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Origins and Global Dissemination of *Siluriformes* A Phylogenetic Perspective on Historical Trajectories

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Abstract Catfishes (order *Siluriformes*), arguably the most diverse and widely ranging freshwater fishes with a diversity of ecological niches on all but one continent, Antarctica. Their evolutionary origin and global dispersal are of particular importance for reconstructing freshwater biogeographic history and delineating lineage diversification patterns in aquatic habitats. Here, we build the phylogenetic framework of *Siluriformes* from mitochondrial and nuclear molecular information, date the divergence, and describe prevailing lineages with distinctive geographical signatures. By integrating fossil records, paleogeographic reconstructions, and modern biogeographic modeling approaches (such as DEC and BioGeoBEARS), this study proposes that South America may have been the evolutionary cradle of catfishes. It suggests that catfishes could have achieved transcontinental dispersal through ancient river connections, continental drift, and climatic fluctuations. In addition, the study explores regional adaptation and niche differentiation across various ecosystems, as well as the close interplay between local evolutionary responses and global expansion. This research provides a comprehensive perspective on the evolutionary history of catfishes and offers practical insights for freshwater biodiversity conservation and future biogeographic predictions.

Keywords *Siluriformes*; Phylogeny; Biogeography; Global dispersal; Freshwater fish evolution

1 Introduction

Catfishes, family Order *Siluriformes*, are among the most cosmopolitan freshwater fishes in the world. They possess over 3 600 valid species and 37 accepted families with huge morphological and ecological heterogeneity. Although they are predominantly freshwater inhabitants, some families like *Ariidae* and *Plotosidae* have taken over the ocean (Chen et al., 2024). Molecular studies have now documented widespread cryptic diversity in *Siluriformes*. For instance, species delimitation using sequences has revealed some molecular operational taxonomic units (MOTUs) in such species as the *Silurus asotus* complex and discovered that species richness is not actually reflected in the genus (Roxo et al., 2019; Ditcharoen et al., 2019). Similarly, phylogenetic study of sisorid catfishes has revealed divergent lineages adapted to high-speed rivers encircling the Tibetan Plateau and eastern Himalayas, testifying to the evolutionary diversification of the group.

Catfishes are integral components of freshwater ecosystems. They have ecological roles in nutrient cycling, sediment bioturbation, and regulation of prey populations. Economically, they play a central role in the fisheries and aquaculture of the world. Large species, such as the Mekong giant catfish (*Pangasianodon gigas*), are among the world's largest freshwater fishes and are important to local fisheries (Lujan et al., 2017). Moreover, genera like Loricariidae are popular in the aquarium fish market where genera like *Hypostomus plecostomus* are adequately represented in aquariums worldwide. However, there is an ecological imbalance when catfish species are invasive. For example, the introduction of armored catfish (*Pterygoplichthys* spp.) into alien ecosystems has posed ecological problems because of their burrowing behavior and competition with native species (Vilardo et al., 2023).

Understanding the history of origin and dispersal of *Siluriformes* is important for freshwater biogeographic and evolutionary studies. Catfish lineage histories have been elucidated by phylogenetic analysis. Mitogenomic analysis, for instance, has suggested a Pangaean origin of siluriforms in the Early Cretaceous followed by further diversification correlated with continental drift. Phylogenetic use allows scientists to make inferences of historical biogeographic patterns, infer the timing of divergence, and reconstruct evolutionary relationships. These analyses have indicated that diversification in sisorid catfishes in China matches geological processes like the Tibetan Plateau's uplift, indicating that there is a correlation of tectonic processes with species evolution.

2 Phylogeny and Lineage Evolution of Catfishes

2.1 Taxonomic history and phylogenetic controversies of catfishes

Catfish (*Siluriformes*) systematics are of long-standing dispute, and morphologically based early assumptions were in contrast with molecular data. Big catfish families' relationships and the placement of some genera, i.e., *Prietella*'s polyphyly within *Ictaluridae* and Olyra longicaudata's placement, were controversial and in an unstable state with the advent of new data (Janzen et al., 2023; Patil et al., 2024). Monophyly of *Siluriformes* is robust, but relationships between families and some subfamilies and genera remain contentious, provoking ongoing taxonomic revision (Pinna and Mario, 2016; Wang and Wang, 2024).

