

PHYLOGENETIC RELATIONSHIPS OF THE GENUS *GARCINIA* (CLUSIACEAE) PRESENT IN SRI LANKA

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Introduction

The Clusiaceae is a family of plants that encompasses about 37 genera and 1610 species of trees and shrubs, often with milky sap and fruits or capsules for seeds. It is primarily tropical, more so than many plant families it shows a large amount of variation in plant morphology (for example, 3 to 10 petals, fused or un-fused petals, and many other traits). According to the AGP II classification, the family is placed under the order Malpighiales (Judd *et al.*, 2002). During the recent revision of the flora of Sri Lanka, 10 *Garcinia* species have been identified as occurring in the country, with 5 of them being considered as endemics (Kostermans, 1980). They are *G. quaesita*, *G. zeylanica*, *G. ternstroemia*, *G. thwaitesii* and *G. hermonii* which are mainly confined to the wet zone lowlands. Questions are raised to the endemicity of *G. echinocarpa* due its occurrence in the closest land mass India. Among other non endemic species, *G. spicata* is mainly distributed in dry and arid zones and *G. morella* in dry and wet zones while *G. mangostana* and *G. xanthochymus* are restricted to the lowlands of the wet zone (Kostermans, 1980). The objective of the present study was to carry out a phylogenetic analysis of the genus *Garcinia* occurring in Sri Lanka, using morphological and anatomical data to

determine their phylogenetic relationships and to compare with a phylogeny proposed using a numerical analysis (Pathirana and Herat, 2004).

Materials and Methods

The morphological characters of all the 10 species of *Garcinia* occurring in Sri Lanka were coded using herbarium specimens deposited at the National Herbarium, Royal Botanic Gardens Peradeniya, Sri Lanka and at least 10 specimens were studied for each species. The data were also supplemented with the available literature. In most cases the floral and fruit characters were coded using *A Revised Handbook to the Flora of Ceylon* (Kostermans, 1980). The anatomical characters were coded using a recent study done by Pathirana and Herat (2004). A data matrix was constructed by coding 44 characters and character states using the computer program MacClade. The data were analyzed using the computer program PAUP 4.0. For all analyses, heuristic searches were performed initially under the unordered and equal weighting criteria of Fitch parsimony with 10 replicates, random sequence addition, tree bisection connection and branch swapping. Initially characters were not weighted. The characters were weighted based on the RI (Retention Index) and a bootstrap analysis was carried out to find support for the separation of the monophyletic

clades. The resulting trees were rooted using the mid point rooting option.

Results and Discussion

Initial heuristic search under Fitch criterion yielded 11 most parsimonious

trees each with a tree length of 124, CI - 0.621 and RI - 0.520. The successive weighting of characters based on RI resulted in only one most parsimonious tree with a tree length of 56.56, CI - 0.752, RI - 0.725 (Figure 1).

