



Seahorse genome and its unique male pregnancy and pelvic fin loss

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Seahorse *Hippocampus*, belongs to the family Syngnathidae, has a complex array of morphological innovations and reproductive behaviors. Seahorse is regarded as a model fish in this family because of its well-evolutionary body plan and male pregnancy, moreover, some characteristics, such as toothless tubular mouth, and absence of caudal and pelvic fins. We report the genome sequence of a tiger tail seahorse, *Hippocampus comes*, which was done using the Illumina HiSeq 2000 platform, and the filtered reads were assembled using SOAPdenovo to yield a 501.6 Mb assembly (N50 contig size and N50 scaffold size of 34.7 kb and 1.8 Mb; 23,458 genes in the genome were predicted). Comparative genomic analysis finds higher protein evolutionary rates in the *H. comes* compared to other teleost fish. We find *Patristacin* gene has six gene duplications during the brood pouch development and male pregnancy. This is an interesting instance of a gene family (C6AST subfamily) that has undergone expansion independently in different teleost lineages and shows new expression patterns and functions associated with similar evolutionary innovations. The *H. comes* genome also shows loss of enamel matrix protein-coding P/Q-rich SCPP genes, which might have led to the loss of mineralized teeth, as well as a master control limb development gene, *tbx4*. Knockout of *tbx4* in zebrafish recapitulated the 'pelvic fin-loss' phenotype of seahorses, linking genotype to phenotype. This finding shows the *tbx4* plays a major role in the pelvic fin formation in teleost fishes. This work has been accepted as an article research in *Nature* recently.

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