



Species diversity within the *Helvella crispa* group (Ascomycota: Helvellaceae) in China

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Abstract

The white saddle-mushroom, a well-known European species, has long been named as *Helvella crispa* in China. In this study, phylogenetic analyses of combined ITS, nrLSU, *tefl-α*, *rpb2* and *mcm7* sequence data, showed that the Chinese *H. crispa*-like samples represent a species complex, which contains at least six phylogenetic species. Three of these species, *H. involuta*, *H. orienticrispa* and *H. pseudoreflexa*, are introduced as new species in this paper. The remaining two taxa are not described due to paucity of material. Among the six phylogenetic species, *H. zhongtiaoensis* is more closely related to European *H. crispa* than the remaining Chinese species. They are provided with descriptions, photographs and are compared with similar species. A key to the Chinese morphologically recognizable taxa of this complex is provided.

Keywords: white saddle-fungi, new taxa, phylogeny, taxonomy

Introduction

The saddle mushroom *Helvella* L. (Helvellaceae, Pezizomycotina) is widely distributed in deciduous or coniferous forests. The type species, *H. crispa* Scop. ex Fr., is a well-known and widely distributed ascomycete, which has been described and illustrated repeatedly by mycologists worldwide (e.g. Abbott and Currah 1988, 1997, Anderson and Ickis 1921, Dissing 1966a, 1966b, 1972, 1979, Harmaja 1979, Hongo and Izawa 1994, Nannfeldt 1937, Weber 1972, 1975, Zhuang 2005). This species is characterized by pale bi- to tri-lobite apothecia, with a pubescent to villose receptacle surface and inrolled to inflexed margin when young, and a white ribbed stipe (Weber 1972). Despite being easily recognized and commonly seen, little is known about the genetic base, variations, and host range within the *H. crispa* group.

Helvella crispa has been regarded as a single species with a wide geographic distribution in China (e.g. Mao 2000, Xu 2002, Ying and Zang 1996, Yuan and Sun 2007, Zhuang 1985, 1995, 1996, 1998, 2004, Zhuang and Yang 2008). However, Cao *et al.* (1990) rejected the monophyly of this species, and introduced *Helvella zhongtiaoensis* as new species. Although Cao *et al.* (1990) made a contribution towards understanding the relationships within the species complex, their study was limited mainly to material collected from a single locality and morphological traits.

In this study, a systematic study of *H. crispa*-like specimens collected throughout China was carried out using both morphological and molecular data. We aimed to accomplish the followings, 1) phylogenetically analyze collections to clarify whether they are conspecific, 2) examine the diversity and host-specificity of the white saddle mushroom in China, and 3) define species taxonomic boundaries of the collections based on morphological, molecular, geographical and ecological traits.