

MITOGENOME ANNOUNCEMENT

 OPEN ACCESS

The phylogenetic analysis of *Acrossocheilus paradoxus* among the *acrossocheilus* base on complete mitochondrial DNA sequence

Honghui Li^a, Xiaodong Wang^b, Yiqin Xiong^a and Xiaoyan Liu^{b,c}

^aInstitute for New Rural Development, Zhejiang University, Hangzhou, China; ^bCollege of Animal Science and Technology, Hunan Agricultural University, Changsha, China; ^cCollaborative Innovation Center for Efficient and Health Production of Fisheries in Hunan Province, Changde, China

ABSTRACT

In our research, we used 17 sets of primers to amplify the complete mitochondrial DNA (mtDNA) of *Acrossocheilus paradoxus*. The total length of the mitochondrial genome is 16 597 bp and deposited in the GenBank with accession numbers KT751364. The gene arrangement and transcriptional direction were similar to other bony fishes which contained 37 genes (13 protein-coding genes, 2 ribosomal RNA and 22 transfer RNAs) and a major non-coding control region. Most genes were encoded on the H-strand, except for the ND6 and 8 tRNA genes, encoding on the L-strand. The nucleotide skewness for the coding strands of *A. Paradoxus* (GC-skew = -0.24, AT-skew = 0.07) is biased toward A and C. The negative GC-skew ranges from -0.35(ND6) to -0.21(CO1) and the AT-skew showed more positive varying from -0.23(ND4L) to 0.42(ND6). The phylogenetic analysis demonstrated that *Acrossocheilus* clustal together as one group.

ARTICLE HISTORY

Received 18 December 2015
Accepted 22 December 2015

KEYWORDS

Acrossocheilus paradoxus;
base composition;
mitogenome; phylogenetic

In animal phylogenetic analysis, choose a suitable marker is important to reconstruct the animal evolutionary process. Mitochondria are double-layered membrane-bound organelles, found in nearly all eukaryotic cells with some unique characteristics, such as small size (16K), high abundance, maternal inheritance, lack of recombination and rapid evolutionary rate (Curole & Kocher 1999; Chen et al. 2012). It has being considered as a natural marker and widely applied in population genetic and evolutionary studies (Ballard & Whitlock 2004; Rand 2008).

Acrossocheilus paradoxus was assigned to Cypriniformes; Cyprinidae; Cyprinus, *Acrossocheilus* which was mainly located in ChangJiang river. In this study, we obtained the dorsal myotome and preserved in 95% ethanol. Total genomic DNA was extracted from fin tissues using Blood & Cell Culture DNA Kit (QIAGEN, USA) according to the manufacturer's recommendations. For a better understanding of genetic status and the evolutionary study, we focused on the genetic information contained in the complete mitochondrial genomes of the fish.

The mitochondrial genome has been deposited in the GenBank with accession number KT991436. The mitochondrial genome was 16 597 bp in length, including 13 protein-coding genes, 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes and 1 control region (D-loop).

The gene arrangement and transcriptional direction were the similar to those of the typical teleosts mitogenomes (Li et al. 2010; Chen et al. 2012). Except for ND6 gene and eight tRNA genes (tRNA-Gln, Ala, Asn, Cys, Tyr, Ser (AGY), Glu and Pro), all other genes were encoded on the H-strand. All the 13 protein-coding genes contain the same start codon ATG

except the gene CO1, which contains GTG instead. However, the termination codons of the 13 protein-coding genes are varied, 5 genes (ND1, CO1, ND4L, ND5, ND6) ended with TAA, 5 (CO2, CYTB, ND2, ND3, ND4) with T-, ATP6 and CO3 stopped with TA – while ATP8 stopped with TAG.

The length of 22 tRNA genes ranged from 65 to 76 bp. All tRNA genes appeared to exhibit typical cloverleaf structure except for tRNA-Ser (AGY), which lost the dihydrouridine arm and formed a simple loop. Among the 22 tRNA, 3 tRNA clusters were observed with IQM (tRNA-Ile, tRNA-Glu and tRNA-Met), WANCY (tRNA-Trp, tRNA-Ala, tRNA-Asp, tRNA-Cys and tRNA-Tyr) and HSL (tRNA-His, tRNA-Ser and tRNA-Leu).

As observed in other bony fish, the G contents were lowest (17.24%) (Oh et al. 2007). The AT-skew and GC-skews always show high inter or intra-phylum variation, which might affect phylogenetic analyses (Nesnidal et al. 2011). The nucleotide skewness for the coding strands of *A. Paradoxus* (GC-skew = -0.24, AT-skew = 0.07) is biased toward A and C. A similar trend has been observed in other teleost mitogenomes: the negative GC-skew ranges from -0.35(ND6) to -0.21(CO1) and the AT-skew showed more positive varying from -0.23(ND4L) to 0.42(ND6).

