





A PRELIMINARY MOLECULAR PHYLOGENY OF SYNGNATHIDAE

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DISCUSSION In this dataset, maximum parsimony and Bayesian analyses appear to be more sensitive to character sampling than to taxon sampling, stressing the importance of increased sampling of molecular markers. The sensitivity of our data to smaller character sampling forced us to consider only 17 of 60 taxa and four of six markers, or un arraning dehead. In our arrand datacter forced us to consider only 17 of 60 taxa and four of six markers from our growing dataset. In our current dataset, we do not have the same number of taxa for each gene and only 17 taxa are represented by data for all four genes. We analyzed trees from maximum parsimony and Bayesian analyses on a variety of character combinations including individual genes, ribosomal genes and the combined partitions with the exclusion of taxa with missing data.

None of the individual genes recovered similar None of the individual genes recovered similar topologies except for the consistent pairing of the weedy and leady sea dragons, *Phycodurus eques* and *Phyloptexy taeniolatus*.
 Both analyses of the combined data were identical except for the placement of *Idiotropicsis lumnizear* (Figure 1).
 Of all our analyses, the combined analysis provided the best support for the systematic relations determined by the earlier morphological work of Heraid (1959) and Dawson (1985), namely Hallichthys (previously Acentronura) and *Hippocampus* as sister tax.

Hippocampus as sister taxa. The combined analysis does not support the

division of syngnathids into two subfamilies, the Syngnathinae and Hippocampinae. Syngnthinae ar to be paraphyletic.

At this stage of our study, single gene or small partitions of our overall dataset produce unpredictable and inconsistent topologies, regardless of the number of OTUs. Greater sampling of molecular markers is needed to recover a more robust phylogenetic hypothesis.

generated, spanning over 50 genera and 5 genes. generated, spanning over 50 genera and 5 genes. Analysis of individual genes resulted in poorly supported phylogenies and inconsistent relationships (data not shown). However, maximum parsimony and Bayesian analyses recovered similar topologies for each partition analyzed and recovered nearly the same tree in combine analysis of the 12S, 16S, COI and RP1 (Figure 1). More extensive taxon sampling and additional nuclear sequence data are required to further evaluate evolutionary relationships among this unjue aroun of evolutionary relationships among this unique group of fishes. We are sampling additional taxa for the genes presented and have begun sequencing the mitochondrial genes ND1, cytochrome b (cyt b) and other nuclear markers to further explore the evolutionary relationships of the Syngnathid fishes

INTRODUCTION

A modern DNA-based hypothesis of the phylogenetic relationships among Syngnathid fishes is a scientific priority for documenting and conserving marine biodiversity.

Syngnathid fishes are a diverse, unique and charismatic group that include 54 genera and at least 278 vaiid species of pipefishes, seahorses, sea dragons and pipehorses. They have a highly unusual reproductive strategy, exhibiting sex role reversal and male pregnancy with live birth in many species.

 Many syngnathids are heavily exploited for traditional Chinese medicines and the aquarium trade and they occur in some of the ocean's most threatened habitats.

Conservation and management of syngnathids is undermined by their challenging alpha taxonomy and their systematic relationships are unresolved at multiple levels. Many genera are monotypic, yet no study has measured the degree of evolutionary uniqueness of these lineages.

A robust phylogenetic hypothesis of syngnathid Particular physicenesis of syngheating relationships will aid in their conservation. Unresolved phylogenetic relationships make species identification inaccurate and misleading. Management plans are difficult to implement and the status of each species remains undefined.

 Here, we present DNA sequence data derived from four markers: the nuclear intron RP1 of the 57 ribosomal protein; the mitochondrial cytochrome oxidase I (COI) and ribosomal RNA 12S and 16S genes. Preliminary analyses recover a phylogenetic hypothesis for seventeen genera, including several poorly known and monotypic genera and seven genera that have never before been sequenced.

METHODS

METHODS Specimens were obtained in collaboration with multiple museum collections and directly from the field. Extraction, amplification and sequencing of DNA were performed using standard techniques. ABI 310XL chromatograms were assembled and confirmed in Sequencher 4.7 (Gene Codes Corp.) and BioEdit 7.0.3 (Hall, 1999). Sequences published on Genbank were used to expand our taxon sampling in 12S and 16S rRNA datasets (Wilson et al., 2001) and to fill im signin mitchondrial data (Kawabara et al. and to fill in missing mitochondrial data (Kawahara et al., 2007). Phylogenetic relationships were reconstructed using arsimony and Bayesian likelihood methods, with node upport calculated through full heuristic bootstrap resampling parsin

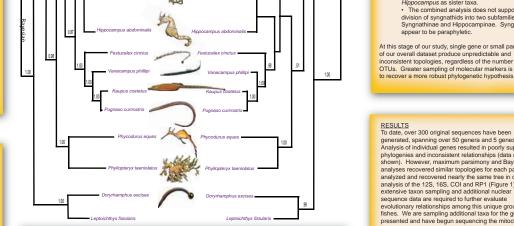


Figure 1. Trees recovered from Bayesian and maximum parsimony analyses of combined character sets 12S, 16S, COI and RP1. Node support is indicated by posterior probabilities in the Bayesian tree on the left, and by bootstrap support values on the right.

NEXT STEPS

1) Additional taxon sampling for the genes presented.

2) Increased character sampling. We have begun sequencing the mitochondrial genes cytochrome b (cyt b) and NADH 1 and other nuclear markers to further explore the evolutionary relationships of the Syngnathid fishes.



ACKNOWLEDGMENTS

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