



A phylogenetic analysis and new delimitation of *Crepidiastrum* (Asteraceae, tribe Cichorieae)

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Abstract

The systematic position of *Paraixeris humifusa* (Asteraceae) is hard to define, because the circumscription of *Paraixeris*, *Youngia* and *Crepidiastrum*, three closely related genera in subtribe Crepidinae (Cichorieae), is not clear. This paper reports on the relationships between 30 species in subtribe Crepidinae, based on an analysis of nucleotides from one nuclear (ITS) and three chloroplast DNA regions (*trnL-F*, *rps16* and *atpB-rbcL*). The phylogenetic analyses used maximum parsimony with maximum likelihood inference. The monophyly of *Crepidiastrum* in the most recent generic classification of Shih & Kilian (2011) is explored. The results show that 12 species in *Crepidiastrum* constitute a monophyletic group, and that *Paraixeris humifusa* should be treated as *Youngia humifusa*.

Introduction

The tribe Cichorieae, especially the subtribe Crepidinae and the taxonomically related genera such as *Crepidiastrum* Nakai (1920: 147) and *Youngia* Cassini (1831: 88) are difficult groups, because of the weedy nature of some species that are highly polymorphic (Babcock & Stebbins 1937, Shih 1997, Peng *et al.* 1998). The generic ranking as well as the evolution of the tribe Cichorieae are not clear, presenting difficult definitional problems. The genus *Ixeridium* (Gray 1858: 397) Tzvelev (1964: 388) is easily distinguished from *Youngia* and *Crepidiastrum* by its slender long-beaked achenes (Pak & Kawano 1992, Gao 2007). But it has been difficult to distinguish the three genera of *Paraixeris* Nakai (1920: 155), *Youngia* and *Crepidiastrum* through traditional morphology and pollen morphology (Babcock & Stebbins 1937, Kitamura 1942, Shih 1993, 1997, Gao 2007, Sennikov & Illarionova 2008, Wang *et al.* 2009).

The molecular phylogenetic analyses by Enke & Gemeinholzer (2008) revealed that the *Youngia-Crepis-Ixeridium* subclade (including *Crepidiastrum*) was one of the two subclades of the Crepidinae clade, consisting predominantly of Eurasian taxa. The fact that the generic limits as well as the evolution of this subclade is always not clear, makes it difficult to understand their relationships through morphology alone. Saito *et al.* (2006) provided molecular evidence for repeated hybridization events involved in the origin of *Crepidiastrum* × *nakaii* Ohashi & Ohashi (2007: 339). Four hybrids were described by Ohashi & Ohashi (2007). A new hybrid *Crepidiastrum* × *semiauriculatum* was reported by Yamamoto *et al.* (2009: 224). The intergeneric hybridization between *Crepidiastrum*, *Paraixeris* or *Youngia* (Ohashi & Ohashi 2007, Yano & Ikeda 2009) make it more difficult to understand the relationships among the three genera and the relationships between species within a particular genus.

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