2.2 Phylogenetic relationships revealed by molecular data

Mitochondrial and nuclear gene molecular phylogenies have clarified most of the *Siluriformes* relationships (Figure 1). Works at high levels have defined monophyly for all but one family and revealed deep splits, e.g., *Loricarioidei* the most ancient diverging clade, showing that the order is South American in origin (Kappas et al., 2016). Molecular information has further validated polyphyly in families like *Bagridae* and *Prietella*, and has taxedonomically reclassed subfamilies like *Hypoptopomatinae* and *Hypostominae* (Roxo et al., 2019; Patil et al., 2024). Multilocus approaches and DNA barcoding have remained at the core of resolving cryptic diversity, as well as of managing relations at deep and shallow levels of taxonomy (Lujan et al., 2017; Patil et al., 2024).

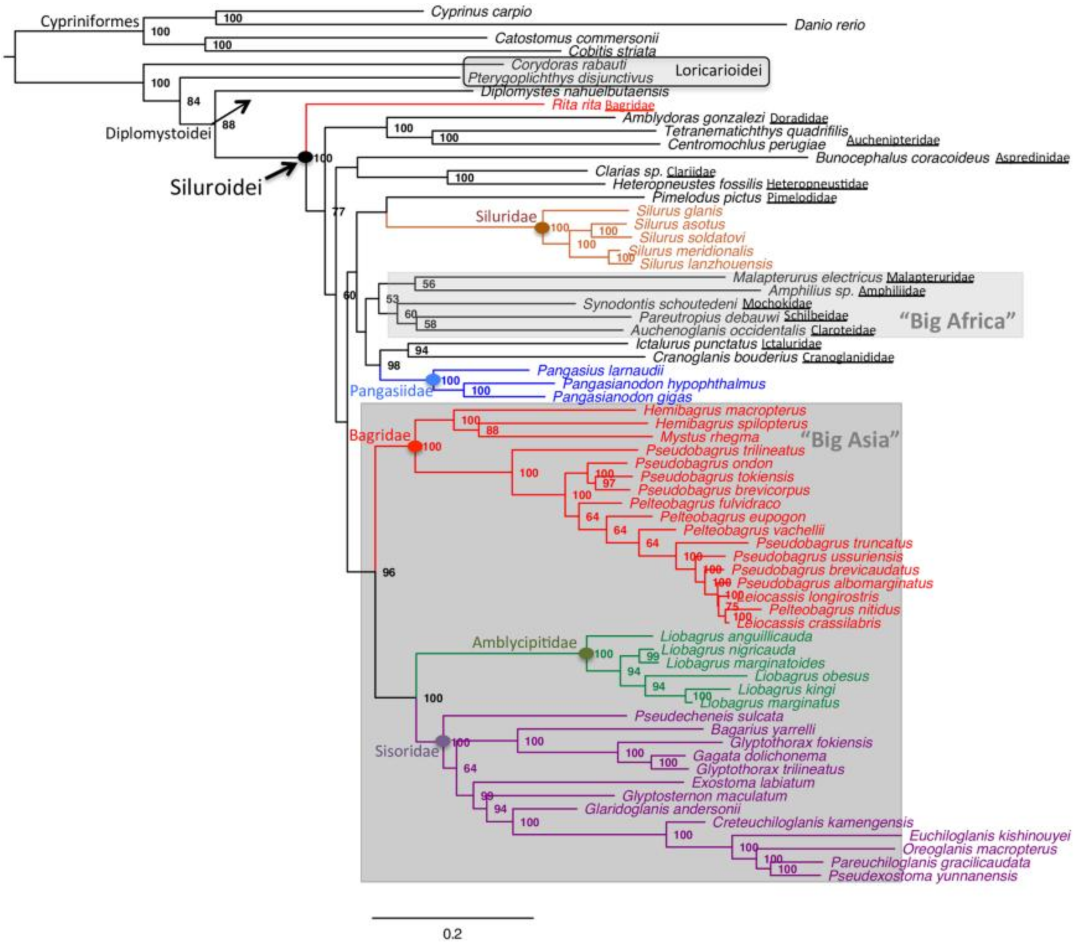

Figure 1 A Time-Calibrated Mitogenome Phylogeny of Catfish (*Teleostei*: *Siluriformes*) (Adopted from Kappas et al., 2016)

