



## A new paludicolous species of *Malaxis* (Orchidaceae) from Argentina and Uruguay

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### Abstract

*Malaxis irmae*, a new orchid species from the Paraná and Uruguay river basins in northeast Argentina and Uruguay, is described and illustrated. It is similar in size and overall floral morphology to *Malaxis cipoensis*, a species endemic to upland rocky fields on the Espinhaço range in Southeastern Brazil, which is its closest relative according to a cladistics analysis of nuclear (ITS) and plastid (*matK*) DNA sequences presented here. However, *M. irmae* is distinguished from *M. cipoensis* by inhabiting lowland marshy grasslands, possessing 3–5 long-petiolate leaves per shoot (vs. 2 shortly petiolate leaves), cylindrical raceme (vs. corymbose), pale green flowers (vs. green-orange flowers) and less prominent basal labellum lobules. *Malaxis irmae* is morphologically also similar to the Brazilian *M. warmingii*, which differs in its much larger plants and prominent basal labellum lobes.

**Key words:** ITS, *Malaxis irmae*, marshy grasslands, *matK*, phylogenetics

### Introduction

As traditionally delimited, the genus *Malaxis* Solander ex Swartz (1788: 119) *s.l.* included about 300 species and had a worldwide distribution (Cribb 2005). However, a recent molecular phylogenetic analysis of tribe Malaxideae (Cameron 2005) showed that *Malaxis s.l.* is polyphyletic. Although much work on the phylogeny and taxonomy of the whole tribe Malaxideae remains to be done to clarify the generic limits, several morphology-based taxonomic studies have started to recognize less-inclusive segregated genera. Some of the current segregates of *Malaxis s.l.* include Old World tropical groups like *Crepidium* Blume (1825: 387), *Dienia* Lindley (1824: sub t. 825) and *Orestias* Ridley (1887: 197) (e.g. Szlachetko 1995, Clements & Jones 1996, Cribb 2005), whereas the New World segregated genera comprise *Crossoglossa* Dressler & Dodson (1993: 148), *Tamayorkis* Szlachetko (1995: 121) and *Crossoliparis* Margońska (2009: 298–299). Excluding such segregates, *Malaxis s.s.*, including *Microstylis* (Nuttall 1818: 196) Eaton (1822: 115), encompasses approximately 120 species restricted to the New World and temperate regions of Eurasia (G. A. Salazar, unpubl. data). Recently, Margońska *et al.* (2012) published a review of “Malaxidiinae” Bentham & Hooker (1883: 463, 465), a polyphyletic assemblage of taxa allegedly distinguishable from other Malaxideae by morphological traits such as column length relative to anther length, angle of the anther relative to the column, position of anther openings, degree of concavity of the stigma and structure of the nectary, but none of these traits is consistent in any of their purported subtribes, the limits of which grossly contradict the results of both, the molecular phylogenetic analysis of Cameron (2005) and Margońska *et al.*’s own cladogram based on ITS sequences (Margońska *et al.* 2012: Fig. 5). Likewise, the cumbersome infrageneric classification proposed in that work, which recognizes sections, subsections and series often based on unreliable characters (e.g. “Raceme apically dense and conical” vs. “Raceme dense and distinctly cylindrical all along its length”, a feature that often varies in the same plant depending on the stage of development of the inflorescence), results in grouping together disparate plants and segregating in different

for water-logged habitats is shared, besides *M. warmingii*, by several other species, including South American *M. hieronymi* (as noted above) and Mexican *M. zempoalensis*. From our analysis, it is clear that the preference for wet places has evolved more than once in this genus. Although our sample of species of the genus is too sparse to draw conclusions at this time, the relationships recovered suggest that habitat divergence/specialisation may have played a role in promoting speciation in *Malaxis s.s.*, which is exemplified by the contrasting habitat preferences of *M. irmae* and *M. warmingii* with respect to *M. cipoensis* (the closest relative of *M. irmae* among the taxa we sampled). This and other interesting evolutionary questions, however, will have to be revisited when a more thorough sample of the genus is available for molecular phylogenetic study.

Barros (1996) placed *M. cipoensis* in *Malaxis* section *Umbellulatae* (Ridley 1888: 315) Barros (1996: 33) and *M. warmingii* in *M.* section *Spicatae* Ridley (1888: 315). The latter is obviously superfluous as it includes the (lecto-) type species of *Malaxis* (*M. spicata*), whereas our phylogenetic analysis shows that *M. cipoensis* belongs in the same clade as *M. spicata*, thus demonstrating that these infrageneric taxa are of little use. These and other infrageneric groups (e.g. those in Margońska *et al.* 2012), will have to be thoroughly assessed when the phylogenetic relationships in the genus are better understood.

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