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Research note

The systematic position of *Sophora inhambanensis* (Fabaceae: Sophoreae)

J.S. Boatwright a,b,*, B.-E. Van Wyk b

^a Compton Herbarium, South African National Biodiversity Institute, Private Bag X7, Claremont 7735, Cape Town, South Africa ^b Department of Botany and Plant Biotechnology, University of Johannesburg, PO Box 524, Auckland Park 2006, Johannesburg, South Africa

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Abstract

The phylogenetic position of *Sophora inhambensis* (one of only three species of *Sophora* that occur in Africa — the others are the widespread *S. tomentosa* and *S. velutina*) is inferred from an analysis of internal transcribed spacer (ITS) sequences for the core genistoid legumes. This species was thought to be closely related to the Podalyrieae based on chemical data (alkaloids and seed flavonoids), but molecular data indicates that it is strongly supported within the genus *Sophora*, close to the type species, *S. tomentosa*. *Sophora velutina* also groups with *Sophora* sensu stricto.

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The tribe Sophoreae (Fabaceae) is a polyphyletic assemblage with constituent genera scattered throughout the phylogenetic tree of the Papilionoideae (Lewis et al., 2005). The "Sophora group" of genera, which includes the type species S. tomentosa L., is placed within the core genistoids (sensu Crisp et al., 2000) along with the largely African tribes Crotalarieae and Podalyrieae (Boatwright et al., 2008a; Crisp et al., 2000). The genus Sophora L. is poorly represented in Africa, with only three of the ca. 50 species occurring on the continent. Of these species, Sophora inhambanensis Klotzsch is the only endemic, occurring along the coast of East and southern Africa. Two other species, S. tomentosa (widespread in the coastal Paleotropics and coastal Eastern Brazil) and S. velutina Lindley (widespread in Asia), also occur in Africa, the latter with a localised, African-endemic subspecies (subsp. zimbabweensis Gillett and Brummitt) described from Zimbabwe (Brummitt and Gillett, 1966).

Sophora inhambanensis shares with other Sophora species, notably S. tomentosa, the imparipinnately compound, pubescent leaves, unspecialised, yellow, ebracteolate flowers with free stamens and moniliform pods. However, chemotaxonomic similarities between the Podalyrieae and S. inhambanensis were discussed by Van Wyk (2003), who suggested a possible

E-mail address: S.Boatwright@sanbi.org.za (J.S. Boatwright).

relationship of this species with the genera of the Podalyrieae. Similar chemotaxonomic signatures were found in the genus *Cadia* Forssk. (also Sophoreae) and DNA analyses (Boatwright et al., 2008a) confirmed its relationship to Podalyrieae, to which it was accordingly transferred. In light of similar chemotaxonomic evidence, the phylogenetic position of *S. inhambanensis* and the other African species of *Sophora* needs to be clarified before generic circumscriptions of *Sophora* can be ascertained.

Leaf material of *S. inhambanensis* (Van Wyk 3574, JRAU; FN813570) and *S. velutina* (Van Wyk 4229, JRAU; FN813569) were extracted and the internal transcribed spacers of rDNA (ITS) amplified and sequenced following the procedures outlined in Boatwright et al. (2008b). These sequences were combined with ITS data for taxa from the Podalyrieae, Crotalarieae, Genisteae, Thermopsideae and Sophoreae s.s. (voucher information for these are given in Boatwright et al., 2008a, b). *Styphnolobium japonicum* (L.) Schott was included as outgroup. Two additional sequences of *Sophora tomentosa* were also included from GenBank (AY725482, Heenen et al., 2004; DQ499085, Wright et al., 2006).

The nrITS matrix consisted of 699 characters, 326 of which were constant, 373 variable and 259 parsimony informative. Parsimony analysis resulted in 2500 trees with a tree length (TL) of 1173 steps, a consistency index (CI) of 0.51 and a retention index (RI) of 0.76 (Fig. 1). The Podalyrieae (including *Cadia*)

^{*} Corresponding author.

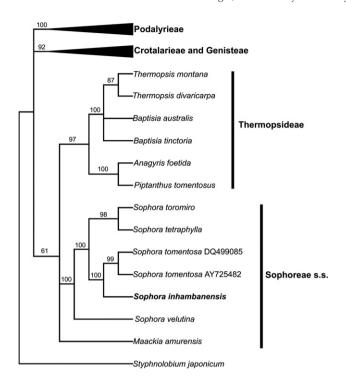


Fig. 1. Strict consensus tree of 2500 shortest length trees from the analysis of the ITS data set for the core genistoids (TL=1173; CI=0.71; RI=0.76). Numbers above the branches are bootstrap percentages above 50%.

are strongly supported as monophyletic (100 bootstrap support, BS), with Crotalarieae and Genisteae as sister groups (92 BS). Thermopsideae (97 BS) and Sophoreae s.s. are early diverging within the core genistoids and *Sophora* s.s. is strongly supported as monophyletic (100 BS). *Sophora inhambanensis* is placed with the other *Sophora* species with strong support (100 BS) close to the type of the genus, *S. tomentosa* (100 BS), and not close to the Podalyrieae.

In a phylogenetic study of the tribe Podalyrieae, Boatwright et al. (2008a) transferred the genus Cadia Forssk. from Sophoreae to the Podalyrieae, based on morphological, cytological, chemical and molecular data. Cadia shared with the Podalyrieae a similar chromosome base number, several morphological characters, as well as similar alkaloids and flavonoids. These authors mention the uncertain position of S. inhambanensis and the need to ascertain its phylogenetic placement, based on evidence presented by Van Wyk (2003). The latter author indicated a possible relationship of this species with the genera of the Podalyrieae and Cadia, citing the presence of carboxylic acid esters of alkaloids (unique outside of the Podalyrieae, after the transfer of *Cadia*) and the isoflavone 3'-hydroxydaidzein as major seed flavonoid. This, as well as the absence of α -pyridone alkaloids (present in some Sophoreae), strongly suggests that there is a direct link between S. inhambanensis and genera of the tribe Podalyrieae. Morphologically, however, this species is very similar to *S. tomentosa* and *S. velutina*.

From the analysis of the ITS data it is clear that S. inhambanensis is placed within the genus Sophora and not closely allied with the Podalyrieae. This indicates that the similarities in chemical patterns are more likely the result of convergence, rather than common ancestry. Analysis of molecular data with a broader sample of Sophora species is needed to determine the exact relationships of S. inhambanensis to other Sophora species, but the current data indicates that it is closest to S. tomentosa. Studies of alkaloid and flavonoid distributions with a more comprehensive sampling may also provide insights into the chemical patterns discussed by Van Wyk (2003), and their phylogenetic implications. Further taxonomic and molecular studies on African Sophora species will provide insights into the relationships with other species in the genus and give more clarity regarding the origin of S. velutina subsp. zimbabweensis, which is uncertain (Brummitt and Gillett, 1966), considering its highly localised and disjunct distribution. The possibility that the plant or its seeds may have been introduced to southern Africa in prehistoric times cannot be ruled out.

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