



Amana wanzhensis (Liliaceae), a new species from Anhui, China

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Abstract

Amana wanzhensis, a new species from Ningguo County, Eastern China, is described and illustrated. *A. wanzhensis* is similar to *A. erythronioides* in sharing villous tunics and oblanceolate leaves, but differs from it by having shorter bracts (0.1–0.5 cm long), yellow anthers, and deciduous tepals.

Keywords: ITS, Lilioideae, taxonomy, *trnL* intron, Tulipeae

Introduction

The genus *Amana* Honda (1935: 20) includes 4–5 species, endemic to Eastern Asia (Tan *et al.* 2007). This genus is overlapping with *Tulipa* Linnaeus (1753: 305) in many morphological character-states, and generic delimitation is confused. Many taxonomists considered *Amana* and *Tulipa* as synonyms (Sealy 1957, Mao 1980, Ohwi 1992, Tamura 1998, Shen 2001); however, other authors treated them as two distinct genera based on morphological characters and biogeography (Wu 2003), morphological (Tan *et al.* 2005) and molecular phylogenies (Peruzzi *et al.* 2009 and literature cited therein). *Amana* is characterized by 2–3(–4) opposite or verticillate bracts at the upper part of flowering stem, and is endemic to eastern Asia. *Tulipa* has no bracts on scape and distributed from Middle Asia to West Europe (Christenhusz *et al.* 2013).

There are four species of *Amana* in China (Wu 2003). Recently, one new species, *Amana kuocangshanica* D.Y.Tan & D.Y.Hong in Tan *et al.* (2007: 443) has been discovered.

During our fieldwork in Ningguo County, Anhui Province, China, in 2012, a unknown species with a lot of populations was discovered. Our further examination and analysis indicated that it was a new species by having a unique combination of character-states in *Amana*.

Materials and methods

Population sampling:—A total of 15 individuals of 4 *Amana* species were sampled, and at least two individuals were collected for each species (Table 1). All sequences from this study and two ITS region sequences (EU912095 and HE656028) from *A. erythronioides* (Baker) D.Y.Tan & D.Y.Hong in Tan *et al.* (2007: 441) were used as ingroups, while two sequences (JQ776498 and JQ280387) from *Tulipa saxatilis* Baker (1883: 168) was used to be combined one sequence as outgroup for the phylogenetic analysis. New sequences for *Amana* were produced in the present study, while all other sequences were retrieved from GenBank. The specimens and GenBank accession number in this study are listed in Table 1.

Molecular phylogeny

Sequences, homogeneity between data partitions, and homogeneity of nucleotide base frequencies across taxa:—Twenty-three new sequences were obtained. Sequence lengths of partial ITS region and *trnL* intron were 617 bp and 497 bp, respectively. The combined alignment of partial ITS region and *trnL* intron was 1114 bp. Because the partition homogeneity test for the nrDNA ITS region and cpDNA *trnL* intron data showed character congruence ($P = 1.00$), we combined partial ITS region and *trnL* intron to obtain 16 combined sequences (including outgroup taxa) revealing 10 haplotypes (Table 1) for the phylogenetic analyses. A chi-square test indicates that there was no significant compositional heterogeneity of bases among these haplotypes ($\chi^2 = 46.81$, $df = 27$, $P > 0.01$), and thus the biasing effects on the phylogenetic analyses could be eliminated (Jermiin *et al.* 2004).

Phylogenetic analyses:—The Bayesian and MP analyses based on the combination of partial ITS regions and *trnL* intron resulted in almost identical tree topologies, and the posterior probability (PP) values from the Bayesian analysis were all higher than the bootstrap (BS) values from the MP analysis. Figure 2 showed the partitioned Bayesian tree along with the PP and BS values obtained by MP methods. All haplotypes from *A. erythronioides*, *A. wanzhensis*, and *A. edulis* formed a single moderately supported clade (PP = 0.93, BS = 67), while the haplotype corresponding to *A. anhuiensis* (Hap9) was found to be outgroup of this clade. All haplotypes from *A. erythronioides* formed a monophyletic group (PP = 0.99, BS = 92), while all haplotypes from *A. wanzhensis* formed another monophyletic group (PP = 1.00, BS = 93). *A. erythronioides* and *A. wanzhensis* were reciprocally monophyletic, and these two species formed a clade (PP = 0.95, BS = 79) that was sister to *A. edulis* from which all haplotypes formed a monophyletic group (PP = 1.00, BS = 95). Phylogenetic relationships estimated using BI and MP methods were almost identical, and both methods suggested that *A. wanzhensis* is an independent lineage, distinct from *A. wanzhensis*.

Acknowledgements

We thank Prof. De-Qun Wang for the help in the field work. We express our gratitude to Prof. Zhen-Yu Li, Xiao-Hua Jin for critical review of manuscript. The authors are also grateful to Yun-Xi Zhu for the drawings, Dr. Qun Zhao for phylogenetic analysis. This study was supported by the special fund for Traditional Chinese Medicine (NO. 201007008\201207002\201407002), special fund for public health of Traditional Chinese Medicine (NO. [2011]76\2012]13\2013]135) and special protection of biological diversity of department environmental protection of China.

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