

Foreword

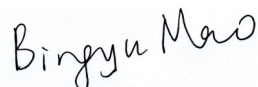
The State Key Laboratory of Genetic Resources and Evolution, located at the Kunming Institute of Zoology, Chinese Academy of Sciences (CAS), is a leading research center in genetic resource conservation and evolutionary biology. In this special issue of *Zoological Research* on “Animal Genetic diversity, development and evolution”, we have compiled 12 review and research articles from the Key Lab as well as 4 related articles from external authors, covering, among other topics, genetic biodiversity, molecular phylogeny, evolution of gene families, and the use of mitochondrial DNA in the study of adaptive evolution and tumor evolution.

Based on previous cytogenetic, morphological and molecular data, Hu JY et al summarized the higher-level phylogeny of *Laurasiatheria*, one of the richest and most diverse superorders of placental mammals. The genus *Trachypithecus* is the most diverse langur taxon, distributed in southwestern China and south and southeastern Asia. He K et al reconstructed the phylogeny of the 16 recognized *Trachypithecus* species using mitochondrial and nuclear genes. Wang CY et al reported on the identification of the processed medicinal insect *Catharsius molossus* by means of DNA barcoding, hopefully stimulating similar studies. Wang F et al cloned the heat shock protein 60 cDNA of *Neobenedenia melleni* (a capsalid monogenean parasite on fish skin) and studied its expression change under different temperatures and salinity. Wang JH et al and Wang XA et al respectively discussed the establishment of fibroblast-like cell lines of the endangered Crested ibis (*Nipponia nippon*) and the local fish *Anabarilius grahami* (Cypriniformes: Cyprinidae).

Due to its rapid mutation ratio, mitochondrial DNA has been widely used in molecular evolutionary studies. In this issue, Chen X et al reviewed recent progress on its applications in molecular phylogeny, evolution of energy metabolism and adaptation. Different from normal cells, tumor cells generate energy *via* glycolysis even under aerobic conditions. In tumor cells, somatic mutations on the energy metabolism related genes (including mitochondrial ones) occur at a high frequency. Whether this is involved in the switch of the energy metabolism pathways is examined by Liu J and Kong QP. Meanwhile, Shi QH et al reported on the complete mitochondrial genome of the Painted Jezebel, *Delias hyparete*.

During conjugation of the protozoa *Paramecium caudatum*, four haploid nuclei formed during the first two meiotic prezygotic divisions, of which only one survived. In the study by Wang YW et al, cytoplasmic microtubules (cMTs) were observed surrounding the surviving nuclei during the third prezygotic division, providing a new clue to the mechanism of its survival. The regulation of mRNA stability through RNA binding proteins plays an important role in embryonic development. In this issue, Xia YJ et al also showed that XZFP36L1, an RNA binding protein, is involved in *Xenopus* neural development. XZFP36L1 is expressed in specific brain regions in *Xenopus* embryos, and its overexpression inhibits neural differentiation and can lead to severe neural tube defect.

Ye DD et al reviewed the bioinformatics pipelines for metagenomic analysis and Zhang & Su provided validation for an approach for peak identification for ChIP-seq data with no controls. This issue also includes reviews on the evolution of neurotransmitter gamma-aminobutyric acid, glutamate and their receptors; advances in the study of the nucleolus; and current progress on the study of ovarian germ stem cells in mammals.



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