Phylogenetic analysis was performed using the mitochondrial genomes of 14 fish species from the Cyprinidae. Each of the datasets was aligned using ClustalX (Thompson et al. 1997) and analyzed by neighbor-joining (N-J) in MEGA 4.0, and bootstrap analysis was performed with 1000 replications. The result demonstrated that all the *Acrossocheilus* clustal together as one group. The *Alburnus*, *Gnathopogon* and *Hemibarbus* clustal together as another group. The *Chanodichthys mongolicus*

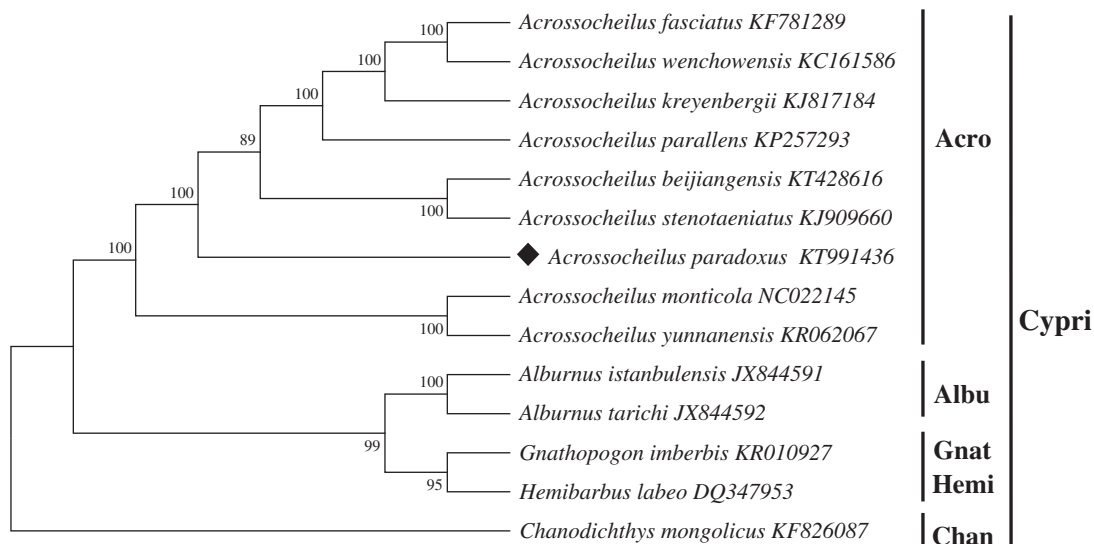


Figure 1. An MP tree (maximum parsimony) of the phylogenetics based on mitochondrial genome sequences of various percoid fishes. Abbreviations after species indicate family names. Acro, Acrossocheilus; Albu, Alburnus; Gnat, Gnathopogon; Hemi, Hemibarbus; Chan, Chanodichthys; Cypri, Cyprinidae .

as the out group. The *A. Paradoxus* in our research was joined with other *Acrossocheilus* and in the middle position (Figure 1).

Declaration of interest

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

References

- Ballard JW, Whitlock MC. 2004. The incomplete natural history of mitochondria. *Mol Ecol.* 13:729–744.
- Chen DX, Chu WY, Liu XL, Nong XX, Li YL, Du SJ, Zhang JS. 2012. Phylogenetic studies of three sinipercid fishes (Perciformes: Sinipercidae) based on complete mitochondrial DNA sequences. *Mitochondrial DNA.* 23:70–76.
- Curole JP, Kocher TD. 1999. Mitogenomics: digging deeper with complete mitochondrial genomes. *Trends Ecol Evol. (Amst.)* 14:394–398.
- Li J, Xia R, Mcdowall RM, Lopez JA, Lei GC, Fu CZ. 2010. Phylogenetic position of the enigmatic *Lepidogalaxias salamandroides* with comment on the orders of lower euteleostean fishes. *Mol Phylogenet Evol.* 57:932–936.
- Nesnidal MP, Helmkampf M, Bruchhaus I, Hausdorf B. 2011. The complete mitochondrial genome of *Flustra foliacea* (Ectoprocta, Cheilostomata) – compositional bias affects phylogenetic analyses of lophotrochozoan relationships. *BMC Genomics.* 12:572.
- Oh DJ, Kim JY, Lee JA. 2007. Complete mitochondrial genome of the multicolorfin rainbowfish *Halichoeres poecilopterus* (Perciformes, Labridae). *Korean J Genet.* 29:65–72.
- Rand DM. 2008. Mitigating mutational meltdown in mammalian mitochondria. *PLoS Biol.* 6:35.
- Thompson JD, Gibson TJ, Plewniak F. 1997. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res.* 25:4876–4882.