

Commentary

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Snow carps as an emerging model for polyploid genome evolution

For more than half a century, snow carps (Schizothoracinae) have occupied a central place in Chinese zoological research. Distributed across the Qinghai–Xizang Plateau, this remarkable group has inspired extensive studies in taxonomy, biogeography, cytogenetics, conservation, and adaptive evolution (Cao et al., 1981; Gu et al., 2024). Snow carps have evolved remarkable adaptations to high-altitude environments and high ploidy levels. Moreover, their diversification has long been viewed as one of the most compelling examples of vertebrate evolution associated with the uplift of the Qinghai–Xizang Plateau. Yet despite this rich research history, snow carps have remained largely absent from the genomics era.

The principal obstacle has been their unusual genomes. All extant snow carps are polyploids, carrying duplicated chromosome sets generated through whole-genome duplication (WGD). Unlike allopolyploids formed through hybridization between species, snow carps possess predominantly autopolyploid genomes derived from genome doubling within a single ancestral lineage. Because homologous chromosomes remain highly similar, distinguishing and assembling duplicated chromosome copies has proven exceptionally difficult, and analyzing these copies is equally challenging. As a consequence, many longstanding questions concerning the origin, diversification, and adaptation of snow carps have remained unresolved.

The study by Xie and colleagues (Xie et al., 2026b) addresses this challenge by providing a practical strategy for assembling haplotype-resolved autopolyploid genomes. Using a combination of PacBio HiFi and Oxford Nanopore Technologies (ONT), High-throughput Chromosome Conformation Capture (Hi-C) scaffolding, and chromosome-specific read binning, the authors generated fully phased genomes for representative snow carp species (Figure 1A; *Schizopygopsis younghusbandi* and *S. curviliatus*). Beyond providing valuable genomic resources, this framework opens the door for integrating decades of ecological and evolutionary studies on snow carps with modern comparative genomics.

The most important contribution of the study, however, lies not in genome assembly itself but in what the genomes reveal about the process of rediploidization. Following WGD, duplicated chromosome sets must eventually regain diploid-like inheritance through a process known as rediploidization (Ohno, 1970). This transition is essential because it allows

duplicated genes (ohnologs) to diverge and acquire new evolutionary functions. Although rediploidization has been recognized as a key step in the evolutionary consequences of WGD (Wolfe, 2001), its initiating mechanisms have remained elusive.

By exploiting the recent polyploid history of snow carps, the authors capture rediploidization at an unusually early stage. Their analyses propose that chromosome fusions act as the mechanism to trigger the transition from tetrasomic to disomic inheritance (Figure 1B). Rediploidization begins near fusion sites and subsequently spreads along chromosome arms. Notably, chromosome termini retain tetrasomic inheritance, which may be related to the formation of multivalent pairing configurations. Importantly, not all chromosomes undergo rediploidization simultaneously (Figure 1C). Some chromosomes (Wave 1) represent the earliest rediploidized regions and were established in the common ancestor of all snow carps, whereas others occurred in specific lineages (Wave 2) or specific species (Wave 3). This finding provides one of the clearest explanations yet for the initiation and progression of rediploidization in autopolyploid vertebrates.

The implications extend far beyond snow carps. Ancient whole-genome duplications are thought to have played a fundamental role in vertebrate evolution, including the genome duplications that occurred near the origin of vertebrates (Dehal & Boore, 2005). Comparative genomic studies have suggested that these ancestral events were followed by extensive chromosome rearrangements, including multiple chromosome fusions (Huang et al., 2023). The observation that chromosome fusions initiate rediploidization offers a plausible mechanism for how duplicated vertebrate genomes transitioned toward diploid inheritance following ancient WGDs. Although additional mechanisms such as inversions may also contribute, the study suggests that chromosome fusions could represent one of the general drivers of early rediploidization across vertebrate evolution.

Equally intriguing is the discovery that different snow carp lineages appear to occupy different positions along the rediploidization continuum. Comparative analyses indicate that highly specialized lineages exhibit more extensive rediploidization than basal lineages, suggesting that genome stabilization has progressed unevenly during the radiation of the group. This observation raises an important evolutionary question: does progressive rediploidization enhance adaptive potential? Whether advanced rediploidization promotes adaptation to extreme high-altitude environments remains

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Received: 30 July 2026; Accepted: 18 August 2026; Online: 19 August 2026

Foundation items: This work was supported by the National Natural Science Foundation of China (U23A20249)

