

8. Summary

This thesis investigates the phylogenetic relationships of sedentary polychaetes using molecular sequence data. The results are presented in five chapters (chapter 2-6), which are based on two published and three submitted manuscripts. A general introduction (chapter 1) and a general discussion (chapter 7) are given.

In Chapter 2: *A contribution to sedentary polychaete phylogeny using 18S rRNA sequence data*, Chapter 3: *New insights into polychaete phylogeny (Annelida) inferred from 18S rDNA sequences*, and Chapter 4: *18S rDNA and polychaetes*, polychaete phylogeny is investigated using a larger taxon sampling. Due to an enhanced taxon sampling, evidence for the monophyly of many of the investigated traditional polychaete families is presented and the usefulness of 18S rRNA gene sequence data for the inference of the phylogenetic position of “enigmatic” taxa is demonstrated. Thus a close relationship between the unsegmented Echiura and the Capitellidae is strongly supported by all analyses independent of the chosen method.

In Chapter 5: *Phylogenetic relationships and evolution of Orbiniidae (Annelida, Polychaeta) based on molecular data*, the phylogenetic relationships of orbiniids are inferred by using nuclear 18S rRNA gene and mitochondrial 16S rRNA gene data. The results are discussed in respect to phylogenetic hypotheses, which have been derived from morphological data by previous authors. Judging the results of the present molecular analysis, it is reasonable to conclude that the morphological characters which are presently used for genus diagnosis in the Orbiniidae are not phylogenetically informative enough for cladistic analysis. No support is found for the traditional classification as well as for the hypothesis that taxa of the Protoariciinae represent juveniles of Orbiniinae. Instead, in the case of *Protoaricia oerstedii* strong support for a progenetic origin is given.

Chapter 6: *Molecular phylogeny of lugworms (Annelida, Arenicolidae) inferred from three genes*, deals with the relationships of arenicolids. The monophyly of maldanids and arenicolids is sustained by this analysis. A previously proposed progenetic evolution of *Branchiomaldane* finds additional support in this analysis.

All these results demonstrate the usefulness of 18Ss sequence data to address questions concerning phylogenetic hypotheses of annelid relationships on different hierarchical levels..