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

GUANG-YAN WANG¹²₄, YING MENG¹²₃, TAO DENG¹ & YONG-PING YANG¹²₃⁵

¹Key Laboratory of Biodiversity and Biogeography, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China.
²Plant Germplasm and Genomics Center, the Germplasm Bank of Wild Species, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, China.
³Institute of Tibetan Plateau Research at Kunming, Chinese Academy of Sciences, Kunming 650201, China.
⁴University of the Chinese Academy of Sciences, Beijing 100049, China.
⁵Author for correspondence. E-mail: yangyp@mail.kib.ac.cn.

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. thibetica* 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.


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*, *matK*, and *trnL–F*).
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).

References


Zwickl, D.J. (2006) Genetic algorithm approaches for the phylogenetic analysis of large biological sequence data sets under the maximum likelihood criterion. Ph.D. dissertation, The University of Texas at Austin, Austin, Texas, USA.