

An 18 S rDNA based molecular phylogeny of the Mysidacea (Crustacea)

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The phylogeny of the Mysidacea, an order of small, mostly hyperbenthic peracarid crustaceans, was studied using the base sequence of the 18S rDNA gene. 25 species, belonging to the most important taxa, were analysed. To this end the DNA of the specimens was isolated and the gene amplified in a PCR-reaction, using two oligonucleotide primers. These primers flanked the 18S region of the DNA, which was to be amplified. The technique used for sequencing the gene was the dideoxymethod developed by Sanger. The sequences were automatically aligned using ClustalW 1.74. The resulting alignment was improved by hand using DCSE to obtain the optimal alignment. Aligning is a very important step because the alignment expresses the distance between two species and is the basis of the derived phylogeny. As a next step, molecular phylogeny was inferred using three different methods: Neighbour Joining (NJ), Maximum Parsimony (MP) and Maximum Likelihood (ML). The programs used were, for NJ, TreeconW and PAUP* version 4.04b4, for ML, PAUP* version 4.04b4 and for ML, Puzzle 4.0.2 and FastDNAmI version 1.2.1. Generally the results from these three methods, using the different programs, are very similar. The Leptomysini are clearly monophyletic, but the genus *Mysidopsis*, is, in its present definition, polyphyletic. The Gastroasaccinae, without the genus *Anchialina*, are monophyletic as well and the traditional division in genera within the taxon is supported. The Mysini are clearly not monophyletic. On the basis of these data, this problem can be solved by incorporating the clade, consisting of *Neomysis*, *Acanthomysis* and *Holmesimysis*, in the Leptomysini. The genus *Mysidium* cannot be placed unambiguously in the phylogeny using this set of data. The results from the analyses, using the three different methods, also clearly show that the 18S rDNA does not contain enough information to fully resolve relationships between the higher taxonomical units within the Mysidacea.