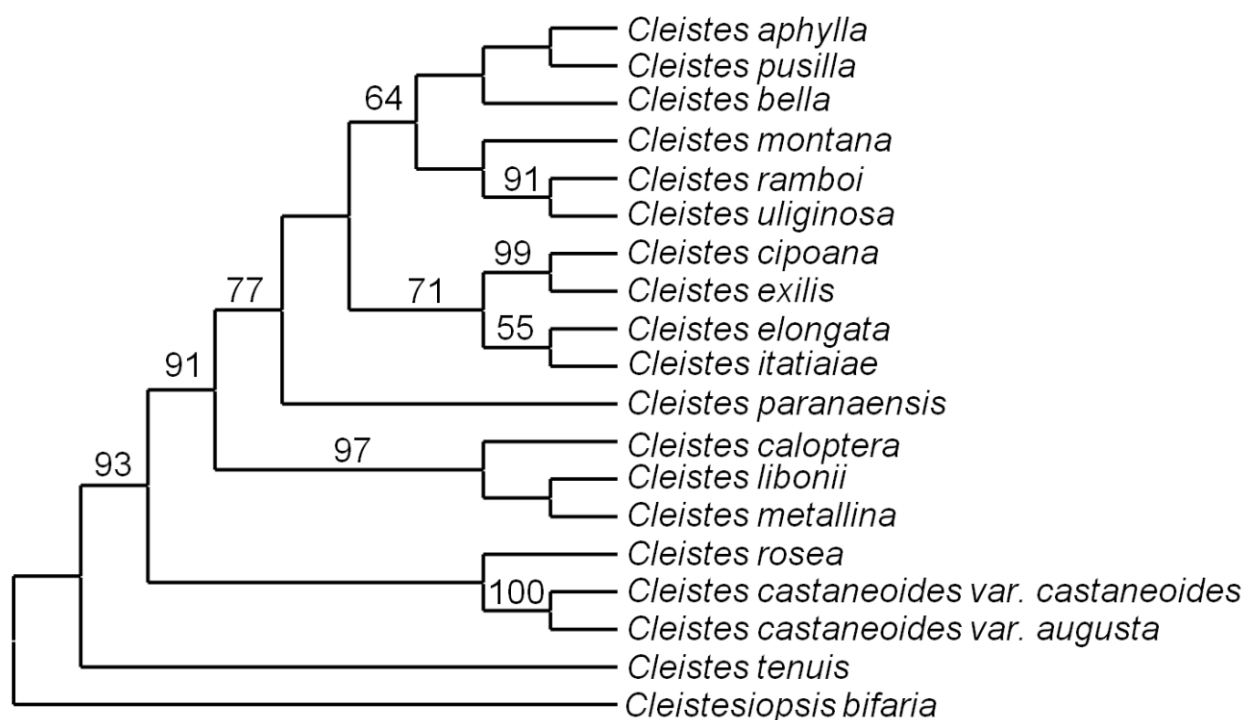


Figure S5. Bootstrap consensus tree based on the maximum likelihood analysis from *rbcL* (cpDNA) sequences of *Cleistes* (Orchidaceae, Vanilloideae). Bootstrap values >50% are given above branches.

