



Hedyotis nanlingensis (Rubiaceae), a new species from South China[#]

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[#]In: Delprete, P.G. & Dessein, S. (Editors), Festschrift volume dedicated to Timothy Motley (1966–2013). *Phytotaxa* 206: 1–132. (2015)

Abstract

A new species, *Hedyotis nanlingensis* from Guangdong province, China, is described and illustrated. It is morphologically similar to *H. nankunshanensis* but differs in the smaller and more slender habit, the sessile leaves, the usually two to three secondary veins on each side of the midvein, the inflorescences with monochasial branching and the shorter style in the long-styled flowers. DNA barcoding analysis demonstrates that all accessions from *H. nanlingensis* form a monophyletic lineage closely related to *H. cantoniensis*.

Introduction

The genus *Hedyotis* L. (1753: 101) and *Oldenlandia* L. (1753: 119) are two of the largest genera within the tribe Spermaceae of Rubioideae (Groeninckx *et al.* 2009). Their circumscriptions and classifications are controversial and have been disputed for many years because of their confused taxonomic delimitation and lack of molecular evidence (Terrell & Robinson 2003). Recent phylogenetic analyses, based on the Asian samples, showed that the *Hedyotis*-*Oldenlandia* complex is polyphyletic and suggested that *Hedyotis* should only include species with erect, robust herbs or shrubs, entire stipules with glandular-serrate margins, and diplophragmous capsules (Guo *et al.* 2013, Wikström *et al.* 2013). Following this delimitation, the genus is essentially restricted to Asia and the Pacific. There are about 75 *Hedyotis* species in China, most of them endemic to China and often with a restricted distribution (Chen & Taylor 2011; Guo & Wang 2011).

During fieldwork in Nanling National Nature Reserve, Guangdong Province, China, we collected a woody herb belonging to *Hedyotis* under secondary broad-leaf forests or pine forests. It is morphologically similar to *Hedyotis nankunshanensis* R.J. Wang & S.J. Deng (Deng & Wang 2012) in its terete stems and terminal inflorescences, but detailed comparison showed that the two species differ from each other in habit, length of leaf petiole, number of secondary veins, flower arrangement in the inflorescence sub-axes, and the style length in the long-styled flowers. Therefore, a new species is here described and illustrated. We also conducted a molecular phylogenetic analysis based on the internal transcribed spacers of nuclear rDNA (ITS) and plastid *petD* sequences in order to elucidate its phylogenetic relationship.

Material and methods

All morphological data in the description of the new species were observed and measured by the authors. The methods for extracting and sequencing nrITS and *petD* follow Guo *et al.* (2011) and the Bayesian analyses refer to Wen & Wang (2012). The sequences of other taxa included in the analysis were downloaded from Genbank (Table 1). ITS of nrDNA and plastid *petD* were chosen as they have proven to be good markers within *Hedyotis* to discriminate between species (Guo *et al.* 2011).

Hedyotis nanlingensis R. J. Wang, *sp. nov.* (Fig. 1)

Type:—CHINA. Guangdong province: Yangshan county, Chengjia Town, Nanling National Nature Reserve, long-styled flowers and young fruits, 24°55' N, 112°57' E, 1420 m, 29 August 2012, R.-J. Wang & S.-J. Deng 2188 (holotype IBSC, isotypes IBSC).