

The seahorse genome provides new insights into the evolution of its specialized morphology

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Supported by the National Natural Science Foundation of China and the Strategic Priority Research Program of the Chinese Academy of Sciences, the research team led by Prof. Lin Qiang (林强) at the CAS Key Laboratory of Tropical Marine Bio-resources and Ecology (LMB), South China Sea Institute of Oceanology, Chinese Academy of Sciences, uncovered the seahorse genome and the evolution of its specialized morphology, which was published in *Nature* as a cover article (2016, 540: 395–399).

Seahorses are regarded as an important environmental indicator species in the marine ecosystem, and they are widely distributed along the coast sea water. The seahorse has a novel morphology that includes a toothless tubular mouth, a body covered with bony plates, a male brood pouch, and the absence of caudal and pelvic fins. Besides, the seahorse also has specialized physiological and behavioral characteristics, and the brood pouch of the male seahorse provides a special immune and nutrient metabolism system for their offspring during the gestation period. This finding was published in *Biology Open* as a cover story.

In order to explore the adaptation of seahorses to the environment and better understand the evolution process, Lin's team started the study of seahorse genome in 2013. The whole genome of the tiger tail seahorse (*Hippocampus comes*) was sequenced and *de novo* assembled. Comparative genomic analysis identified that the evolutionary rate of the seahorse is the fastest in teleosts with the whole genome sequenced (Figure). The seahorse has small numbers of olfactory receptor genes (OR) through comparing with other ray-finned fish genomes. It also lacks enamel matrix protein-coding proline/glutamine-rich secretory calcium-binding phosphoprotein genes, which might have led to the loss of mineralized teeth. Comparative genomic analysis identified that the seahorse genome lost great numbers of conserved noncoding elements (CNEs), which are involved in the development of the limbs and skeletal system.

Male pregnancy is a unique developmental feature of the seahorse and pipefish. The astacin family of *cbast* metalloprotease genes, which are responsible for hatching of embryos, has undergone tandem duplications given rise to six genes. Of the six duplicated *pastn* genes in the seahorse, five are highly expressed in the male brood pouch, suggesting that they may be involved in male pregnancy. The loss of pelvic fins in the seahorse is associated with evolution of an armour-like covering of its body and gain of an elongated, flexible, substrate-gripping tail. A regulator gene, *tbx4*, is found lost in the seahorse genome. Knockout of *tbx4* in zebrafish showed a ‘pelvic fin-loss’ phenotype similar to that of seahorses. The loss of the *tbx4* gene may have a role in the loss of pelvic fins in seahorses. These results provide important clues for elucidating the molecular mechanism of pelvic fin loss during fish evolution. It is of great significance to deepen the understanding of the biological characteristics of the seahorse and the evolution status of the teleost.

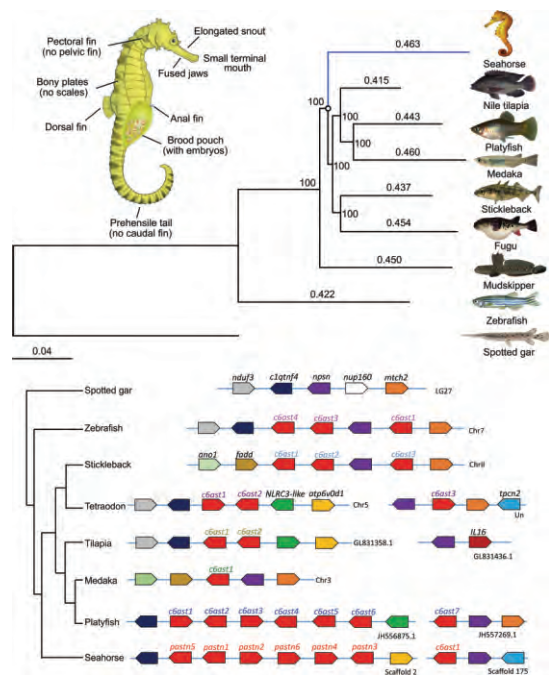


Figure High evolutionary rate and expansion of the *patristacin* gene family in seahorses.