



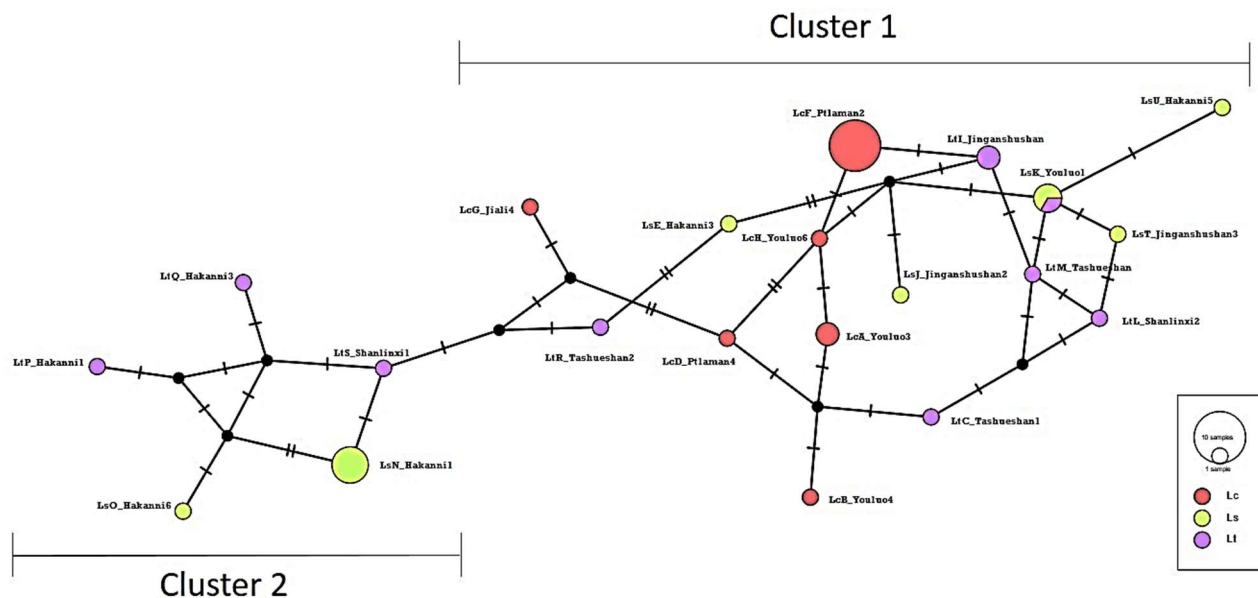
## Supplement

The following supplementary materials are available for this article: Hwang, S.-Y., Y.-S. Li, T.-P. Lin. 2022. Incomplete lineage sorting and secondary admixture results in the paraphyly of *Lecanorchis cerina*, *L. suginoana*, and *L. thalassica* (Orchidaceae) in Taiwan. *Taiwania* 67(3): 366-376. doi: 10.6165/tai.2022.67.366

