

MITOGENOME ANNOUNCEMENT

Intraspecific mitochondrial variations between *Rhinogobio typus* from the Yellow River and Yangtze RiverLikun Jiang¹, Baohua Chen¹, Jianxin Feng², Shahid Mahboob^{3,4}, and Khalid A Al-Ghanim³¹College of Life Sciences, Shanghai Ocean University, Shanghai, China, ²Henan Academy of Fishery Sciences, Zhengzhou, China, ³Department of Zoology, College of Science, King Saud University, Riyadh, Saudi Arabia, and ⁴Department of Zoology, GC University, Faisalabad, Pakistan**Abstract**

The complete mitochondrial genome of the first individual *Rhinogobio typus* collected from the Yellow River were sequenced and compared with the previously reported complete mitochondrial sequence of *Rhinogobio typus* from the Yangtze River. The length of their circular mitochondrial genome was determined to be 16 599 and 16 608 bp respectively. The comparison of two mitochondrial genomes revealed 237 base pair substitutions and 17 insertions or deletions (indels), including 182 base pair substitutions and 2 indels in protein-coding region. Phylogenetic tree was constructed based on complete mitogenomes of the two populations and closely related 13 teleost species to assess their phylogenetic relationship and evolution.

Keywords

Mitochondrial genome, polymerase chain reaction, *Rhinogobio typus*, Yellow River, Yangtze River

History

Received 30 June 2015

Accepted 9 July 2015

Published online 11 August 2015

Rhinogobio typus, belonging to *Cyprinidae* and *Cypriniformes*, is a genus of common food fish endemic to China. Although it has small-or-middle body size (commonly 15–35 cm in length and 50–300 g in weight for mature individuals) and a relatively slow growth, the population size is considerably large, making it a good source of food. The main food type of *Rhinogobio typus* is benthic invertebrates, such as aquatic insects and mollusks. *Rhinogobio typus* is usually believed to be distributed only in upper and middle basin of Yangtze River and Minjiang River (Wang et al., 2015). However, samples have been recently collected at Xingyang on the Yellow River for the first time.

In order to provide genetic tools for finding the differences between it and its normal congeners lived in traditional habitats, we sequenced its entire mitochondrial genomes and compared the results with the sequence of entire mitochondrial genomes of a common individuals living in Yangtze River (downloaded from NCBI, GenBank: KJ631750.1). In this study, total genomic DNA was extracted from blood tissues by DNasy Blood & Tissue Kit (Qiagen, Hilden, Germany). In addition, totally nine PCR primer

pairs were designed according to the mitochondrial genome of *Rhinogobio typus* (Yan et al., 2014) in Yangtze River from NCBI. The complete mitochondrial genome sequence of *Rhinogobio typus* inhabiting in the Yellow River (*R. typus* I) is 16 599 bp in length, which is equal to the length of previously reported mitochondrial genome of the sample from the Yangtze River (*R. typus* II). The new mitochondrial genome sequence has been submitted to DDBJ with the accession number KP883295. The genome of *R. typus* I have a genomic organization and structure identical to *R. typus* II (13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and a noncoding control region) (Wang et al., 2013). Additionally, the nucleotide base composition of *R. typus* I is 29.4% for A, 28.8% for C, 14.6% for G and 27.2% for T. Compared with the genome of *R. typus* II, there are 254 site differences observed between the two mitochondria genomes, including 17 insertions or deletions (indels). Among these differences, 8 base pair substitutions and 10 indels are located in rRNAs; 2 base pair substitutions and 2 indels are in tRNAs; 182 base pair substitutions and 2 indels are in protein coding region; and 12 base pair substitutions are in ATPs. These variations between two distinctive populations provide us very useful resource to develop genetic markers or tools for discrimination of the Yellow River population from Yangtze River population.

We then performed phylogenetic analysis and constructed the tree based on mitochondrial genome sequences of *R. typus* I, *R. typus* II and those 13 closely related species to validate the taxonomy and phylogenetic relationships (Wu et al., 2010). We performed maximum likelihood analysis in MEGA6 with 1000 bootstrap replicates (Jiang et al., 2014). The topology clearly illustrated phylogenetic relationship of *R. typus* I, *R. typus* II and their related species (Figure 1).

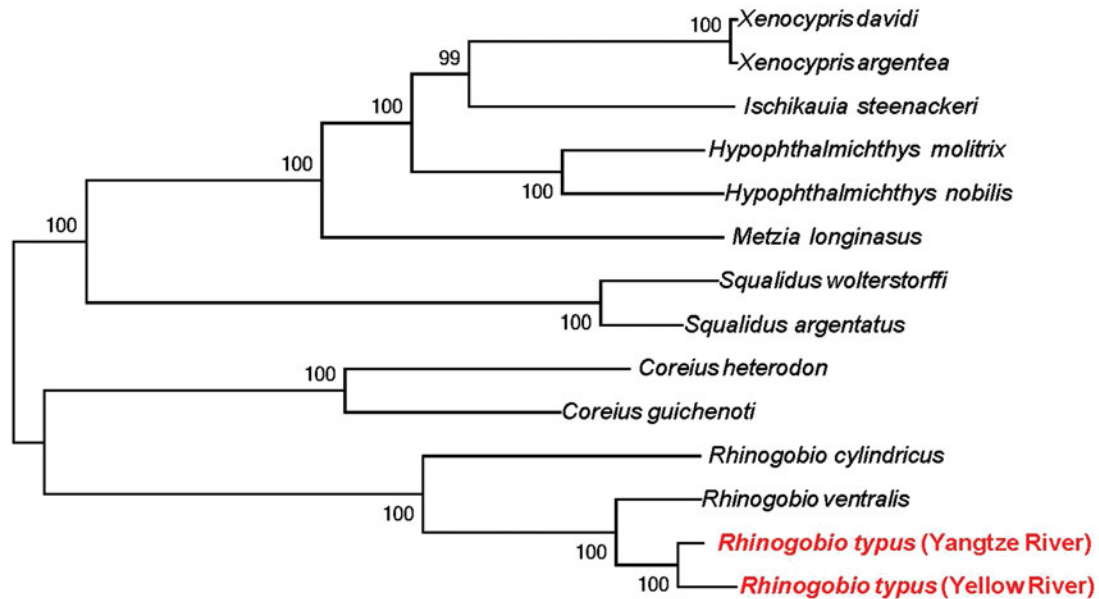


Figure 1. The phylogenetic tree of two mitochondrial genomes of *Rhinogobio typus* from Yellow River and Yangtze River with thirteen closely related species. *Genbank accession numbers of species used in the tree: *Rhinogobio typus* (Yangtze River): KJ631750.1, *Rhinogobio ventralis*: KF529530.1, *Rhinogobio cylindricus*: KF724884.1, *Coreius guichenoti*: JF906108.1, *Coreius heterodon*: JF906110.1, *Hypophthalmichthys molitrix*: KJ746949.1, *Hypophthalmichthys nobilis*: KJ746966.1, *Xenocypris argentea*: AP009059.1, *Xenocypris davidi*: KF039718.1, *Metzia longinasus*: KF955011.1, *Squalidus argentatus*: KF926824.1, *Squalidus wolterstorffi*: AP011392.1, *Ischikauia steenackeri*: AB239601.1.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

We acknowledge grant supports from National Infrastructure of Fishery Germplasm Resources of China (2006DKA30470-009). The authors would like to extend their sincere appreciation to the Deanship of Scientific Research at King Saud University for funding this Research (No. RG 1435-012).

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