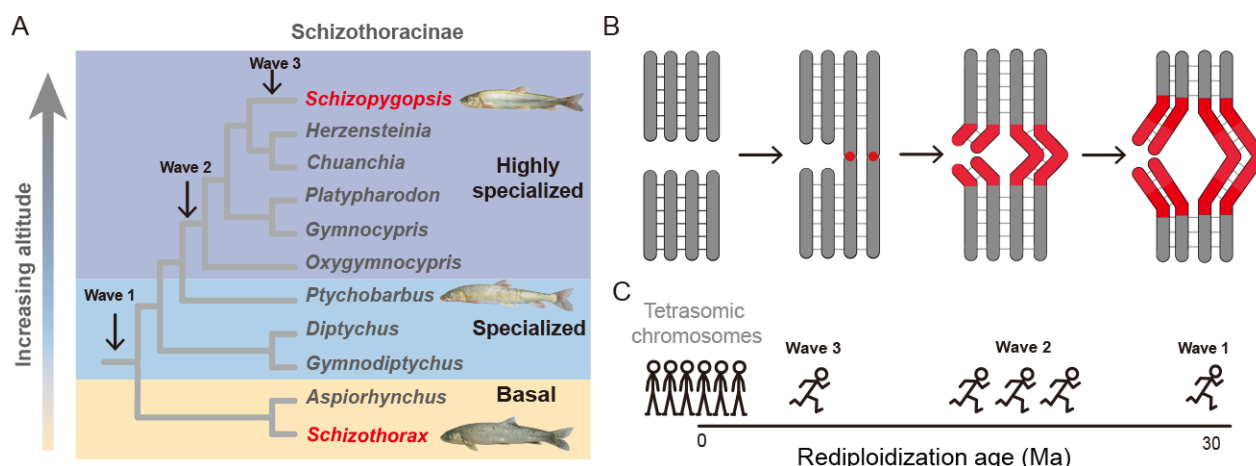


Figure 1 Chromosome fusion-driven and asynchronous rediploidization in snow carps.

A: Snow carps can be classified into three evolutionary grades: basal, specialized, and highly specialized groups, with the degree of specialization and rediploidization increasing with elevation. Wave 1 includes chromosome fusion of Chromosome (Chr) 19–Chr22; Wave 2 includes Chr08–Chr16, Chr04–Chr15, and Chr20–Chr23; and Wave 3 includes Chr11–Chr14 specific to *Schizopygopsis*. The two species shown in red have fully phased genomes. Animal illustrations are adapted from Xie et al. (2026b). **B:** Proposed model of chromosome fusion-driven rediploidization. At the early stages of tetraploidy, the genome exhibits tetrasomic inheritance. Following asymmetric chromosome fusion, two fused homologous chromosomes and two unfused chromosomes are generated. This suppresses recombination between the fused and unfused chromosomes, allowing both chromosome pairs to gradually establish disomic inheritance. Regions surrounding the fusion site are the first to transition from tetrasomic to disomic inheritance, followed by progressive expansion toward chromosome ends. **C:** Stepwise progression of rediploidization. The *S. younghusbandi* genome contains five chromosome fusion events distributed across three waves. Each human-shaped icon represents an individual chromosome fusion event. The estimated rediploidization age refers to the time span since the corresponding chromosome fusion event occurred. These observations demonstrate that rediploidization occurs asynchronously across chromosomes rather than simultaneously.

speculative, but the new genomic framework now makes this hypothesis testable.

The study also highlights unresolved questions concerning the polyploid origin of snow carps themselves. The timing, number, and phylogenetic distribution of genome duplication events have long been debated, with competing hypotheses proposing either a shared ancestral WGD or multiple independent polyploidization events (Li et al., 2024; Wang et al., 2026). By using genome-wide ohnologs extracted from the haplotype-resolved genome assembly, the present work provides a working strategy to resolve these controversies. Looking forward, more haplotype-resolved genomes spanning the full taxonomic diversity of the group will provide a comprehensive understanding of the evolutionary history of snow carp polyploids.

As more high-quality assemblies become available (Xie et al., 2026a), snow carps are poised to emerge as one of the most informative vertebrate systems for studying polyploid genome evolution. Compared with ancient autopolyploids such as salmonids and sturgeons, snow carps experienced a more recent polyploidization and have not undergone extensive chromosomal rearrangements. In addition, snow carps provide a unique opportunity to investigate chromosome behaviors, a feature that cannot be readily studied in ancient autopolyploids. By transforming a classic model of Xizang Plateau evolution into a genomic model of polyploid evolution, this study establishes snow carps as a promising system for understanding how whole-genome duplication generates evolutionary novelty.

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