Image Caption: Image is best-scoring maximum-likelihood tree of 62 ingroup siluriforms and four cypriniform outgroup species obtained from the partitioned (12-3-R-T) RAxML analysis of 15 557 positions (Adopted from Kappas et al., 2016)

2.3 Methods of phylogenetic tree construction and divergence time estimation

Phylogenetic trees for catfishes have been constructed using various methodologies including neighbor-joining, maximum likelihood, maximum parsimony, and Bayesian inference. Genome-scale data sets and partitioned analyses within a combination with fossil calibrations and relaxed molecular clocks are used in current studies to obtain divergence time estimates (Kappas et al., 2016; Roxo et al., 2019). Such approaches have returned robust chronograms, suggesting that lineage divergences of large catfish happened during the Early Cretaceous and that following radiations were connected with continental drift and paleogeographic occurrences (Kappas et al., 2016; Roxo et al., 2019; Li et al., 2024).

2.4 Regional lineage divergence and evolutionary pathways of representative clades

Regional diversity in catfishes is ancient and recent in origin (Figure 2). For example, the African *Clariidae* have multiple independent origins of anguilliform body types, and Neotropical *Loricariidae* possess profound lineage diversity with large river basin and Andean uplift connections (Roxo et al., 2019). Repeated invasions of cave habitats by ictalurid catfishes in North America reflect parallel evolution and complex biogeographic histories (Janzen et al., 2023). Molecular phylogenies have revealed convergent evolution within small interstitial catfishes of the Amazonian and Atlantic forest systems, and novel subfamilies and clades in *Trichomycteridae* and *Loricariidae*, and highlighted the dynamic evolutionary histories of *Siluriformes* (Lujan et al., 2017; Costa et al., 2020).

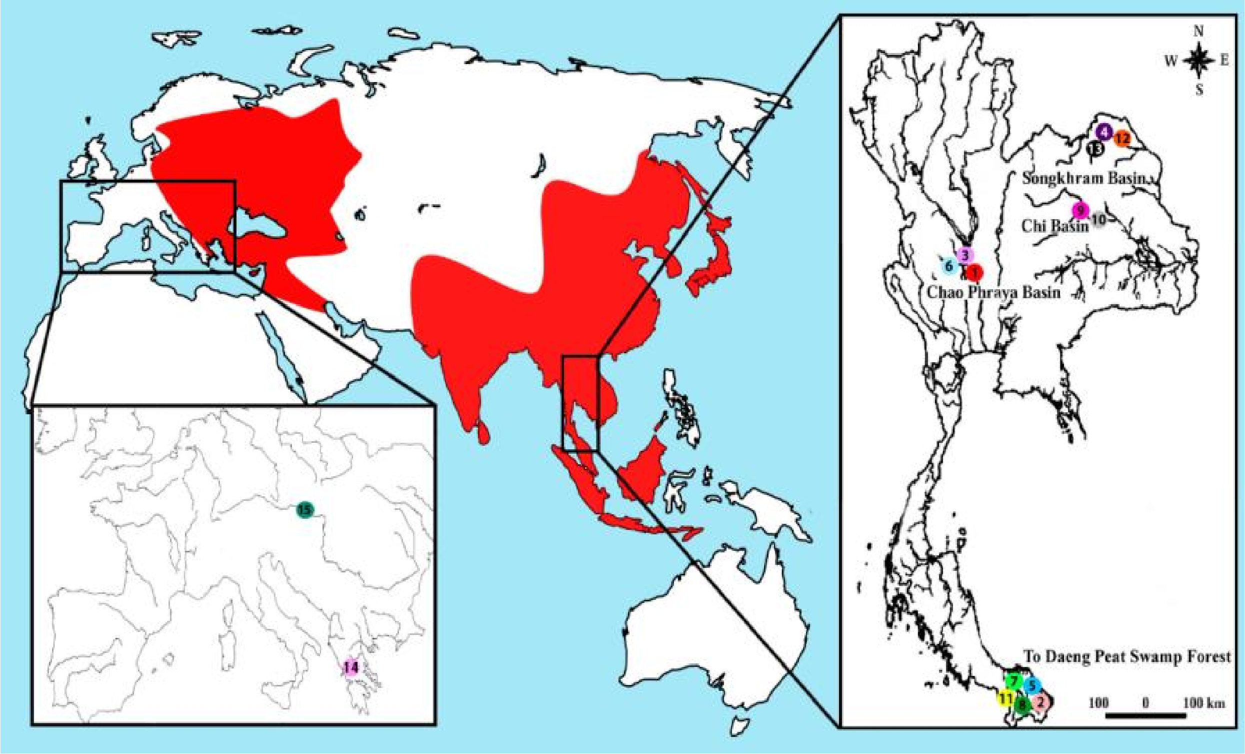

Figure 2 Current distribution of catfish (red) (Adopted from Ditcharoen etet al., 2019)

