

Towards a phylogeny of the Cucurbitaceae — S. S. Renner, A. Weerasooriya, and M. E. Olson*; Dept. of Biology, Univ. Missouri-St. Louis & The Missouri Botanical Garden, renner@umsl.edu; *Inst. de Biología, Universidad Nacional Autónoma de México, molson@ibiologia.unam.mx
 In consultation with: C. Jeffrey (morphology and classification), S. Swensen (rbcL phylogeny), D. Decker-Walters (Benincaseae), and W. de Wilde (*Trichosanthes* and relatives)

Abstract

Cucurbitaceae comprise 760 species in 120 genera and are most species-rich in tropical and subtropical Africa/Madagascar and Central and South America. Phylogenetic relationships in Cucurbitaceae have been inferred from morphology, but an explicit family-wide character analysis is not available nor are family-wide molecular data, hindering inference of fruit and flower evolution, and reconstruction of geographic links. Our goal is to generate parallel data sets for representatives of all genera to strengthen the morphology-based classification of the family (Jeffrey, 1990) and to test hypotheses about the ages and geographic spread of major clades within cucurbits.

The tree shown (Fig. 1) is based just on trnL-F sequences and contains 47 genera that represent all tribes and subfamilies. Additional genera already sequenced include *Acanthosicyos*, *Cucumella*, *Cucurbita*, *Cyclanthera*, *Fevillea*, *Hodgsonia*, *Melothria*, *Peponium*, *Sicyos*, and *Solena*.

DNA regions being sequenced are the chloroplast trnL-F region, the rpl16 intron, the rbcL gene (lab of S. Swensen), and the mitochondrial nad1 B/C intron and partial exons.

Results so far indicate that Benincaseae, Melothriaceae, and Trichosantheae may be polyphyletic and that genera often fall out along geographic, rather than current tribal lines.

The oldest cucurbit seeds and fruits come from the Lower Tertiary London Clay, and fruits of *Trichosanthes* are commonly reported from Late Miocene and Pliocene floras of Europe and Russia.

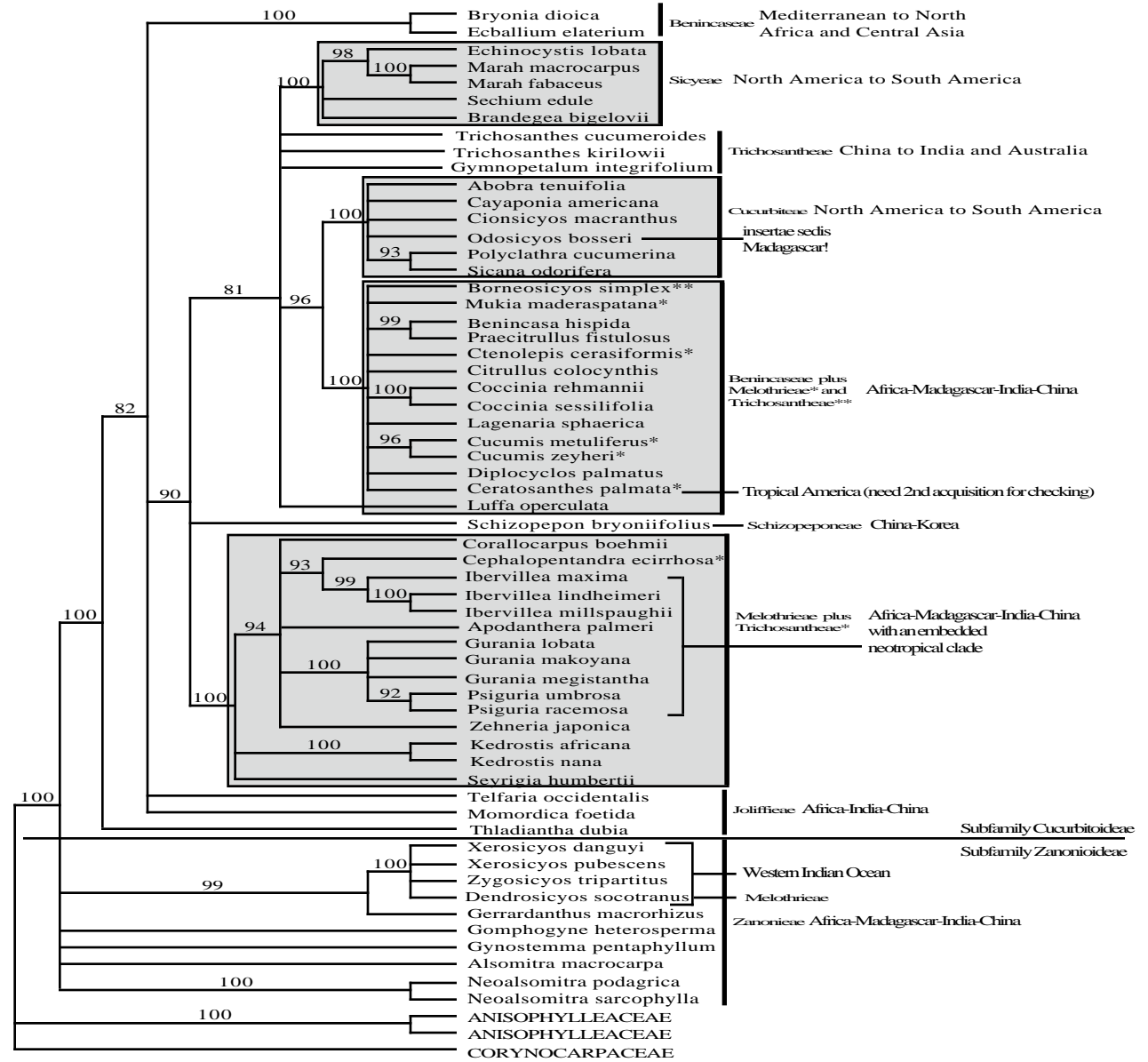


Fig. 1. Phylogenetic relationships in Cucurbitaceae determined by Bayesian inference from chloroplast spacer sequences (trnL-F e-f; 529 bp). The analysis used the GTR model, with four Monte Carlo Markov Chains run for 100 000 generations, using a random tree as a starting point. Trees were sampled every 10th generation, the first 4000 discarded as burnin, and the remaining 6000 used to construct this consensus with the posterior probabilities shown on the branches.

