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data generally have placed the Commelinaceae as a sister group or close relative to the Pontederiaceae, countering morphological analyses that group the Commelinaceae with families of the Commelinales, including the Eriocaulaceae and Xyridaceae. However, other molecular studies utilizing restriction site data place the Commelinaceae apart from the Pontederiaceae and more in line with the traditionally delimited Commelinales. A cladistic analysis of this complex of monocots will be presented using all available data. Several competing cladistic relationships of the Pontederiaceae to other families will be discussed, including homoplasy of major features in seedling development, leaf morphology, floral anatomy, embryology, and palynology.

- 548** SINHA, N. AND ELIZABETH A. KELLOGG.* Section of Plant Biology, University of California, Davis, CA 95616 and Harvard University Herbaria, Harvard University, Cambridge, MA 02138.
The evolution of C₄ photosynthesis.

C₄ photosynthesis, an adaptation to warm environments, involves changes in the expression of multiple genes governing photosynthesis, intermediary metabolism, and leaf morphology. Such complexity should be difficult to evolve, yet the pathway has arisen multiple times in the flowering plants, and at least four times in the grass family alone. This paradox might be resolved if we could determine what aspects of the pathway are absolutely required for its function and/or which parts appear earliest either in ontogeny or phylogeny. Such investigations also address whether the pathway could be considered an "apomorphic tendency" where it occurs.

In the grass family, the pathway has arisen at least four times in a single clade. We compared the photosynthetic pathways across all four origins to determine whether the pathway is genetically and developmentally identical wherever it occurs. Data from the literature show that close vein spacing is a common feature of all C₄ origins, whereas decarboxylating enzymes differ.

We investigated gene expression of C₄ enzymes using immunolocalization procedures. The only gene expression patterns common to all origins of the pathway are an elevation of PEPC in mesophyll tissue and an increase of Rubisco expression in bundle sheath. All other changes in photosynthesis and metabolic genes are lineage-specific. LHCP protein expression may be reduced in the bundle sheath or not, malic enzyme and PPDK may be strongly expressed in bundle sheaths or expressed throughout the leaf. The central aspect of the pathway are thus the change in carbon acceptor, from RuBisCO to PEPC, and the decrease in vein spacing. This suggests that the evolution of the pathway is controlled by a regulator upstream of PEPC and *rbcS*, and that the regulator may be one that is also involved in determination of vascular development. Regulation of other genes (e.g. malic enzyme, LHCP) is not central to the evolution of the pathway.

- 549** SMITH, JAMES F.*, KIM D. BROWN, CYNTHIA L. CARROLL, AND DAVID S. DENTON.
Department of Biology, Boise State University, 1910 University Drive, Boise, Idaho, 83725. -
Tribal relationships within the Gesneriaceae: An assessment of three data sets.

No previous classification system for the Gesneriaceae has relied on cladistic analyses, and only a few have undertaken an investigation of the family as a whole. Instead, each has concentrated on either the New World, or Old World taxa. Recent investigations have utilized both morphological and molecular data to assess the tribal relationships within the Gesneriaceae. Morphological data have provided support for the monophyly of the neotropical Gesnerioideae and inclusion of the tribe Coronanthereae in this subfamily, but did not result in a monophyletic Cyrtandroideae. Tribal relationships were largely in congruence with traditional classification schemes for the Gesnerioideae with the exception of the Gloxinieae, and were in congruence with the Cyrtandroideae for all tribes except the large heterogeneous Didymocarpeae. A cladistic analysis of *ndhF* sequences has provided support for the monophyly of both Gesnerioideae and Cyrtandroideae, the placement of Coronanthereae in Gesnerioideae and congruence for tribal relationships within Gesnerioideae except for Gloxinieae. The *ndhF* sequences have provided evidence for monophyly of only the tribe Klugieae within the Cyrtandroideae. Although there are areas of congruence between the two analyses, there are also discrepancies. A third data set may resolve discrepancies between the two. Sequences of *rbcL* strongly support the monophyly of the family, but have provided little resolution among the genera. In order to assess more accurately the relationships of the tribes within this family, characters that are in conflict between the different data sets are examined in an attempt to determine the source of discrepancy.

- 550** SONDENAA, ANGELA C.* AND DOUGLASS M. HENDERSON. Department of Biological Sciences, University of Idaho, Moscow, Idaho 83544. -Reproductive biology, pollination, and floral rewards in the rare *Douglasia idahoensis* Henderson.

The Idaho mountain primrose (*Douglasia idahoensis*) is a regional endemic of central Idaho that occurs in small, isolated populations, and has low fecundity. Concern for its viability prompted an investigation of its reproductive biology at Square Mountain, Idaho. Breeding system experiments indicated that *D. idahoensis* is a