



## **A phylogenomic analysis of Syngnathidae based on high-throughput sequencing of more than 1000 genetic regions**

\*\*\*\*Please note the additional authors 7 and 8 given in the institution block.\*\*\*\*

Josefin Stiller, Healy Hamilton, Sj Longo, Np Saarman, Graham Short, P Wainwright

**Presenting Author:** Josefin Stiller

Author 7 WB SIMISON, Author 8 GW ROUSE, Author 1 and 8 Scripps Institution of Oceanography, University of California San Diego, USA, Author 2 NatureServe, Arlington, Virginia, USA, Author 3 and 6 University of California Davis, USA, Author 4 Yale University,

Syngnathidae are a charismatic group that is increasingly being studied for their intriguing reproductive mode and unique morphology. In order to give a perspective on the evolution of syngnathids, including biogeographic trends and evolution of morphological and life history characteristics, a well-resolved and taxonomically-broad phylogeny is needed. Previous studies were often limited in taxonomic breadth and had little resolution at deeper nodes due to the limited availability of genetic markers. These studies have found incongruence in phylogenetic signal from different types of markers and sampling schemes. The incongruence observed leave some important questions such as the phylogenetic placement of seahorses and the taxonomic relationships among congeneric species from the Atlantic and Indo-Pacific unresolved. The advent of high-throughput sequencing of numerous loci for phylogenetics will largely resolve the topology of deeper nodes, shifting the bottleneck to the acquisition of samples and towards bioinformatic analysis of the data. We have sourced >265 individuals, representing 177 species of pipefishes, pipehorses, seadragons and seahorses from museum collections, aquaria and personal field collections. We will generate genomic data for these samples using targeted capture of 1340 ultraconserved elements (UCEs). The resulting phylogenetic tree will be integrated with fossil and biogeographic information to date key nodes of the phylogeny. This taxonomically comprehensive genome-scale analysis and time-calibrated phylogeny will be an important resource for syngnathid biologists interested in studying the evolutionary history of this remarkable clade of fishes.

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