

MICROPALAEONTOLOGY NOTEBOOK

The molecular phylogenetic status of *Elphidium williamsoni* (Haynes, 1973) as inferred from partial 18S-rDNA sequences

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Comparative studies on DNA nucleotide sequences have revolutionized our understanding of the phylogenetic relationships of many organisms and have become an important tool in evolutionary, ecological and palaeobiological inquiry. We have analysed partial small-subunit 18S sequences (srDNA) of *Elphidium williamsoni* (Haynes, 1973), a common intertidal benthic foraminiferid from the North Sea. The molecular phylogenetic analysis of the ribosomal rDNA sequence data indicate that *E. williamsoni* constitutes a well-defined genetic entity that is closely related to *Elphidium aculeatum*.

Elphidium williamsoni is a prominent and frequently encountered foraminiferid in the North Sea and other tidal flats. It was originally described by Williamson (1858) as *Polystomella umbilicata* and subsequently renamed by Haynes (1973). Because of its phenotypic similarities with other elphidiids, this species has been frequently confused with, for example *E. excavatum* or *Cribronion alvarezanum* (see Haynes for discussion). The molecular data provided here, and their direct comparison to other benthic foraminifera including one elphidiid, may therefore provide additional insight into the taxonomic status and the validity of this species.

Individuals of the foraminiferid *Elphidium williamsoni* were collected in October 1997 from the intertidal mud flats of the Crildumersiel at the outer Jade Bay near Wilhelmshaven, North Sea (see Langer *et al.*, 1989 for details). The mud flats are characterized by fine-grained, muddy sediments containing high contents of organic material. In the laboratory, specimens were transferred into petri dishes, examined and cleaned under a stereo microscope. Living specimens of *E. williamsoni* were picked out separately and placed into clean glass dishes containing filtered seawater. A single specimen was then ground in 1.5 ml reaction tubes and genomic DNA was immediately extracted, amplified by the PCR method, cloned and sequenced as has been described in Langer & Leppig (2000). The amplified product is located at the 3' end of the foraminiferal 18S gene and comprises 835 base pairs (bp). A total of three clones were sequenced successfully and all of them had identical sequences. The foraminiferal nucleotide sequence reported in this study has been submitted to GenBank and assigned accession number AF286476. The sequence of *E. williamsoni* is somewhat shorter than those of other benthic foraminifera, but of approximately equal length to *E. aculeatum* (779 bp, GenBank Acc. No. Z69618).

The srDNA molecular phylogeny of benthic foraminifera (Fig. 1) reveals a pattern of evolution that is largely congruent with the evolutionary hypothesis deduced from the fossil record and comparative biological studies (see also Pawlowski *et al.*, 1997; see however Pawlowski, 2000). The root of the tree is represented by *Allogromia* (a taxon with an uncalcified proteinaceous test), followed by skeletonized unilocular, bi-triserial, and low-trochospiral agglutinated and other hyaline-perforate taxa and a distantly related clade of the porcelaneous miliolids (*Peneroplis* and *Quinqueloculina*). Molecular phylogenetic analysis of *Elphidium williamsoni* from the North Sea and comparison with other benthic foraminifera shows that this species is closely related to *E. aculeatum* but represents a distinct genetic entity. The comparison of 575 unambiguously aligned sites shows both elphidiid taxa to differ by 2.5%. Full-length analysis of the entire gene fragment between *Elphidium aculeatum* and *E. williamsoni* shows both species to differ by more than 11%, a genetic distance that is congruent with its phenotypic treatment as a separate species.

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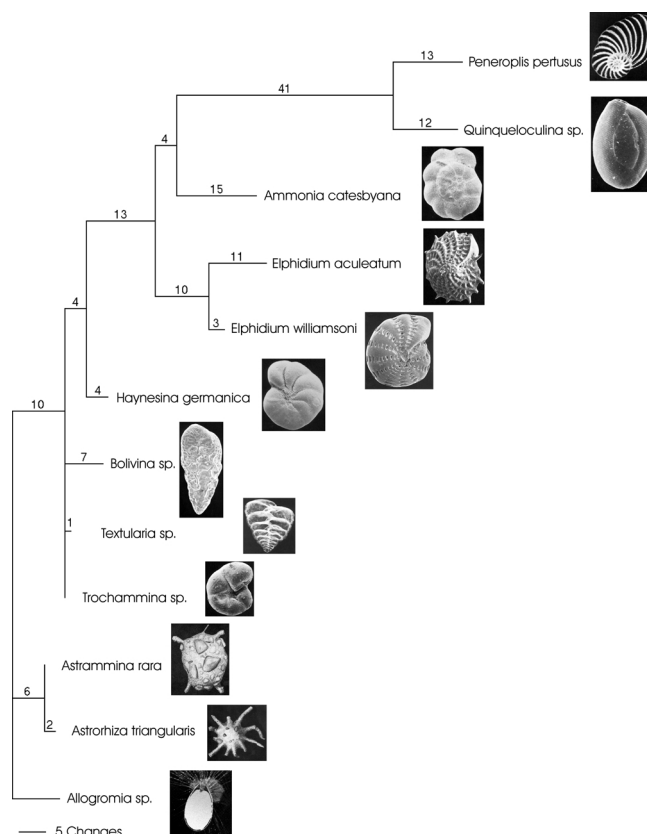


Fig. 1. Molecular phylogenetic analysis was conducted by employing the phylogenetic software program PAUP (for analytical details see Langer & Leppig, 2000). The analysis is based on 575 unambiguously aligned sites and includes sequences from species with the following GenBank Accession numbers: X86093, Z69609, Z69608, Z69612, Z69610, Z69613, AF190724, AF286476, Z69618, AF190872, Z69605 and Z69604. Note that the pictures of taxa attached to the tree do not represent the original specimens sequenced. The srDNA nucleotide alignment of all sequences is available from the author on request.

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