3 Geographical Origin and Evolutionary Centers

3.1 Hypotheses of freshwater fish origins in the context of ancient supercontinents

Evolution and global distribution of the freshwater fishes, including *Siluriformes*, are linked with the initial dissolution of supercontinents Pangaea and Gondwana. Vicariance hypotheses purport that fragmentation of the continents led to isolation and independent development of the large freshwater fish clades on different continents. However, both vicariance and episodes of long-distance dispersal have built up the current distributions as suggested by the fossil record and molecular evidence, with complex biogeographic processes tracing back to the Late Cretaceous and Cenozoic era (Capobianco and Friedman, 2018; Verma et al., 2024).

3.2 Support from fossil records and stratigraphic distributions for inferring origin sites

Fossil evidence from the Central Indian Late Cretaceous–Early Paleocene documents the initial diversification of the order *Siluriformes* and attests to their presence in the freshwaters such as lakes and rivers. The paleogeographic occurrence of these fossils and their South American counterparts implies that the areas underwent significant paleobiogeographic connectivity, which may have been promoted by the Phanerozoic history of Pangaea break-up and reorientation of the drainage basins related to massive geological activity like Deccan Traps volcanism (Verma et al., 2024). Stratigraphic data and fossil horizons possess confidence intervals of origin times for freshwater fish clades, which affirm the worth of reconciling paleontological and molecular information (Capobianco and Friedman, 2018).

3.3 Origin timing and possible source regions supported by molecular clock data

Molecular clock estimates, which are dated against the fossil record, assign the origin of the most important freshwater fish clades, for example, *Siluriformes*, to the Cretaceous (around 120~95 million years ago for Characiformes, and 125~95 million years ago for *Lepidosireniformes*). These ages are typically congruent with estimates based on fossils and suggest early diversification of *Siluriformes* and their sister groups was concurrent with Gondwanan break-up, supporting a southern hemisphere origin followed by radiation and dispersal (Capobianco and Friedman, 2018). Local literature also places Western Amazonia as a major evolutionary center and dispersal donor of South American freshwater fishes (Cassemiro et al., 2023).

3.4 The role of geological events in early distribution

Massive geological processes, such as mountain formation, river rearrangement, and volcanism, have played a pivotal role in the organization and radiation of freshwater fishes. For example, Andean mountain formation and rearrangement of South American river systems started rapid speciation and dispersal, notably in Western Amazonia, which was a center of origination for subsequent diversification (Cassemiro et al., 2023). In India, volcanism of Deccan Traps and associated drainage oscillations influenced the primary distribution of *Siluriformes*, and afterwards, worldwide events like the Cretaceous–Paleogene extinction and associated climatic changes influenced evolutionary directions (Guinot and Cavin, 2016; Verma et al., 2024). These geological events in conjunction with climatic fluctuations have given rise to regional radiations as well as world-wide patterns of dispersal in *Siluriformes* and other freshwater fishes (Luo et al., 2025; Beltrán‐López et al., 2025).

4 Global Dispersal Routes and Distribution Patterns

4.1 South America as a potential center of diversity and dispersal origin

South America has widely been accepted as a major hotspot of biological diversity and a likely center of origin for many freshwater fish clades, including *Siluriformes*. The geologically and hydrologically complex history of the continent, especially in the Amazon basin, has favored high endemism and species richness. Western Amazonia, in particular, has been recognized as a source region for freshwater taxa dispersal and diversification, with its unstable river networks and rich habitats providing evolutionary opportunities and constraints.

4.2 Hypothetical migration routes of lineages in Africa, Asia, and North America

Freshwater fish dispersal routes have been shaped by ancient and recent geologic processes. As an example, Gondwanan breakup and subsequent continental drift favored initial vicariant events, while later contacts—e.g., land bridges and river captures—subsequently allowed intercontinental migrations. South American to African and Asian migration has perhaps occurred over ephemeral land bridges or by marine barrier crossing under conditions of lowered sea level. In North America, dispersal would have been affected by river system formation and reorganization, and also by the existence of land bridges during glacial times.

