New England Botanical Club - Minutes of the 1009th Meeting
3 September 2005
Karen Lombard, *Recording Secretary*

The 782nd meeting of the New England Botanical Club, being the 1009th since its original organization, was held on Friday, September 3, 2005, in the Lecture Room of the Fairchild Biochemistry Building, Divinity Avenue, Cambridge MA.. There were 35 members and guests in attendance.

Council Vice President, Karen Searcy, introduced Tatyana Livshultz, who gave a talk entitled "Systematic Studies in the Apocynaceae: Implications for the Evolution of Complex Pollination Mechanisms. Dr. Livshultz is currently a Mercer Fellow at Arnold Arboretum at Harvard University. She will move shortly to Omaha, Nebraska to take a position as Assistant Professor in the Biology Department. Dr. Livshultz gave an introduction to the Apocynaceae and then discussed complex pollination mechanisms and phylogeny within this family.

The Apocynaceae contains 400 genera and about 5000 species with the majority of the diversity in the tropics. In the Northeastern U.S. only 10 genera are present (6 native) and 31 species (25 native) and only two genera are native to New England (*Apocynum* and *Asclepias*). The family is characterized by milky latex, paired fruits, a secretory stylehead, and contorted propeller-like corollas. One member of the family, *Catheranthus roseus,* is used medically for chemotherapy and the-well known monarch butterfly (*Danaus plexippus*) feeds - the genus *Asclepias*. Another species is used as a hallucinogen (*Tabernanthe iboga*) by the Bwiti religion of West Africa and another as food in Southeast Asia (*Telosma cordata*).

The family has been classified into five subfamilies, the Rauvolfioideae, Apocynoideae, Periplocoideae, Secamonoideae, and the Asclepiadoideae by Endress & Bruyns (2000), based on increasing complexity in pollination morphology. Endress and colleagues have hypothesized two evolutionary trends, one of which focuses on the attachment and functional integration of the anthers and stylehead and the other on the amount of aggregation of pollen grains with each subfamily. The ancestral mechanism is hypothesized to be similar to modern Rauvolfioideae where the pollen is in monads. Intermediate phases involve the anthers attaching to the stylehead to form a barrier "cone" , presumably to reduce self-pollination, dispersal of pollen in tetrads, and restriction of stylehead secretion to five discrete zones. The most highly modified subfamily is the Asclepiadoideae with style head secretion molded into five solid structures, known as translators, which hold pollinia (each pollinium is a fused mass of all the pollen grains from one anther sporangium). The pollinating insect carries away the translator and attached pollinia to another flower.

Dr. Livshultz and colleagues decided to test the hypothesis that the subfamilies represent increasing complexity by making predictions about the phylogeny within the Apocynaceae based on the pollination mechanisms and pollen aggregation and then testing this with a genetic sequenced based phylogeny. She tested 153 species using molecular and morphological data.

Results have demonstrated that the subfamilies are not stages in an evolutionary trend, but that several characters have evolved multiple times. Reconstruction of ancestral states shows that translators have evolved at least twice and aggregate pollen has evolved three times independently. This work suggests that the subfamilies will need to be reorganized and it appears that biogeographic distributions may be the key to understanding evolution in this family. An early researcher, John Macfarlane suggested in 1933 that a group of African Apocynaceae are most closely related to the Asclepiadoideae in spite of their relatively unmodified floral morphology. It is unclear how he made this conclusion, however, the new phylogenetic research supports his work. In addition, one species in eastern North American of the Apocynoideae, *Trachelospermum difforme*, was thought to be the only representative of the genus on this continent with the remaining 13 species in Asia; instead it belongs to an almost exclusively American lineage. This species will need to be renamed as a result of this research.