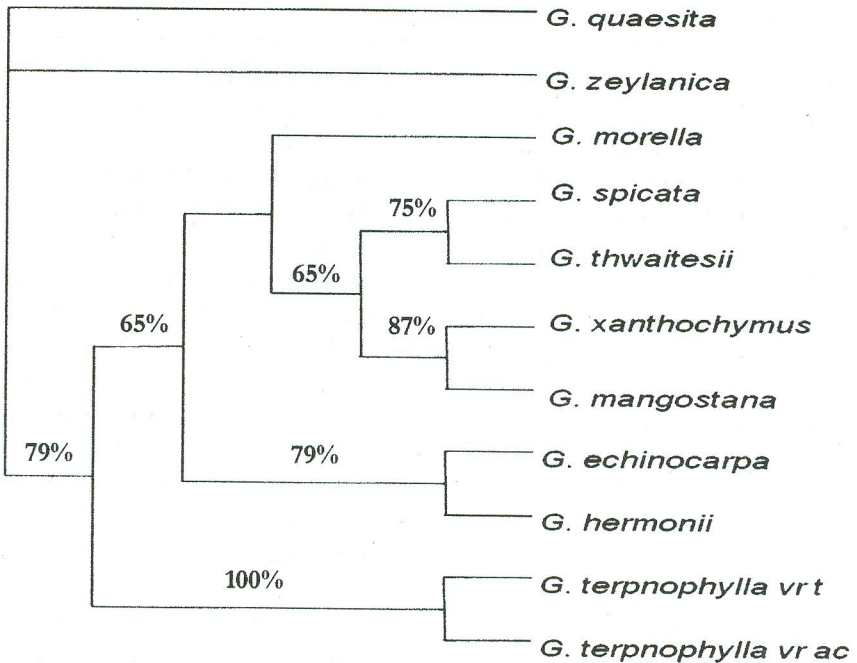


Figure 1. The Most Parsimonious tree resulting from the analysis of morphological and anatomical data and the bootstrap values.

Based on the phylogenetic analysis carried out using morphological and anatomical data, the genus *Garcinia* occurring in Sri Lanka was recovered as a monophyletic group. By considering the 50% majority rule consensus tree, *G. quaesita* and *G. zeylanica* (endemics) evolved separately from the basic stock. Characters such as the presence of the grooves of the ovary and the presence of ribs in the fruit supports the clade with a CI value of 1.00. The two varieties of *G. terpnophylla*, *G. terpnophylla* var. *terpnophylla* and *G. terpnophylla* var. *acuminata* form a

strong monophyletic clade (100% bootstrap) strengthening their position in belonging to the species. The two varieties differ from each other by the presence of acute leaf base in *G. terpnophylla* var. *terpnophylla* and caudate base in *G. terpnophylla* var. *acuminata*. This monophyletic clade is the sister to a large monophyletic group enclosing, *G. morella*, *G. spicata*, *G. thwaitesii*, *G. xanthochymus*, *G. mangostana*, *G. echinocarpa* and *G. hermonii*. It is interesting to note that the doubtful endemic species *G. echinocarpa* forms a strong monophyletic clade

with endemic *G. hermonii* with a bootstrap value of 79%. The results of the phenetic analysis (Pathirana and Herat, 2004) corroborate with this and Trimén (1893) also considered as *G. echinocarpa* endemic to Sri Lanka. However, Kostermans (1980) considers *G. echinocarpa* as non endemic to Sri Lanka, as he had doubts due its occurrence in India. According to the majority rule consensus tree, *G. morella* is the sister group to the clade bearing, *G. spicata*, *G. thwaitesii*, *G. xanthochymus* and *G. mangostana*. *Garcinia morella* is clearly separated from the clade, and the presence of druse crystals in the epidermis supports this with CI value of 1.00. Non endemic *G. spicata* and endemic, *G. thwaitesii* recovered as a monophyletic group with 75% bootstrap value supporting their common origin. The remaining two cultivated species *G. mangostana* and *G. xanthochymus* recovered as a monophyletic group, with the bootstrap value of 87%.

The results of the present study does not totally agree with the phenetic analysis, where the study suggests the basic stock responsible for the evolution of endemic Sri Lankan taxa are mainly the non endemics *G. mangostana*, *G. morella*, *G. spicata* and *G. xanthochymus*. *G. thwaitesii* and *G. hermonii* have evolved on two evolutionary lines from the basic stock through *G. xanthochymus*. Similarly, *G. quaesita* evolved from the stock through *G. morella*, giving rise to *G. echinocarpa*. Further, *G. echinocarpa* is considered as the most specialized species. Based on the overall anatomical data and ecological distribution it is considered as an

endemic species. This could be due the reason as the phenetics mainly concentrates on total similarity while the cladistics gives more weight for character evolution and synapomorphic characters.

Conclusion

The phylogenetic analysis of *Garcinia* occurring in Sri Lanka recovered as a monophyletic group. The doubtful endemic taxa, *G. echinocarpa* forms a strong monophyletic clade with endemic *G. hermonii* with a bootstrap value of 79%. The results of the present investigation do not corroborate the phenetic analysis carried out using anatomical data. The set of morphological data coded in the present study could be supplemented with molecular data in order to gain more support for the monophyletic groups and the endemic taxa and using an outgroup for rooting.

References

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