

Elucidating the taxonomic status of *Uvaria* sp. (Annonaceae) from Thailand using morphology and molecular phylogenetics

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<<Abstract

Introduction

Uvaria L. (Annonaceae, Annonoideae, Uvarieae, Uvariinae) is a large genus consisting of about 171 species widely distributed in Palaeotropics plus Australia [1]. Members of the genus are mostly lianas [2]. Although species of *Uvaria* exhibit diverse floral morphologies, they all share a stellate indumentum, which facilitates identification to genus even in the absence of flowers and/or fruits. In Thailand, there are ca. 24 species of *Uvaria* reported. Recent expeditions in Chanthaburi Province, southeastern Thailand have yielded unidentifiable gatherings of *Uvaria*. This study aims to elucidate the taxonomic status of this *Uvaria* sp. through comprehensive morphological comparisons coupled with molecular phylogenetic inferences.



Materials and Methods

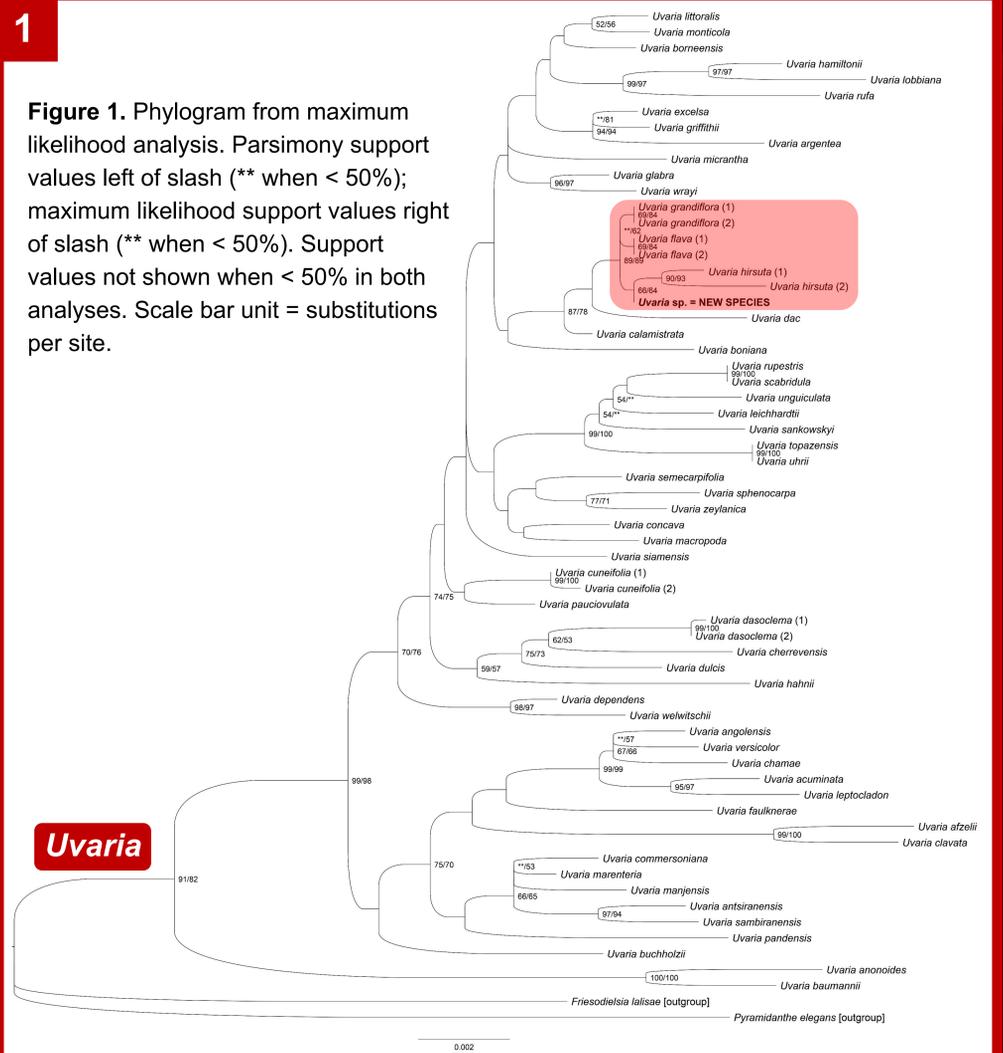
A molecular phylogeny of *Uvaria* (62 accessions) was reconstructed using five plastid DNA regions (*matK* and *rbcl* exons; *trnL* intron; *psbA-trnH* and *trnL-trnF* intergenic spacers). Two representatives of other Uvarieae genera were assigned as outgroups: *Friesodielsia lalisae* Damth., Baka & Chaowasku and *Pyramidanthe elegans* (Hook.f. & Thomson) Bangk. & Chaowasku. The methods for generating and aligning DNA sequences as well as settings of the phylogenetic tree reconstruction used in the present study followed [3]. Parsimony and maximum likelihood phylogenetic analyses were performed.

Results, Discussion and Conclusion

As depicted in the phylogenetic tree reconstructed (Figure 1), the genus *Uvaria* was recovered as a monophyletic group with moderate to strong support. *Uvaria* sp. belongs to a strongly supported clade that also includes three other species: *U. flava* Teijsm. & Binn., *U. grandiflora* Roxb. ex Hornem. and *U. hirsuta* Jack. Although *Uvaria* sp. is sister to a strongly supported clade comprising two accessions of *U. hirsuta* (with weak support), its morphology more closely resembles *U. grandiflora*. However, *Uvaria* sp. is dissimilar from both *U. grandiflora* and *U. hirsuta* by different combinations of traits, such as leaf base, inflorescence position, degree of petal reflexion at anthesis (Figure 2), number of stamens per flower (Figure 2) and monocarp surface. Therefore, based on morphological and molecular phylogenetic evidence, *Uvaria* sp. deserves recognition as a new species.

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Figure 1. Phylogram from maximum likelihood analysis. Parsimony support values left of slash (** when < 50%); maximum likelihood support values right of slash (** when < 50%). Support values not shown when < 50% in both analyses. Scale bar unit = substitutions per site.



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Figure 2. Floral morphology of *Uvaria* sp. (left), *U. grandiflora* (middle) and *U. hirsuta* (right). Photographs by Anissara Damthongdee (*U. grandiflora*), Anutra Satayakul (*Uvaria* sp.) and Cerlin Ng (*U. hirsuta*).

References

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