

## PHYLOGENETIC ANALYSES WITHIN THE SUBCLASS NAUTILOIDEA AND COMPARISON TO EXISTING EVOLUTIONARY SCENARIOS

SHELLENBERG\*, Stephen A. and BOTTJER, David J., Department of Earth Sciences, University of Southern California, Los Angeles, CA 90089-0740, U.S.A. (e-mail: schellen@earth.usc.edu, dbottjer@earth.usc.edu)

The cephalopod subclass Nautiloidea represents one of the early metazoan pioneers of the pelagic realm as well as the root stock of the subclasses Ammonoidea and Coleoidea. Although ammonoids have historically garnered greater interest given their high abundance and excellent biostratigraphic utility, early to middle Paleozoic nautiloids express morphologic diversity arguably greater than that of the ammonoids. This diversity has led to numerous questions (and answers) with regard to functional morphology, paleoecology, and evolutionary trends within the Nautiloidea.

Requisite for accurate and precise answers to such questions is a classification that best reflects the true phylogeny. The major structure of the existing classification of the Nautiloidea was erected by a relatively small number of systematists. These workers derived their evolutionary scenarios (*sensu* Eldredge, 1979) under the paradigm of evolutionary taxonomy. As such, homology, degree of divergence, *a priori* character weighting, and adaptational narrative are often deeply entrenched within their evolutionary scenarios, but generally not in an explicit manner. Such an approach makes hindsight determination of the rationale and justification for the existing classification over a great number of other possibilities difficult.

A cladistic approach is currently underway to explore evolutionary relationships within the Nautiloidea for the following methodological reasons: 1) The method requires critical comparison of taxa to erect discrete characters and character states and careful determination of each character state for each taxon. 2) The data and method are inherently explicit versus non-comparable intuitive or poorly documented classifications (*i.e.*, evolutionary taxonomy). 3) The analysis implicitly strives to recognize the most parsimonious hypothesis of evolutionary relationship.

Cladistic analyses may be conducted at any rank, yet each employed terminal taxon is assumed to be a monophyletic clade. Use of high-rank taxa may therefore defeat the entire purpose of the cladistic analysis, whereas utilizing individual species also proves problematic (*e.g.*, record completeness, etc.). As such, the ongoing cladistic study involves both familial- and generic-rank analyses within individual nautiloid orders. Upon completion of analysis of all orders, taxa at each rank across the subclass will be pooled and re-analyzed with comparison to one another (*i.e.*, families versus genera as terminal taxa) as well as to the existing classification.

Such iterative cladistic analyses will produce the most parsimonious hypothesis of relation within the Nautiloidea. The cladogram may then serve as a testable, biologically meaningful platform for exploring the group's evolution in response to external stimuli (abiotic and biotic) and internal constraints during the Paleozoic.

Eldredge, N. 1979. Cladism and common sense, p. 165-198. *In* J. Cracraft and N. Eldredge, (eds.), *Phylogenetic Analysis and Paleontology*. Columbia University Press, New York.