



## *Musa ruiliensis* (Musaceae, Section *Musa*), a new species from Yunnan, China

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### Abstract

A new species *Musa ruiliensis*, which occurs in Yunnan, China, is described based on morphological characters and molecular phylogeny. It belongs to *Musa* sect. *Musa* (former *Rhodochlamys*) and has close relationship with *Musa chunii* Häkkinen and *Musa rubinea* Häkkinen & C.H.Teo. A detailed description, chromosome cytology ( $2n = 2x = 22$ ) and phylogenetic position are provided.

**Key words:** *Musa*, *Musa ruiliensis*, section *Musa*, Yunnan

### Introduction

*Musa* Linnaeus (1753: 1043) is the largest genus in Musaceae with about 70 species, distributed from the East Himalayas, through Malaya, Borneo, New Guinea, and to North Australia. A general framework of *Musa* with five sections (sect. *Musa*, sect. *Rhodochlamys*, sect. *Callimusa*, sect. *Australimusa* and sect. *Ingentimusa*) was realized and has been widely accepted by subsequent botanists in the following decades. This classification was mainly derived from two bases: (1) Cheesman (1947) divided genus *Musa* into four sections: *Musa* (= *Eumusa*) ( $2n = 2x = 22$ ), *Rhodochlamys* ( $2n = 2x = 22$ ), *Callimusa* ( $2n = 2x = 20$ ) and *Australimusa* ( $2n = 2x = 20$ ) based on the basic chromosome number, the size and shape of seed, and the orientation and arrangement of flowers, which has been widely used for almost half a century without significant modifications (De Langhe 2000); Argent (1976: 111) created section *Ingentimusa* to accommodate *M. ingens* N.W.Simmonds (1960: 198), an exceptional species with unique basic chromosome numbers ( $n = x = 7$ ). Recently, based on the evidence from molecular phylogenetic studies on the genus *Musa* (Gawel & Jarret 1991, Gawel *et al.* 1992, Jarret *et al.* 1992, Jarret & Gawel 1995, Shepherd 1999, Ude *et al.* 2002, Nwakanma *et al.* 2003, Wong 2002, Wong *et al.* 2003, Bartoš *et al.* 2005, Heslop-Harrison & Schwarzacher 2007, Li *et al.* 2010, Liu *et al.* 2010, Nayar 2010, Christelová *et al.* 2011, Hřibová *et al.* 2011, Xavier *et al.* 2011), Häkkinen (2013) reconstructed species of *Musa* into two sections: sect. *Musa* and sect. *Callimusa*.

Wild species of banana family have been a taxonomically difficult group due to the large fleshy nature of the plants, ephemeral aspect of the flowers (Liu *et al.* 2002), and poor representation in herbaria (Argent 1976, Häkkinen & Väre 2008). In the last decade, extensive field observations were made by botanists in diversity centers of *Musa*, such as India, southwestern China, Vietnam etc., and many new species were identified (i.e., Häkkinen 2004, 2005, 2006, 2009, Häkkinen & Meekiong 2004, Häkkinen & Wallace 2007, Häkkinen & Teo 2008, Häkkinen & Wang 2008, Sabu *et al.* 2013). The new species described here is from Southwestern Yunnan, China, apparently belonging to the section *Musa* (former section *Rhodochlamys*) because of its brightly colored bracts. In the current study, morphological details were described and the phylogenetic position of this organism was investigated based on 3 chloroplast DNA loci (*atpB-rbcL*, *rps16* and *trnL-F*). In addition, a cytological experiment was conducted to count the number of chromosome.

newly-acquired cpDNA sequences were aligned with the original cpDNA matrix containing 35 taxa of *Musa* and four out-group species (*Heliconia caribaea* Lam., *H. psittacorum* L.f., *Orchidantha chinensis* T. L. Wu, and *Ravenala madagascariensis* Sonn.) from three of the most closely related families in Zingiberales (Li *et al.* 2010, Kress *et al.* 2001, Kress & Specht 2005) using CLUSTAL X version 1.81 (Thompson *et al.* 1997) and manually adjusted in the program Se-AL version 2.0a 11 (Rambaut 2002). Phylogenetic analyses were conducted on a combined matrix including all of these three regions using maximum parsimony (MP) in PAUP\*v.4.0 b10 (Swofford 2002) and Bayesian methods in MrBayes v. 3.2.1 (Ronquist & Huelsenbeck 2003, Ronquist *et al.* 2012). Both MP and Bayesian trees suggested the close relationship of *M. ruiliensis*, *M. chunii* and *M. zaifui*, which is consistent with the morphological classification. Moreover, the new species *M. ruiliensis* and *M. chunii* are resolved to be the most closely related to each other with strong support (BS = 91%; PP = 1.00) and these two species form a clade sister to *M. zaifui* but with poor support (BS = 61%; PP = 0.99) (Fig. 4).

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