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### 农学院参与的海马研究成果以封面文章发表于Nature杂志

2016年12月23日 (点击: 880)

鲁东大学农学院王凯博士参与、农学院兼职教授林强研究员主持的海马研究成果, 2016年12月15日于*Nature*期刊发表封面研究论文(Article) "The seahorse genome and the evolution of its specialized morphology" (海马基因组及其特异体型进化机制)。这是我校教师首次以鲁东大学为单位参与在国际顶尖学术杂志*Nature*发表高水平文章。

该研究在首次完成海马全基因组分析的基础上, 揭示了海马在海洋近岸和岛礁栖息过程中的长期适应性进化特征, 揭开了海马雄性育儿之谜, 阐明了海马特异体型进化机制, 为人类重新认识海洋鱼类进化地位和环境适应性开拓了新视角。*Nature*同期短文(Symbolic Seahorse: *The genome sequence of this unusual creature offers clues to its unique traits.*)评价了本文基于基因进化特征挖掘探索了海马体型与繁殖进化的重要性, 并对海马资源保护提出了关切。

林强研究员是中科院南海所研究员, 我校生科院99级优秀毕业生, 他带领的研究团队在海马研究领域居世界领先地位。农学院于2013年聘请林强研究员为兼职教授, 农学院的水产养殖团队与林强研究员积极开展海马方面的相关合作研究, 在海马研究领域取得了一系列成果。(撰稿: 赵丽丽, 审核: 程显好)

论文链接: <http://www.nature.com/nature/journal/v540/n7633/full/nature20595.html>

同期评论链接: <http://www.nature.com/news/sequence-reveals-genes-behind-bizarre-sea-horse-traits-1.21149>



Nature封面论文(海马: Evolution at a gallop)

## ARTICLE

OPEN

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## The seahorse genome and the evolution of its specialized morphology

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Seahorses have a specialized 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. Here we report the sequencing and *de novo* assembly of the genome of the tiger tail seahorse, *Hippocampus comes*. Comparative genomic analysis identifies higher protein and nucleotide evolutionary rates in *H. comes* compared with other teleost fish genomes. We identified an astacin metalloprotease gene family that has undergone expansion and is highly expressed in the male brood pouch. We also find that the *H. comes* genome lacks enamel matrix protein-coding proline glutamine-rich secretory calcium-binding phosphoprotein genes, which might have led to the loss of mineralized teeth. *rfx4*, a regulator of hindlimb development, is also not found in *H. comes* genome. Knockout of *rfx4* in zebrafish showed a 'pelvic fin-loss' phenotype similar to that of seahorses.

Members of the teleost family Syngnathidae (seahorses, pipefishes and seadragons) (Extended Data Fig. 1), comprising approximately 300 species, display a complex array of morphological innovations and reproductive behaviours. This includes specialized morphological phenotypes such as an elongated snout with a small terminal mouth, fused jaws, absent pelvic and caudal fins, and an extended body covered with an armour of bony plates instead of scales<sup>1</sup> (Fig. 1a). Syngnathids are also unique among vertebrates due to their 'male pregnancy', whereby males nourish developing embryos in a brood pouch until hatching and parturition occurs<sup>2</sup>. In addition, members of the subfamily Hippocampinae (seahorses) exhibit other derived features such as the lack of a caudal fin, a characteristic prehensile tail, and a vertical body axis<sup>3</sup> (Fig. 1a). To understand the genetic basis of the specialized morphology and reproductive system of seahorses, we sequenced the genome of the tiger tail seahorse, *H. comes*, and carried out comparative genomic analyses with the genome sequences of other ray-finned fishes (Actinopterygii).

## Genome assembly and annotation

The genome of a male *H. comes* individual was sequenced using the Illumina HiSeq 2000 platform. After filtering low-quality and duplicate reads, 132.13 Gb (approximately 190-fold coverage of the estimated 695 Mb genome) of reads from libraries with insert sizes ranging from 170 bp to 20 kb were retained for assembly. The filtered reads were assembled using SOAPdenovo (version 2.04) to yield a 501.6-Mb assembly with an N50 contig size and N50 scaffold size of 34.7 kb and 1.8 Mb, respectively. Total RNA from combined soft tissues of *H. comes* was sequenced using RNA-sequencing (RNA-seq) and assembled

*de novo*. The *H. comes* genome assembly is of high quality, as >99% of the *de novo* assembled transcripts (76,757 out of 77,040) could be mapped to the assembly; and 243 out of 248 core eukaryotic genes mapping approach (CEGMA) genes are complete in the assembly.

We predicted 23,538 genes in the genome of *H. comes* based on homology and by mapping the RNA-seq data of *H. comes* and a closely related species, the lined seahorse, *Hippocampus erectus*, to the genome assembly (see Methods and Supplementary Information). More than 97% of the predicted genes (22,941 genes) either have homologues in public databases (Swissprot, TrEMBL and the Kyoto Encyclopedia of Genes and Genomes (KEGG)) or are supported by assembled RNA-seq transcripts. Analysis of gene family evolution using a maximum likelihood framework identified an expansion of 25 gene families (261 genes, 1.1%) and contraction of 54 families (96 genes, 0.41%) in the *H. comes* lineage (Extended Data Fig. 2 and Supplementary Tables 4.1, 4.2). Transposable elements comprise around 24.8% (124.5 Mb) of the *H. comes* genome, with class II DNA transposons being the most abundant class (99%; 65 Mb). Only one wave of transposable element expansion was identified, with no evidence for a recent transposable element burst (Kimura divergence  $\leq 5$ ) (Extended Data Fig. 3).

## Phylogenomics and evolutionary rate

The phylogenetic relationships between *H. comes* and other teleosts were determined using a genome-wide set of 4,122 one-to-one orthologous genes (Supplementary Note 4.2). The phylogenetic analysis (Fig. 1b) showed that *H. comes* is a sister group to other percomorph fishes analysed (trickleback, *Gastrophysus altanatus* medaka, *Oryzias latipes*, Nile tilapia, *Oreochromis niloticus*, fugu, *Takifugu rubripes*, and

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