4.3 Influence of hydrological connectivity, marine transgressions/regressions, and climate change

Hydrological connectivity, such as the creation of new river channels or mergers of drainage basins, has significantly contributed to dispersal and gene exchange between freshwater fish populations. Marine transgressions (rise in sea level) and regressions (sea level drop), by contrast, have made barriers create and dismantle each other in turns, regulating both isolation and admixture of lineages. Climate change, particularly during the Neogene and Pleistocene, has imposed habitat availability and connectivity shifts, leading to range expansions, contractions, and sudden diversification events (Wilson et al., 2016; Luo et al., 2020). These processes are reiterated in other taxa, e.g., mangroves and spiders, whose connectivity and dispersal are highly sensitive to environmental conditions and oceanography (Van Der Stocken et al., 2018; Luo et al., 2020).

4.4 Dual impacts of oceanic barriers and land bridges on population isolation and dispersal

Oceanic barriers, such as the Atlantic and Pacific Oceans, have long prevented dispersal of freshwater taxa, promoting allopatric speciation and regional endemism. Periodic closure of land bridges (e.g., the Isthmus of Panama) and stepping-stone archipelagos, on the other hand, have promoted transcontinental dispersal events occasionally. The presence or absence of these contacts, together with ecological requirements and dispersal abilities of species, has regulated the extent of population isolation or admixture. For instance, Miocene marine invasions created effective barriers to Amazonian freshwater biota, while following regressions and the re-establishment of land connections permitted recurrent dispersal and diversification (Moura et al., 2019).

5 Adaptive Evolution in Diverse Ecological Regions

5.1 Regional evolutionary trends in morphological and physiological adaptations to habitat differences

Adaptive evolution in many different ecological regions will lead to severe local specialization, with species evolving special morphological and physiological traits to suit exact habitat requirements. Local adaptive evolution may cause the dominance of certain species in single patches even when all species are capable of inhabiting a range of environments. This is driven by rapid adaptation to local habitats, which can preclude successful colonization by other species and lead to intense niche segregation at the local scale despite overlap at a larger regional scale (Leibold et al., 2018). In addition, flexibility of the primary functional traits, such as phenology and physiological tolerance, enables adaptation across different environments and promotes lineages' abundance and persistence across variable habitats (Cavender-Bares, 2018).

5.2 Niche differentiation and diversification of resource utilization strategies

Niche differentiation is a fundamental process of stable coexistence and diversification in ecological communities. The species may diverge in the utilization of resources, behavior, or metabolic strategy and therefore exploit alternative ecological opportunities and avoid direct competition. The availability of diverse resources, such as nutritional landscapes, can result in the evolution of specialized metabolic traits and resource utilization strategies and therefore adaptive diversification at the species and higher levels (Twining et al., 2020). This may be autocatalytic, with increased diversity fueling further diversification in processes like character displacement and positive diversity-productivity relationships (Calcagno et al., 2017).

5.3 Relationship between geographic isolation and speciation events

Geographic isolation is a key speciation driver because it restricts gene flow and allows populations to diverge ecologically and genetically. Ecological speciation may be initiated at or near environmental gradients or habitat boundaries by local adaptation (Aguirre-Liguori et al., 2017). Over time, isolated populations can build up adaptive divergence that culminates in the creation of new species. The interplay of local adaptation and dispersal limitation further underscores the role of geographic barriers to speciation events (Aguirre-Liguori et al., 2017; Aguilée et al., 2018).

5.4 Synergistic effects between global dispersal and local adaptation

Global dispersal and local adaptation are synergistic in affecting diversity and speciation patterns. Although dispersal aids species in colonizing new habitats and expanding their ranges, local adaptation helps them survive and diverge in novel habitats. Early invaders with rapid evolution to local habitats can monopolize new patches, thus leading to intense local niche segregation and, ultimately, regional neutrality so that species co-occur across landscapes but locally dominate (Leibold et al., 2018). This feedback loop maintains biodiversity at various scales and explains the co-occurrence of both niche differentiation and neutral patterns in the natural world (Leibold et al., 2018; Calcagno et al., 2017).

