



Key Losses in Hox Coding and Regulatory Elements in the Gulf Pipefish

AM Fuiten, S Bassham, CM Small, WA Cresko

Presenting Author: Allison Fuiten

Institute of Ecology and Evolution, Department of Biology, University of Oregon, USA

Abstract: The elongated skull and axial skeleton are key evolutionary novelties of the syngnathid body plan, but their genetic basis remains unclear. Hox genes are organized into conserved clusters in the genome and play a role in axial and craniofacial bone development. Changes in Hox gene expression and cluster content are suggested to underlie macro-evolutionary modifications of the body plan. We hypothesized that changes in Hox cluster content in terms of genes, microRNAs, and regulatory elements have contributed to the evolution of the elongated syngnathid body plan. To test this hypothesis, we sequenced, annotated and confirmed the orthology of 49 Hox cluster genes and seven Hox cluster microRNAs in the fully assembled Gulf pipefish genome. Additionally, we searched for cis-regulatory elements co-localized near Hox genes. Our results indicate that Gulf pipefish have a few key losses in genes and regulatory elements that are potentially related to the derived axial and craniofacial traits found in the pipefish lineage. The Hox 7 genes, which have been hypothesized to be associated with rib loss, have been lost in pipefish and appear to have deteriorated independently in the pufferfish. We found a unique loss of the *eve1*, a *hox-ba* cluster gene expressed during teleost tooth development. We identified a convergent loss of the *mir-196b* microRNA in the *hox-ba* cluster, which is known to affect the number of vertebrae that develop in teleost fish. We conclude that a subset of pipefish Hox genes may be associated with body plan diversification via differential regulation and gene loss.

Keywords: Evolution, Genomics