An attempt to reconstruct phylogenetic relationships within Caribbean nummulitids: simulating relationships and tracing character evolution

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Phylogenetic analysis and trees based on molecular data are broadly applied and used to infer genetical and biogeographic relationship in recent larger foraminifera. Molecular phylogenetic is intensively used within recent nummulitids, however for fossil representatives these trees are only of minor informational value. Hence, within paleontological studies a phylogenetic approach through morphometric analysis is of much higher value. To tackle phylogenetic relationships within the nummulitid family, a much higher number of morphological character must be measured than are commonly used in biometric studies, where mostly parameters describing embryonic size (e.g., proloculus diameter, deuteroloculus diameter) and/or the marginal spiral (e.g., spiral diagrams, spiral indices) are studied.

For this purpose 11 growth-independent and/or growth-invariant characters have been used to describe the morphological variability of equatorial thin sections of seven Carribbean nummulitid taxa (Nummulites striatoreticulatus, N. macgillavry, Palaeonummulites willcoxi, P.floridensis, P. soldadensis, P.trinitatensis and P.ocalanus) and one outgroup taxon (Ranikothalia bermudezi). Using these characters, phylogenetic trees were calculated using a restricted maximum likelihood algorithm (REML), and results are cross-checked by ordination and cluster analysis. Square-change parsimony method has been run to reconstruct ancestral states, as well as to simulate the evolution of the chosen characters along the calculated phylogenetic tree and, independent - contrast analysis was used to estimate confidence intervals. Based on these simulations, phylogenetic tendencies of certain characters proposed for nummulitids (e.g., Cope's rule or nepionic acceleration) can be tested, whether these tendencies are valid for the whole family or only for certain clades. At least, within the Carribean nummulitids, phylogenetic trends along some growth-independent characters of the embryo (e.g., first chamber length and P/D ratio) and some growth-invariant characters of the chamber sequence (e.g., backbend angle, initial chamber base length and chamber length increase) are evident.