6 Biogeographic Models and Phylogeny-Based Methodological Applications

6.1 Biogeographic models integrating distribution and lineage data

Recent advances in biogeographic modeling underscore the integration of species distribution data with phylogenetic relationships to further our knowledge of historical and spatial lineage patterns. Multi-level Bayesian geostatistical models currently allow for simultaneous prediction of species presence and geographic pattern of morphological traits, while allowing for a consideration of genetic affinity and spatial autocorrelation. These integrated frameworks augment biogeographic projections with higher precision and help to address uncertainty in traditional species distribution models that do not account for phylogenetic structure (Humphreys et al., 2019). Other emerging methods combine ecological niche modeling with phylogenetic data in the construction of ancestral distributions, and in the estimation of environmental tolerances and extinct ranges of lineages (Guillory and Brown, 2021).

6.2 Practical applications of integrating phylogenetics with geographic information systems (GIS)

Phylogenetic information combined with GIS enables spatially explicit analysis of evolutionary and ecological patterns. The approach enables the geographic representation of the geographic ranges of lineages, assessment of spatial patterns of genetic diversity, and testing of alternative biogeographic hypotheses using coalescent simulations and distribution modeling. Integration is particularly valuable in taxa with limited fossil records because it applies both genetic and environmental data to simulate realistic phylogeographic scenarios and give conservation advice.

6.3 Use of paleoclimate reconstructions and ecological niche models to support ancient dispersal pathways

Ecological niche models (ENMs), when projected onto paleoclimate reconstructions, provide evidence of the potential historical range and dispersal route of lineages. By projecting ancestral niches and extrapolating them to ancestral climate conditions, researchers can estimate the range of ancestral taxa and identify climatic corridors or barriers that regulated dispersal and diversification (Guillory and Brown, 2021; Folk et al., 2023). Being coupled with fossil evidence, these models are further strengthened, allowing for more accurate reconstructions of evolutionary history across ancient periods and identifying ecological connectivity through time.

6.4 Predictive value of models for biological invasions and conservation strategy planning

Phylogenetic, ecological, and geographic information are combined into biogeographic models that have high predictive value for anticipating biological invasions and for informing conservation strategies. By simulating the response of species to environmental change and to dispersal barriers, such models can identify areas at risk of invasion, anticipate range shifts under future climate projections, and identify conservation priority areas by evolutionary distinctness and vulnerability (Humphreys et al., 2019; Culshaw et al., 2024). Blending niche modeling, phylogenetics, and paleoclimate information will enhance the ability to predict how lineages will respond to existing and future environmental change.

7 Concluding Remarks

New advancements in molecular phylogenetics and integrative biogeographic inference have shed light on the evolutionary past and worldwide dispersal of *Siluriformes*. Incorporating genomic information, fossils, and new statistical approaches has revealed complex patterns of lineage diversification with robust support for the role of ancient continental break-up and paleogeographic events in shaping catfish distribution. Such approaches have also highlighted the central role of both vicariance and dispersal in creating contemporary diversity and distribution of catfishes worldwide.

In spite of tremendous progress, there are still numerous controversies and lacunae in the data. Fossil-living taxon integration remains challenging, as missing fossil records could possibly create ambiguity regarding phylogenetic placement and divergence time estimation. Choice of phylogenetic methods (e.g., tip-dated Bayesian vs. parsimony) may create different tree topologies, especially when there is a weak character signal or high percentage of missing data in a particular region. Besides, the power of incomplete or ambiguous molecular data, modeling assumptions, and calibration methods continues to influence the validity of phylogenetic inference and biogeographic analysis. These issues assert the need for more robust datasets and open methodology.

The future of evolutionary research on *Siluriformes* is the reconciliation of high-throughput genomic data, statistical phylogenetics, and paleogeographic modeling. Data integration of morphological and molecular datasets from fossil and extant groups will provide a clearer representation of evolutionary history and trait evolution. Simulation-based approaches, null-hypothesis testing, and modeling uncertainty explicitly will make inferences of phylogenetic and biogeographic stronger and more confident. With the appearance of new fossil discoveries and improved paleoclimate reconstructions, these integrative frameworks will provide increasingly accurate ancient dispersal route reconstructions and inform conservation policy for catfishes and other freshwater groups.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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