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Phylogenetic analysis of the tribes Gloxinieae and Gesnerieae (Gesneriaceae): data from ndhF sequences.

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sequenced three cpDNA introns (*rpl16*, *rpoC1*, *ndhA*) and four cpDNA spacers (*zfpA-psal*, *trnL-trnF*, *trnT-trnL*, *atpβ-rbcL*) for a total of over 7 kb of sequence, yet have obtained no phylogenetic resolution. In addition, we have sequenced a 1.65 kb region of a homeologous pair of nuclear-encoded alcohol dehydrogenase (*Adh*) genes. In contrast with the cpDNA sequence data, each of the two *Adh* homeologues yielded an identical and robust topology that is concordant with previous cladistic and phenetic analyses. The enhanced resolution obtained using the nuclear genes reflects an approximately 6-fold increase in substitution rate relative to the plastome spacers and introns. The relative utilities and limitations of each source of data will be discussed.

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JAMES F. SMITH* and SHAWN ATKINSON. Boise State University, ID, USA. Phylogenetic analysis of the tribes Gloxinieae and Gesnerieae (Gesneriaceae): data from *ndhF* sequences.

The neotropical Gloxinieae are one of the larger tribes in the subfamily Gesnerioideae (Gesneriaceae). The tribe contains 19 genera and approximately 230 species. The tribe Gesnerieae contains approximately 100 species with two to four genera depending on the treatment. Recent cladistic analyses of the tribes in the Gesneriaceae have indicated that *Sinningia*, *Paliavana*, and *Vanhouttea* are best removed from the Gloxinieae and placed in a separate tribe, Sinningieae. This study investigates the relationships of all but two of the remaining genera of the Gloxinieae, all but one of the Gesnerieae, and the relationship of the two tribes to each other. The Gloxinieae are found to be monophyletic exclusive of the Sinningieae and the epiphytic genus *Capanea*. *Capanea* is found to be placed best within the Episcieae, a tribe that contains the majority of the epiphytic species in the neotropical Gesnerioideae. The Gloxinieae include a monophyletic Gesnerieae, however, this result is weakly supported and may be an artifact of the analysis. The close sister group relationship of several genera is revealed and support is provided for the combination of *Parakohleria* into *Pearcea*. The two genera *Gesneria* and *Rytidophyllum* are in separate clades indicating that their separate generic status may be warranted.

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SOLTIS, DOUGLAS E.A., PAMELA S. SOLTIS^a, MARK W. CHASE^b, MARK E. MORT^{a*}, VINCENT SAVOLAINEN^b, SARAH HOOT^c, and CYNTHIA M. MORTON^d. ^aDept. of Botany, Washington State University, Pullman, WA 99164. ^bJodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, U. K. ^cDept. of Biological Sciences, University of Wisconsin-Milwaukee, Milwaukee, WI 53201. ^dDept. of Botany, University of Reading, Reading RG6 2AS, U. K. - Inferring complex phylogenies: an empirical approach using three large DNA data sets for angiosperms.

Phylogenetic relationships in large groups of organisms (e.g., angiosperms) remain enigmatic despite extensive study. Elucidating relationships in these large groups will likely require phylogenetic analysis of sequences and morphology representing hundreds of taxa. Due in part to the large number of possible solutions, the feasibility of phylogenetic analysis of large data sets has been much debated. Recently, however, simulation studies by Hillis using an 18S rDNA data set for angiosperms revealed that the model phylogeny for this large data set (228 taxa) could be accurately reconstructed with 5000 bp of sequence. To explore the feasibility of analysis of large data sets empirically, we conducted parsimony searches on a combined 18S rDNA, *rbcL*, and *atpB* data set for 193 taxa. Also analyzed were the individual data sets, as well as all pairwise combinations of these data sets. We also assessed the effects of combining these data sets on the internal support for clades, using the fast bootstrap (PAUP * 4.0). Our results indicate that combining data sets results in greatly enhanced resolution, as well as increased bootstrap support for clades, compared to analyses of individual data sets. Combining data sets also results in uniquely supported clades, i.e., clades that do not receive bootstrap support of 50% or more until two or more data sets are combined. This result is an apparent reflection of the synergism of the underlying signal provided by individual data sets. Another benefit of combining these large data sets is seen in computer run times. Using PAUP * 4.0, none of the individual, or pairwise combinations of data sets, swapped to completion. In contrast, multiple searches of the combined data set, using different starting trees, consistently swapped to completion, with an average run time of 55 hours.

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SOSA, VICTORIA*, DOLORES GONZALEZ AND CRISTINA BARCENAS. Departamento de Sistemática Vegetal, Instituto de Ecología, A.C. Km. 2.5 antigua carretera a Coatepec, 91000 Xalapa, Veracruz, Mexico. - Phylogenetic relationships in *Bletia* (Orchidaceae): inferences from morphological and ITS region of nuclear ribosomal DNA sequence data.

Bletia is a neotropical terrestrial orchid genus that includes 29 species. Most of the species are distributed in the pine-oak forests of the Pacific and central mountains of Mexico. A cladistic analysis based on morphological characters showed that one species considered a separate genus by some authors, *Crybe rosea*, constitutes a monophyletic group with the rest of species of *Bletia*. It also showed that three Cuban species do not belong within this genus. However, high levels of homoplasy obscured their phylogenetic relationships. In an attempt to better understand the phylogenetic relationships of *Bletia*, a cladistic analysis with sequence data from ITS 1 and 2 regions of nuclear ribosomal DNA was performed. Both data sets, morphological and molecular confirmed relationships between *B. urbana* and *B. campanulata* and, *B. roezlii* and *B. punctata*. However, the phylogenetic hypothesis from molecular and morphological analyses differs in some aspects. For example, *B. purpurea* is closely related to *B. reflexa* in molecular analyses while in morphological analyses is closely related to *B. campanulata*.

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ABSTRACTS

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