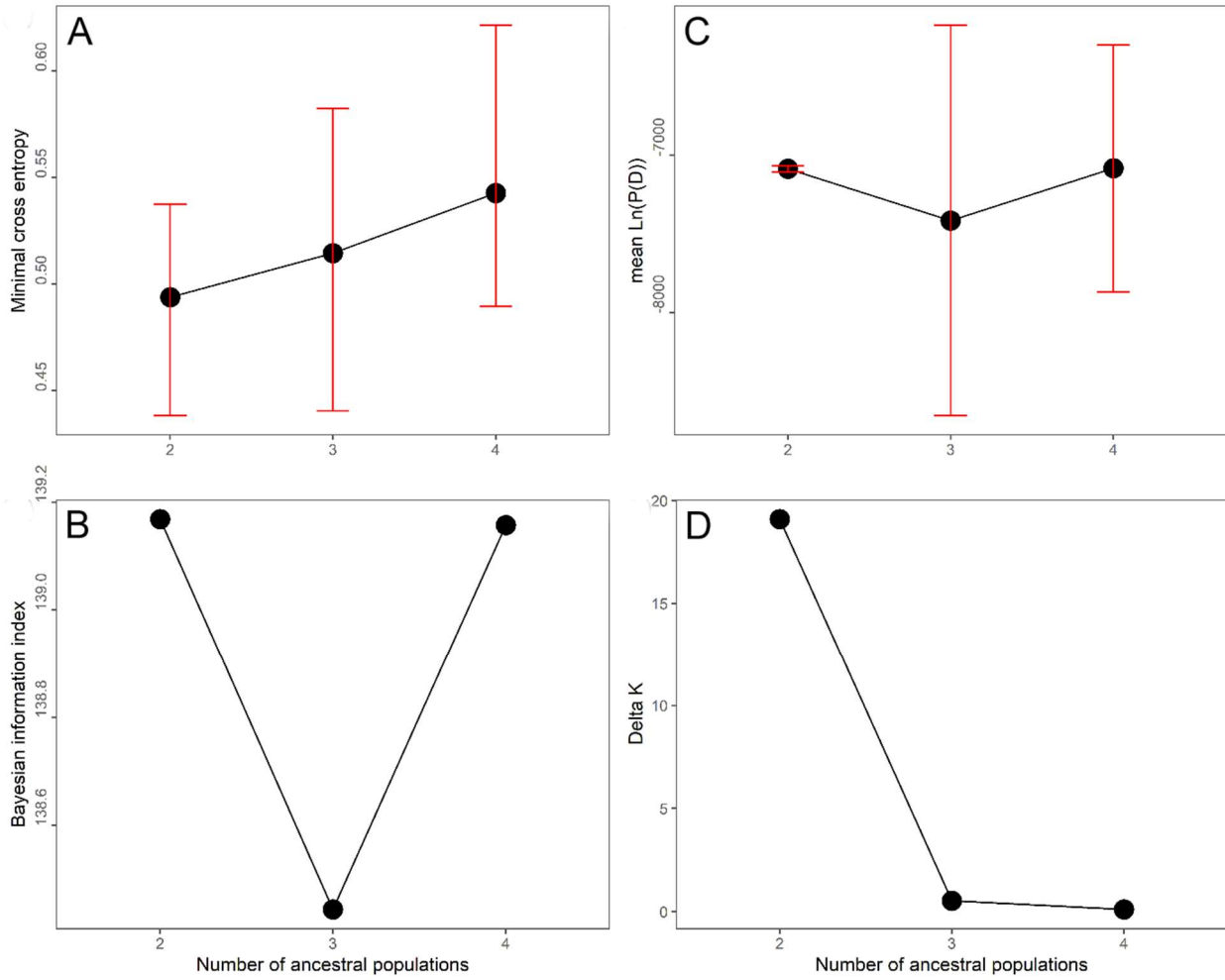
**Table S1.** Primer combinations, number of markers, and error rate per locus in AFLP techniques.

Primer combination	Number of markers	Error rate (%)
E00 CAA + M00 TGT	29	4.48
E00 CAA + M00 GCA	42	4.82
E00 CAA + M00 GGC	31	5.09
E00 CCC + M00 GAT	39	3.27
E00 CGG + M00 TGT	36	4.44
E00 CGG + M00 GAT	43	5.26
E00 CGG + M00 GCA	25	4.01
E00 CGG + M00 GGC	27	4.68
Total	315	4.51

E00 (5'-GACTGCGTACCAATTC-3'); M00 (5'-GATGAGTCCTGAGTAA-3')



**Fig. S1.** The genealogical relationships between haplotypes of *Lecanorchis* species (*L. cerina*, *L. suginoana*, and *L. thalassica*) based on the ITS1 sequences. Species abbreviations (Lc, *L. cerina*; Ls, *L. suginoana*; and Lt, *L. thalassica*) were coded in the front of haplotype names (A–U) and followed with mountain names. The sizes of haplotype circles are proportional to haplotype frequency. The black dots represent unsampled or extinct haplotypes and hash marks indicate the number of mutations between haplotypes.



**Fig. S2.** Evaluation of the genetic homogeneous groups in individuals of the three closely related *Lecanorchis* species (*L. cerina*, *L. suginoana* and *L. thalassica*) based on AFLP variation. The minimal cross entropy (CE) (A) and Bayesian information criterion (BIC) (B) evaluated using the R LEA package. The log likelihood (C) and changes in the log likelihood (D) for different scenarios of groupings evaluated using STRUCTURE