

Heidi Schmidt was approved as the managing editor by the Board of Directors for FNAA in the annual meeting, held in Saint Louis on October 14, 2007. In addition to the existing responsibilities of the managing editor, Heidi will also oversee the main aspects of the illustration process for all FNAAM volumes. Please contact her directly at [heidi.schmidt@mobot.org](mailto:heidi.schmidt@mobot.org) with any questions regarding the illustration protocol or visit the FNAA website at [www.fnaa.org](http://www.fnaa.org) for up-to-date information covering all aspects of the illustration process.

## New Welcome Packet Available for Contributors

*Heidi H. Schmidt, Managing Editor*

An updated Welcome Packet, covering FNAA guidelines for contributing authors, is available in either electronic or hard copy format upon request at [heidi.schmidt@mobot.org](mailto:heidi.schmidt@mobot.org). It includes:

- Overview and timeline of volume production
- Author's checklist for illustration preparation
- Author's checklist for manuscript preparation
- Contact information
- Guidelines for working with illustrations and manuscripts

## Future FNA Volumes With APG Influence

*Richard H. Zander, FNA Lead Editor – Bryophytes*

The FNA Association determined a short while back that future FNA treatments will follow Angiosperm Phylogeny Group (APG; <http://www.mobot.org/MOBOT/research/APweb/>) as best as possible. Details are being discussed and we have several alternative ways of revamping the classification to reflect APG.

Evolution results in both nested clusters of organisms based on analysis of expressed traits and branching lineages of organisms based on analysis of non-coding DNA traits. APG emphasizes the latter

at the expense of the former, often simply mapping expressed traits to inferred molecular lineages. Cronquist's system is a superb explication of nested groups based on expressed traits, and is an evolutionarily based classification. To the extent that APG classification violates such groupings with insistence on monophyly (versus paraphyly, while paraphyly often makes evolutionary sense and is the most parsimonious solution), and on insistence that ancestors never survive (however, although molecules continue to change, stabilizing selection may sustain a morphotype/biorole combination through many molecular splits). Thus, a possible paraphyletic ancestor of molecularly split morphological taxa is explained away as "massive homoplasy" and parallelism or convergence. There is, however, no empirical basis for monophyly as a thing in nature, or for the requirement that a species cannot be phylogenetically complex. A paraphyletic morphologically based group is the evolutionary null hypothesis that is not falsified by even well-supported monophyly of a molecular lineage.

If a molecular monophyletic group in APG is associated with groupings of expressed traits, well and good, but if it contravenes the Cronquistian system, we should find some way to avoid APG if possible and recognize the paraphyletic group. Rejecting the stricture of monophyly does not reject the taxonomic value of the inferred lineage and preserves decades of analysis of evolution of expressed traits.

The paradigm change in systematics is actually the substitution of a tractable problem (determining molecular lineages) for the wearisome, difficult problem of finding an acceptable evolutionary-based classification in the general absence of fossils and the prevalence of parallelism and convergence in expressed traits. But these are two different problems, and this simply substitutes a different basis for classification (phylogenetic) for the evolutionary classification we have been pursuing since Darwin. Lineages do not directly reveal changes in expressed traits that follow selection and drift. The latter may not be recoverable in anything like the detail that lineages can, but we must find some way to preserve what has been inferred about the evolution of expressed traits and

not fragment it in conformance to the enthusiasm of the moment.

As a major work, the FNA will be considerably influential in determining taxonomic concepts and philosophy over the next few decades, and we have a certain responsibility to the future. I believe

that molecular phylogenetics and (Cronquist's) evolutionary classification can be combined judiciously by the appropriate FNA experts with the courage to reject the impedimenta that phylogeneticists have used to promote using lineages alone as a basis of classification.

**FNA MODIFICATIONS TO VOLUMES 6, 7, AND 8: UPDATED DECEMBER 2007**

**Based on Angiosperm Phylogeny Group (Apg) Influence. Updated Dec 2007**

*James Zarucchi, FNA Vice President and Editorial Director*

Sequential APG family numbers added after family in parentheses following E. Haston et al., Taxon 56: 7–12. 2007. We have treatments in hand for nearly all taxa being moved into volumes currently in late-stage production.

**Vol. 6 [Hunt/2008]**

FAMILY	TAXON EDITOR	GENUS/	NOTES SPECIES
Cucurbitaceae (209)	Utech		23/69
Datisceae (211)	Poole	1/1	
Begoniaceae (212)	Poole	1/2	
Elatinaceae (245)	Utech	2/10	
Clusiaceae (257)	Utech	3/3	Removed two genera [see 2 down]
Podostemaceae (259)	Shultz	1/1	Moved here from Vol. 11 – MSS at MBG
Hypericaceae (260)	[Utech]	2/54	<i>Hypericum</i> (50) & <i>Triadenum</i> (4)
Violaceae (263)	Hartman +Rabeler	2/65	
Turneraceae (270)	Poole	2/3	
Passifloraceae (272)	Kiger	1/19	
Muntingiaceae (306)	Kiger	1/1	
Malvaceae (307)	Kiger	53/243	Tiliaceae & Sterculiaceae included
Tiliaceae ( — )	(Kiger)		Included in Malvaceae
Sterculiaceae ( — )	(Kiger)		Included in Malvaceae
Bixaceae (310)	Poole	1/3	
Thymelaeaceae (312)	Boufford	4/6	Moved here from Vol. 11 – MSS at MBG
Cistaceae (315)	Kiger	5/38	
Frankeniaceae (327)	Poole	1/5	<Should have been in Caryophyllales>
Tamaricaceae (328)	Kiger	1/8	<Should have been in Caryophyllales>
Droseraceae (331)	Morin	2/13	<Should have been in Caryophyllales>

**Imported to Vol. 6:** Podostemaceae (from Vol. 11), Thymelaeaceae (from Vol. 11)