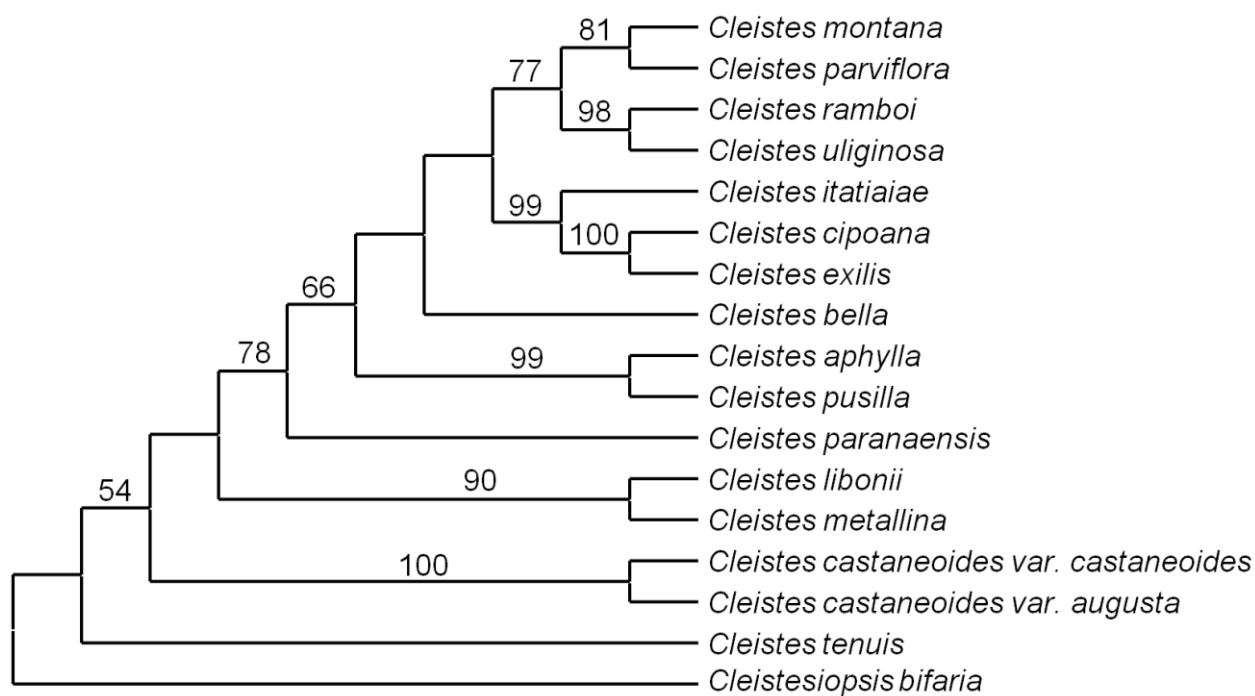


Figure S6. Bootstrap consensus tree based on the maximum likelihood analysis from *rps16* (cpDNA) sequences of *Cleistes* (Orchidaceae, Vanilloideae). Bootstrap values >50% are given above branches.

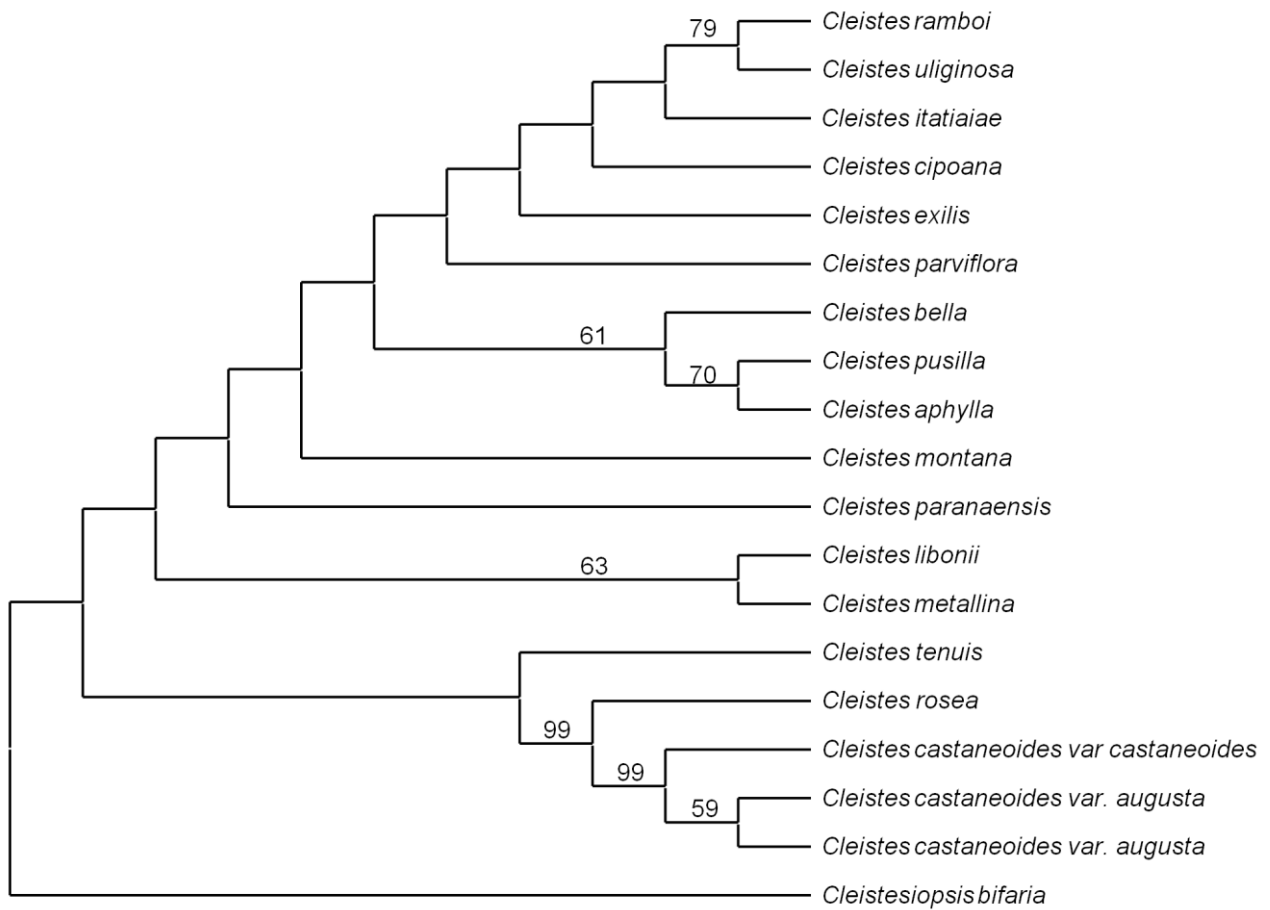


Figure S7. Bootstrap consensus tree based on the maximum likelihood analysis from *trnL-F* (cpDNA) sequences of *Cleistes* (Orchidaceae, Vanilloideae). Bootstrap values >50% are given above branches.