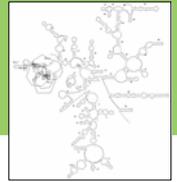


Molecular Morphology of Bivalve 18S rRNA



Susanne Feistel, Gerhard Haszprunar
 BioZentrum der LMU München, Großhadernerstraße 2, 82152 Planegg, Germany
 feistel@zi.biologie.uni-muenchen.de



Introduction

The **PHYLOGENY OF BIVALVES** (Mollusca) consisting of about 20.000 species is still uncertain. Conventional morphology and sequence analyses did not provide conclusive results beyond the four subtaxa Protobranchia, Pteriomorpha, Heterodonta and Schizodontia. This study is concentrated on the **FOLDING PATTERNS OF SLOWLY EVOLVING 18S RDNA** molecules in expectation of finding "deep phylogenetic" information, i.e. pre-Cambrian or Cambrian structural signatures.

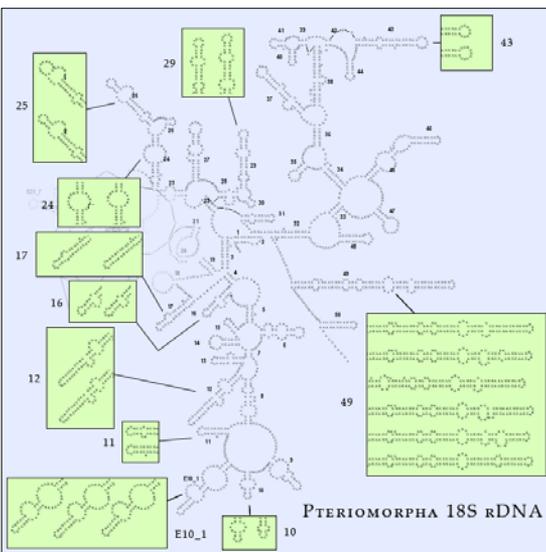
Material & Methods

Sequences of bivalve 18S rDNA with lengths of about 1800 base pairs each, available from Genbank and the European Ribosomal Database, have been studied, with the primary focus on the Pteriomorpha. **SECONDARY STRUCTURES** have been generated by means of a standard procedure (**RNAfold / RNAsalsa** i.e. the "Vienna Server"; **RNAViz, xRNA**) as a primary data-basis (Hofacker 2003, Nucleic Acids Res. 31: 3429-3431).

Constructed by a **MINIMUM GIBBS FREE ENERGY (MFE) PRINCIPLE**, these foldings show high variability, on average at about 40 strand sites.

By contrast, **"NEAR-NATURAL" STRUCTURES** folded with a structural constraint show much less variability and much higher stability of the characters to be classified.

MFE	vs.	Constraint
< 10% conservative great number of characters 6-150 bases per character 80% in double bindings		> 80% conservative few characters 10-30 bases per character 90% in double bindings
phylogenetic groups discernible		phylogenetic groups clearly discernible
too much noise to support deep nodes		no resolution within families promising for deep node resolution



18S rDNA folded with structural information in RNAViz („Near Natural“), highlighted are examples of molecular morphological characters

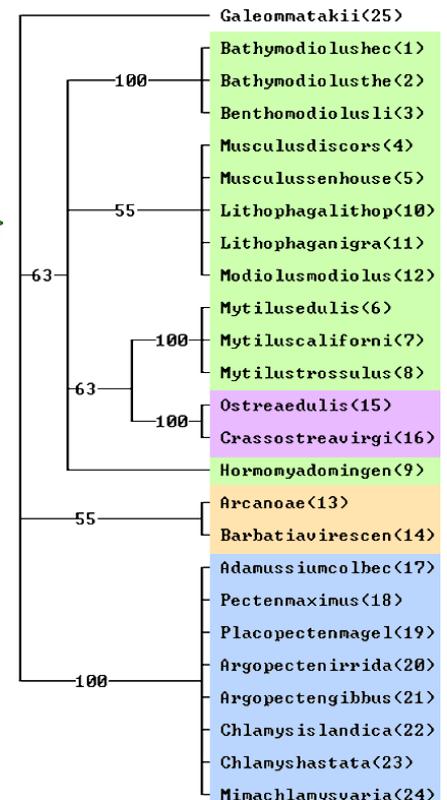
Discussion

MFE foldings are questionable in algorithmic details and currently under discussion. They are generated independent of any natural functionality and thus completely artificial structures. Even small differences in sequences can cause different characters amplified through the folding algorithm.

The current step intended is the **SYSTEMATIC NEAR-NATURAL FOLDING** of bivalve 18S rDNA via the RNAFold / RNAsalsa algorithms and subsequently their morphological analysis. RNAsalsa allows folding of closely related species with only structural information on one species, but at the same time demanding a discussion about folding with a consensus constraint, thus possibly creating artificial similarities. Also, particular detection problems arise from double bindings and secondary and tertiary loop structures. Present efforts concentrate on a systematic solution for these difficulties.

The phylogenetic analysis of the **MFE STRUCTURES** revealed that despite of some phylogenetic information the matrix included too much 'noise' to result in statistic support of deep nodes. In the first preliminary phylograms derived, **PHYLOGENETIC GROUPS WERE CLEARLY DISCERNIBLE BUT ALWAYS INTERSPERSED WITH RUNAWAYS** for unclear reasons. A clear result for bivalve phylogeny could not be found.

← A **"NEAR-NATURAL" FOLDING** shows much less variability in its structure. More than 80% of it is conservative leaving only few and small clusters for morphological analysis. Even more bases than in MFE structures are bound in double bindings thereby restricting the development of new morphological characters through point mutation. A preliminary analysis of a character matrix of 24 pteriomorph species clearly supports previously discerned families – **most taxa remain monophyletic**, with the exception of paraphyletic Mytiloidea. A clear resolution within the families was due to too few characters not to be expected. All the same it promises good results in deeper nodes. →



Simple parsimony analyses of the constraint character matrix of pteriomorph bivalves: Mytiloidea, Arcidae, Ostreidae, Pectinoidea, Outgroup