



The Gulf Pipefish Reference Genome Facilitates Genetic Study of Derived Morphologies and an Evolutionary Novelty

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Abstract: Evolutionary origins of derived morphologies ultimately stem from changes in protein structure, gene regulation, and gene content. Quality reference genomes are powerful resources in any endeavor to understand how these molecular changes have influenced phenotypic evolution. We generated a chromosome-level reference genome for the Gulf pipefish, a well-studied species with many of the derived morphological features embodied by syngnathid fishes, including male pregnancy, a true evolutionary novelty. We documented genetic changes in the pipefish lineage, including gene loss, of conserved developmental genes such as *hox*, *dlx*, *tbx*, and *pitx* families, candidate mechanisms for the evolution of an elongated axis and the loss of ribs, pelvic fins and teeth. We identified marked transcriptional differences related to innate, but not adaptive immunity in pregnant versus non-pregnant brood pouch tissue. For the first time, we describe the genomic organization of rapidly diverging patristacins, duplicated metalloproteases which have evolved exceptional, pregnancy-specific expression patterns in the brood pouch. We also identified ultraconserved elements in the Gulf pipefish genome for phylogenomic analysis, confirming that the syngnathid lineage is an outgroup to the collection of percomorph fish commonly used as vertebrate models. Finally, comparisons of chromosome structure among percomorphs demonstrate a reduction in chromosome number via chromosomal fusions in the syngnathid lineage. These collected findings from the first syngnathid reference genome enable study of the genomic underpinnings of exceptional phenotypic diversity within Syngnathidae, demonstrating that de novo production of high quality and useful reference genomes is within reach of even small research groups.

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