

**A PRELIMINARY STUDY ON SPECIES LIMITS OF THE ENDEMIC GENUS
STEMONOPORUS (DIPTEROCARPACEAE) USING MORPHOLOGICAL DATA**

S.C.K. RUBASINGHE,¹ D.M.D. YAKANDAWALA¹ AND D.S.A. WIJESUNDARA²

¹*Department of Botany, Faculty of Science, University of Peradeniya*

²*Royal Botanic Gardens, Peradeniya*

Stemonoporus is the most species rich dipterocarp genus endemic to Sri Lanka where all the species are categorized as highly threatened or threatened. Since the initial description of the genus *Stemonoporus* by Thwaites in 1854, it has changed to *Vateria* and then to *Vatica* and has now been re-established as a proper genus. The existing taxonomic treatments on the genus are not in agreement with each other and there are no studies on its phylogenetic relationships. The aim of the present study is to re-evaluate the species delimitations and reconstruct the phylogeny of *Stemonoporus*, using a large number of morphological data.

Extensive field visits were made to collect specimens of all major taxa of the genus *Stemonoporus* recognized by Ashton, 1980 and Kostermans, 1992. All collected specimens (150) of the genus *Stemonoporus* were coded for 169 morphological characters and character states in this study. The data clearly suggests that there are many dissimilarities as well as similarities among the taxa. Principal Component Analysis (PCA) and Cluster Analysis (CA) were attempted in order to examine the taxonomic patterns of the data. The dendograms of cluster analyses are poorly resolved mainly due to the fact that the quantitative data of the taxa studied vary greatly. Thus, it can be concluded that the quantitative data cannot be successfully used for evaluating the similarities among species of the genus *Stemonoporus*.

Cladistic analysis was performed with the data matrix of 169, qualitative and quantitative characters. The strict consensus tree of the successively weighted characters recovers the genus as a monophyletic group with good support (100% bootstrap). Twenty-six monophyletic groups (taxa) have been recovered. All the taxa were resolved as monophyletic groups within seven large monophyletic groups. The cladogram tree does not agree with the traditional division of the genus based on the number of stamens, but suggests that there are other strong morphological characters that could be used in the separation of taxa.

Financial assistance by the National Science Foundation, Research Grant RG/2003/BM/02 is acknowledged.