

Molecular evolution of the foraminiferal SSU rDNA: Prospects and pitfalls

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Ribosomal DNA (rDNA) sequences have been extensively used for benthic and pelagic foraminifera as a molecular marker to infer phylogenetic hypotheses. However, molecular phylogenetic studies on a broad taxonomic set of foraminifera are characterized by a generally low resolution caused by the low sequence divergence within the conserved sequence regions that can be unambiguously aligned. Only a few moderately to well-supported lineages (e.g. miliolids, “polythalamous clade”, spinose planktonic taxa) have been identified; the phylogenetic backbone remains completely unresolved. Furthermore, the phylograms’ topologies and the inference of an “all foraminiferal root” appear to be heavily influenced by taxon sampling and outgroup taxa that are used. Using phylogenetic networks, we can visualize the extent and systematic bias induced by incompatible phylogenetic splits that are predominant within the generally alignable portions of SSU (small subunit) rDNA data and thus hindered phylogenetic tree building up to now. We can demonstrate that SSU sequence data of foraminifers cannot be used *ad hoc* to infer an “all-foraminiferal” phylogenetic hypothesis. However, the particular data structure of the foraminiferal SSU showing an alteration between highly conserved and highly divergent sequence portions provides a possibility to evaluate phylogenetic alternatives indicated by network analysis. Identification of evolutionary hotspots for different taxonomic levels can reveal deep insights in the pathways of molecular evolution of the foraminiferal SSU. Sequence motives, e.g. in the DNA region coding for the terminal loop of helix 44, and alignability of variable regions are diagnostic for many taxonomic groups. Thus, an adequate pre-analysis filtering and organisation of the SSU rDNA data and taxa analysed can help to produce a data set assessable for phylogenetic studies, which focuses on particular relationships and evolutionary hypotheses.