Molecular Morphology of Bivalve 18S rRNA

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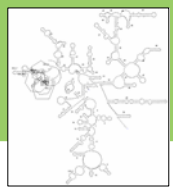


Introduction

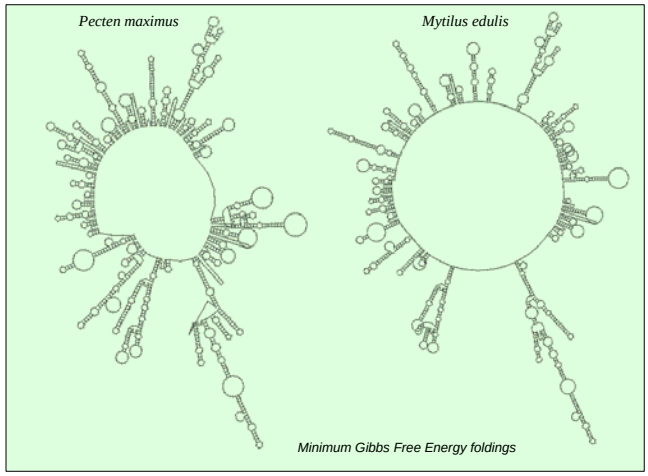
The **PHYLOGENY OF BIVALVES** (Mollusca) consisting of about 20.000 species is still uncertain. Conventional morphology and sequence analyses did not provide conclusive results beyond the four subtaxa Protobranchia, Pteriomorpha, Heterodonta and Schizodonta. This study is concentrated on the **FOLDING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

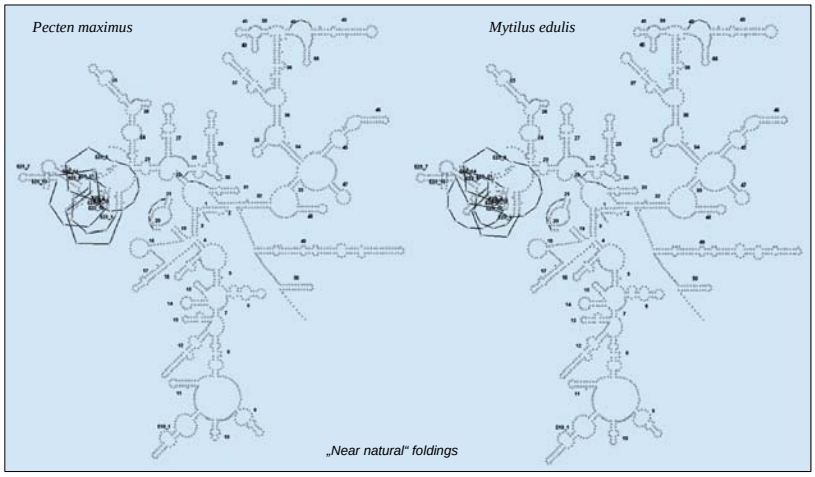
Material & Methods

About 170 sequences of bivalve 18S rDNA with lengths of about 1800 base pairs each, available from Genbank and the European Ribosomal Database, have been studied, covering the four subtaxa. **SECONDARY STRUCTURES** have been generated by means of a standard procedure (**RNAFold** i.e. the "Vienna Server"; **Mfold**, **RNAViz**) 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. They were individually quantified and via sequence alignment homologized for the generation of a species-species property matrix.

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



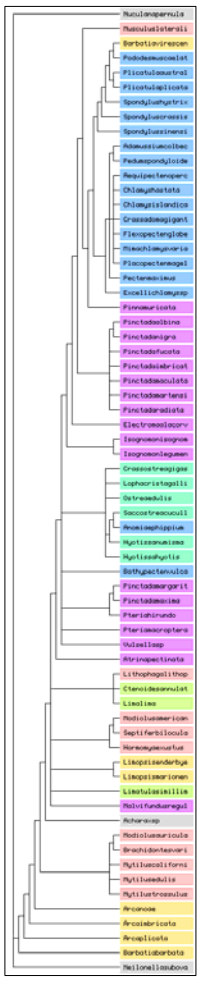


Results

By **VISUAL INSPECTION** of the **MFE STRUCTURES**, a total of more than **500 MORPHOLOGICAL CHARACTERS** of the DNA folding patterns could be detected from the entire set of species. Characters vary between 6 and 150 bases involved, with shorter characters (less than 25 bases) being most frequent. About 80% bases are in double bindings. The phylogenetic analysis 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. More than 80% of the structure is conservative leaving only few and small clusters for morphological analysis.



Simple parsimony analyses of the MFE character matrix of pteriomorph bivalves:
Mytiloida, Arcoida, Limoida, Ostreoida, Pectinoida, Pterioida, Outgroup

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 little differences in sequences can cause different characters amplified through the folding algorithm.

The current step intended is the **SYSTEMATIC COMPARISON OF MFE FOLDINGS WITH NEAR-NATURAL FOLDINGS** via the RNAFold and RNAlifold algorithms. In the latter technique, particular detection problems arise from double bindings and secondary and tertiary loop structures. Present efforts concentrate on a systematic solution for these difficulties.