



Mitogenomic perspectives into sciaenid fishes' phylogeny and evolution origin in the New World

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ABSTRACT

Sciaenid fishes are widely distributed throughout the coastal waters and estuaries of the world. A total of 23 genera of this family are endemic to the Old World. However, evolutionary relationships among Old World sciaenid fishes and their origin have remained unresolved despite their diversity and importance. Besides, hypotheses that explain the origin and biogeographical distribution of sciaenid fishes are controversial. In this study, the complete mitochondrial genome sequences of seven representative sciaenid species were determined and a well-resolved tree was recovered. This new timescale demonstrated that the sciaenid originated during the late Jurassic to early Cretaceous Period. The estimated origin time of sciaenid fish is 208 Mya, and the origin of Old World sciaenid is estimated at 126 Mya. Reconstruction of ancestral distributions indicated a plesiomorphic distribution and center of origin in the New World, with at least one lineage subsequently dispersed to the Old World. Moreover, we conclude that the common ancestors of Old World sciaenid fishes were derived from species of New World.

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1. Introduction

Sciaenid fishes (Croaker or drum fish, family Sciaenidae) are commercially important fish groups in temperate to tropical coastal waters and estuaries throughout the world. They are particularly abundant at the mouths of large continental rivers, but are poorly known as groups that lived in seawater (Sasaki, 1989). This family comprises 67 to 78 genera, of which 23 are endemic to the Old World (Chao, 1986). External morphological features exhibited by the family are diverse, especially in body form and mouth position. Structures related to sound production, gas bladder and otolith structures are also markedly diverse, which is a distinctive feature of this family. Although sciaenid fishes have attracted a great deal of attention from biologists, who have focused on systematics, evolution and zoogeographics, interrelationships of most Old World Sciaenidae genera and the origin of Sciaenidae have remained elusive for a long time.

Morphological disparity among the Old World sciaenid fishes has resulted in numerous conflicting phylogenetic hypotheses (Figs. 1A–H). Chu et al. (1963) classified the sciaenid fishes of China and adjacent areas based on five characters including structure of gas bladder, otolith, sensory pores on snout, lower jaw, and dentition. In their taxonomy, subfamily Argyrosominae and Pseudosciaeninae were sister-groups. The former is composed of the genera *Argyrosomus* and *Nibea*, and the latter of the genera *Atrobucca*, *Miichthys*, *Collichthys* and *Pseudosciaena* (Fig. 1A). Whether the two subfamilies are monophyletic groups or just artificial assemblages has been widely debated (Mohan, 1969;

Taniguchi, 1970; Trewavas, 1962). Trewavas (1962) and Mohan (1969) pointed out that Chu et al.'s classification lacks sampling materials from the Indian Ocean. In contrast to Chu et al.'s taxonomy, Argyrosominae was considered to be polyphyletic in subsequent hypotheses based on more samples and more morphological characters. Taniguchi (1970) and Mohan (1969) suggested a close affinity between *Atrobucca*, *Argyrosomus*, and *Nibea*, although the interrelationships among these genera are uncertain (Figs. 1D and F). Moreover, Taniguchi (1969a, 1969b), Trewavas (1977) and Sasaki (1989) placed *Argyrosomus* and *Nibea* into separate main clades (Figs. 1B, C, G and H). Besides Chu et al.'s conclusion (1963), monophyly of Pseudosciaeninae was also recovered in the study by Taniguchi (1970) in which sciaenid fishes phylogeny was analyzed based on the feature of dentition (Fig. 1E). These results, however, are in conflict with reports by Taniguchi (1969a, 1969b), Mohan (1969), Trewavas (1977) and Sasaki (1989), in which *Miichthys* was not grouped with *Collichthys* and *Pseudosciaena*, but placed into different main clades (Figs. 1B, C, F, G and H). Because of a lack of clear synapomorphies, and often unclear character homology, the ability of these morphological characters to resolve phylogenetic relationships is limited.

Previous molecular investigations of Old World sciaenid fishes phylogeny have relied primarily on partial mitochondrial or nuclear gene sequences, which offered controversial resolutions or support values were in general low (Figs. 1I–Q). Hypotheses based on such short sequences are conflicting and the interrelationship of many genera is still uncertain (Figs. 1I–Q). Deep nodes in the constructed phylogenetic trees were generally weak, suggesting that short sequences might not be sufficient to solve a particularly difficult phylogenetic problem. It has been shown that the use of complete mitochondrial genome

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sequences minus non-coding sequences is more powerful than single gene sequences. Moreover, complete mitochondrial genome is a small-scale genome suitable for complete sequencing and thus provides

substantial amount of DNA and amino acid data for phylogeny reconstruction. Several phylogenetic studies have significantly advanced our understanding of fish evolution by using sequences derived from

