



Molecular phylogeny of *Faberia* (Asteraceae: Cichorieae) based on nuclear and chloroplast sequences

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Abstract

Faberia is a perennial herbaceous member of Asteraceae that is mainly distributed in central and southwestern China. Nuclear (ITS) and plastid (*psbA-trnH*, *rbcL*, *matK*, and *trnL-F*) sequences representing five *Faberia* species were analyzed with maximum parsimony, maximum likelihood, and Bayesian inference, all of which strongly supported the monophyly of *Faberia*. *Faberia nanchuanensis*, *F. cavaleriei*, and *F. faberi* from central China form a well-supported clade. Additionally, *F. sinensis* and *F. tibetica* from southwestern China also form a well-supported clade. Incongruence between nuclear and plastid fragments was interpreted as hybridization or limited character evolution in the plastid DNA. *Faberia* may have descended from hybridization between Lactucinae and Crepidinae. Besides phylogenetic results, *Faberia nanchuanensis* is recorded for the first time from Hunan Province, and *F. sinensis* from the Tibet Autonomous Region.

Key words: China, Compositae, *Faberia*, hybridization, phylogeny

Introduction

Faberia Hemsl. is a perennial herbaceous genus of Cichorieae in Asteraceae. Ling & Shih (1997) recognized four species in the genus and listed another three as potential but imperfectly known members because of a lack of available material. Shih & Kilian (2011) included in the genus seven species that were distributed in central and southwestern China. *Faberia* is characterized by a campanulate or cuneiform involucre, a slender style with papillae or setae, and a brown or pale yellow to white pappus of equal bristles. All species of *Faberia* occur in moist places in woods, or in rocky, grassy places along streams or under waterfalls.

The genus *Faberia* was established based on *F. sinensis* Hemsl., a species endemic to southwestern China (Forbes & Hemsley 1888). Taxonomists held different opinions on the delimitation of this genus. Some botanists considered *Faberia* a separate genus (Hoffmann 1890–1894, Beauverd 1910, Lévillé 1914, Anthony 1934, Shih 1995, Shih & Chen 1996, Ling & Shih 1997, Kilian *et al.* 2009), while others reduced *Faberia* into *Lactuca* L. (Franchet 1895) or into *Prenanthes* L. (Babcock 1947, Lauener 1976, Sennikov & Illarionova 2001, Lack 2007). Sennikov & Illarionova (2008) transferred *Youngia racemifera* (Hook. f.) Babc. et Stebbins, *Y. silhetensis* (DC.) Babc. & Stebbins, and *Y. silhetensis* subsp. *bhutanica* Grierson & Spring. into *Faberia*. Shih & Kilian (2011) associated *Prenanthes glandulosa* Dunn with *Faberia*. Moreover, Kilian *et al.* (2009) and Shih & Kilian (2011) merged *Faberiopsis* Shih & Y. L. Chen with *Faberia*. Liu *et al.* (2012) strongly supported *Faberia* as a separate genus and merged *Faberiopsis* with *Faberia* based on karyological analyses.

Previous studies were restricted to morphological and chromosomal characters; no molecular approach have been undertaken for *Faberia*. DNA data, particularly DNA sequences, greatly contributed to understanding of the phylogeny, evolution, and taxonomy of Asteraceae (Jansen & Kim 1996). In this study, we used nuclear DNA (nrDNA; the internal transcribed spacer of ribosomal DNA; ITS) and plastid DNA (cpDNA; *psbA-trnH*, *rbcL*,

Acknowledgements

We are grateful to Wen-Cai Wang and Yun-Ting Lei for their valuable assistance in revising this manuscript, and to Ze-Long Nie, Dai-Gui Zhang, Liang Xu and Jian-Jun Zhou for providing the materials. The study was supported by grants from the National Natural Science Foundation of China (NSFC 40930209 to H. Sun) and the Ministry of Science and Technology of China, Major State Basic Research Development Program (2010CB951704).

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