

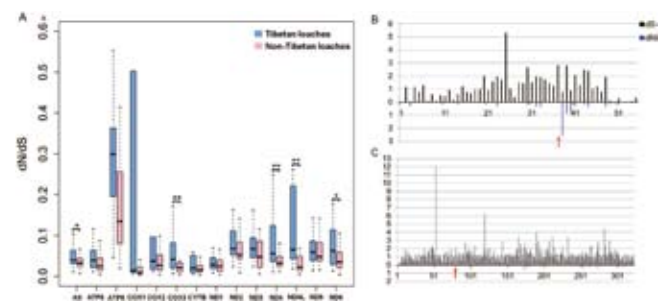
Mitogenomic Analyses Reveal Origin of Tibetan Loaches and their Adaptation to High Altitude

Previous studies have demonstrated the role of selection in mtDNA evolution and detected signals of positive selection in mitochondrial genes in endemic taxa of the Tibetan Plateau. Tibetan loaches are the largest group of Tibetan fishes and well adapted to the Tibetan Plateau. However, understanding of the genetic mechanisms that underlie the adaptations of Tibetan loaches to their high-altitude environment from a mitogenomic perspective is lacking.

A group led by HE Shunping from the Institute of Hydrobiology (IHB), Chinese Academy of Sciences used the mitogenomes of the superfamily Cobitoidea to investigate the origin of Tibetan loaches and their adaptation to high altitude. They provided insights to the origin of Tibetan loaches and the genetic mechanisms for adaptation of fishes to high-altitudes from mitogenomic perspectives.

In this study, IHB researchers analyzed 32 complete, newly determined mitogenomes along with 64 published mitogenomes of the superfamily Cobitoidea to confirm the phylogenetic status of the genus *Triplophysa* within Nemacheilidae. They also dated the origin of the *Triplophysa* lineages, and provided a comprehensive view of the adaptive evolution of the mitogenome in *Triplophysa* species.

They found that the genus *Triplophysa* formed a monophyletic group within Nemacheilidae. The molecular dating time suggested that the lineage leading to the Tibetan loaches approximately originated in 23.5 Ma. This origin time is consistent with the period of recent major uplifts of the Tibetan Plateau in the Early Miocene. Third, Tibetan loaches accumulated more nonsynonymous



Selection pressure analysis and the positive genes identified for *Triplophysa* fishes. (A) Comparisons of average dN/dS ratios for 13 individual protein-coding genes between *Triplophysa* fishes and non-*Triplophysa* fishes. Note: * $0.01 < P < 0.05$, ** $0.001 < P < 0.01$. (B) dN and dS estimated for the positive gene *ATP8* using the FEL analysis method. The red arrow indicates the position of positive selected site. (C) dN and dS estimated for the positive gene *ND1* using the FEL analysis method. The red arrow indicates the position of positive selected site.

mutations than non-Tibetan loaches and exhibited rapid evolution at the mitochondrial genome level. More importantly, the researchers detected two positively selected genes *ATP8* and *ND1* responsible for the high altitude adaptation.

This study is the first indications that the origin and evolution of this group is related to the uplift of the Tibetan Plateau, and also provided investigations to the genetic mechanisms of adaptation to the conditions on Tibetan Plateau in the Tibetan loaches from mitogenomic perspectives.

The study has been published in *Scientific Reports* with the title “Mitogenomic perspectives on the origin of Tibetan loaches and their adaptation to high altitude.”