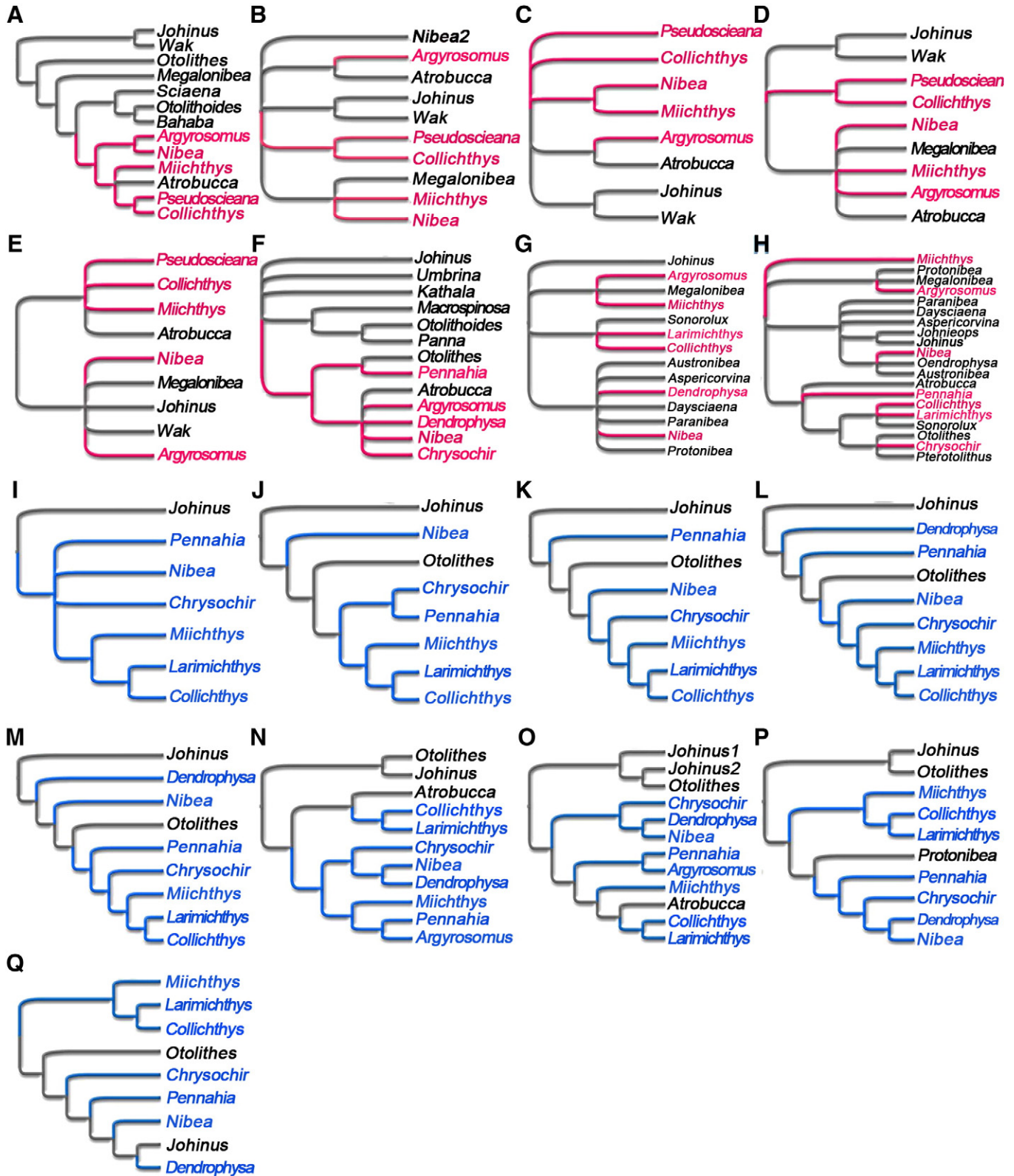


Fig. 1. Alternative phylogenetic hypotheses of the sciaenid fishes. A) Morphology-based hypothesis of Chu et al. (1963). B–D) Morphology-based hypotheses of Taniguchi (1969a, 1969b, 1970). E) Morphology-based hypothesis of Tanguichi in, 1970. F) Morphology-based hypothesis of Mohan (1969). G) Morphology-based hypothesis of Trewavas (1977). H) Morphology-based hypothesis of Sasaki (1989). I–M) Molecular-based hypotheses of Chen (2007), Meng et al (2004) and Tong et al (2007). N, O) Molecular-based hypotheses of Liu et al. (2010). P) Molecular-based hypothesis of Cheng et al. (2010). Q) Molecular-based hypothesis of Ma et al. (2012). Species used in the present study were colored as red (in morphological data-based trees) or blue (in molecular data-based trees).

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