



Goodyera malipoensis (Cranichideae, Orchidaceae), a new species from China: Evidence from morphological and molecular analyses

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Abstract

In this study, we describe a new orchid species, *Goodyera malipoensis*, from Yunnan, China. We have performed morphological and molecular analyses on this new species. A detailed comparison between the newly discovered orchid and other members of *Goodyera* was conducted. The new plant is characterized by having a dense brownish green pubescence on the peduncle. Its ovate-lanceolate petal is unique in *Goodyera* genus. The hypochile is deeply concave-saccate, and inside there are two papillose rows on each side. These features distinguish the new orchid from all other known species of *Goodyera*. The molecular study based on nuclear ribosomal ITS sequence data and morphological differences support *G. malipoensis* as a distinct species.

Key words: Asian orchids, *Goodyera repens*, *Goodyera* phylogenetics, Goodyerinae

Introduction

Goodyera Brown in Aiton (1813: 197; Orchidaceae: Cranichideae) consists of approximately 100 species well represented in southern Africa, Asia, northeastern Australia, Europe, Madagascar, North America and Mesoamerica. There are 29 species in China, 12 of them endemic (Chen *et al.* 2009). *Goodyera* species are terrestrial, lithophytic or epiphytic and have an elongate creeping rhizome. Leaf colour varies from plain light green to blackish, coloured reticulation varies from white to pink and some taxa have a coloured stripe along the mid-vein. Flowers usually have sepals that are dissimilar. The dorsal sepal is concave and connivent with petals, and these form a hood over the column. The lateral sepals are usually connivent with the lip, which is composed of a concave-saccate hypochile and a sessile epichile. There are two pollinia, and each is made of two longitudinal sections that are attached to a small viscidium. They have single anthers with sectile pollinia, and there are hairs at the bases of the labellum that make it relatively easy to distinguish *Goodyera* from related genera (Ormerod & Cribb 2003, Chen *et al.* 2009).

Modern determinations of the phylogenetic relationships of organisms are usually based on both morphological observations and DNA analysis. Molecular studies of orchid taxa have been conducted for higher taxonomic categories (Chase *et al.* 2003, Álvarez-Molina *et al.* 2009, Jin *et al.* 2014, Salazar *et al.* 2014) at the level and at the species level to support description of new species (Li *et al.* 2014). The use of the internal transcribed spacer regions of nuclear ribosomal DNA (nrITS) has become popular because of the relatively high rate of nucleotide substitutions. These studies have permitted systematic comparisons of low-level taxa, such as species within a genus. These species are often difficult to distinguish based on putative diagnostic characters, especially for the groups with similar floral features or highly diverse morphologies, such as *Goodyera* (Shin *et al.* 2002, Górnica *et al.* 2006).

We recently identified three terrestrial populations of *Goodyera* species in Yunnan, China, that are similar in appearance to *G. hispida* Lindley (1857: 183), *G. pusilla* Blume (1858: 31) and *G. hachijoensis* Yatabe (1891: 1). In our study, we describe the diagnostic features of these plants and explore their affinity with similar taxa using DNA sequences (nrITS).

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