

Molecular phylogeny of the Sciaenidae based on the complete mitochondrial sequences

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ABSTRACT

In this study, 45 complete mitochondrial genomes of Sciaenidae species obtained from GenBank were analyzed. Our results suggested that mitochondrial genomes could be an effective marker for resolving the phylogeny of Sciaenidae species. Phylogenetic relationships indicated that *Johnius* species are more ancient species among all the species that were used in this analysis because *Johnius* species stands on the root of the polygenetic tree. However, *Collichthys niveatus* could not separate from *Larimichthys polyactis* based on the complete mtDNA which indicate that these two species needs further study in the future.

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The family of Sciaenidae is commercially important species which is one of the most species of the order Perciformes, with about 70 genera and more than 270 species worldwide distribution (Nelson et al. 2016). Sciaenidae species are very similar in morphology and synonyms always recorded in different regions [such as *Argyrosomus japonicus* and *A. amoyensis* were recorded as *Nibea japonica* and *N. miichthioides*, respectively by Zhu et al. (1963)]. However, *A. japonica* and *N. miichthioides* were recorded as *A. ponicus* and *A. amoyensis* respectively by the fish database of Taiwan (fishdb.sinica.edu.tw), as well as Fishbase (fishbase.org). In addition, few studies have assessed the phylogenetic relationship of the sciaenids, and those that are available do not provide a clear explanation of the relationship among the evaluated taxon.



In this study, 25 Sciaenidae species of 45 complete mtDNA sequences were assessed from GenBank (Supplement Table 1) and were used to analyze their phylogenetic. A 600–900bp tandem repeat sequences were identified between tRNA-Thr and tRNA-Pro among the *Johnius* species. The Maximum Likelihood tree successfully divided the Sciaenidae species and *Thunnus* species, and the most all gene species were well determined except for the *N. coibor*, *Chrysochir aureus*, *Collichthys niveatus*, and *N. miichthioides*. The results of the phylogenetic tree indicated that *Johnius* species is a more ancient species since it stands at the root of the tree (Figure 1). In addition, a 600–900bp tandem repeat sequences were identified among *Johnius* species

making it much larger (Supplement Table 2) than other species in this study.

Nibea species were well claded into a separate group except for *N. miichthioides*, while *N. miichthioides* were divided into groups of *A. ryrosomus*, *N. miichthioides*, and *A. amoyensis* were synonyms determined with otoliths and bladder by Zhu et al. (1963) suggesting that *N. miichthioides* and *A. amoyensis* were the same species. However, complete mtDNA failed to differentiate *A. amoyensis* and *A. japonicus*, these results were in concordance with the study done by Lv (2017), stating that geographical variation may contribute to this confusion.

Chrysochir aureus 1 was divided into the *Protonibea* species, while *C. aureus* 2 and *C. aureus* 3 were claded with *Nibea* species. COI, Cytb, and ND2 were used to determine the phylogenetic relationship among Sciaenidae species, misidentification of morphological species may lead to confusing results (Lv 2017), yet, it may contribute to this strange phenomenon.

Collichthys lucidus were well identified out of *Larimichthys crocea* and *L. polyactis*, but, *Col. niveatus* could not separate from *L. polyactis*. Bioinformatics was used to analyze the phylogenetic relationship among eight Sciaenidae species as elaborated by Sun et al. (2017). Different process results indicate that *Col. niveatus* was very close to *L. crocea* and *L. polyactis*, but much farther from *C. lucidus*. The results produced in this study were supported by analysis done by Sun et al.

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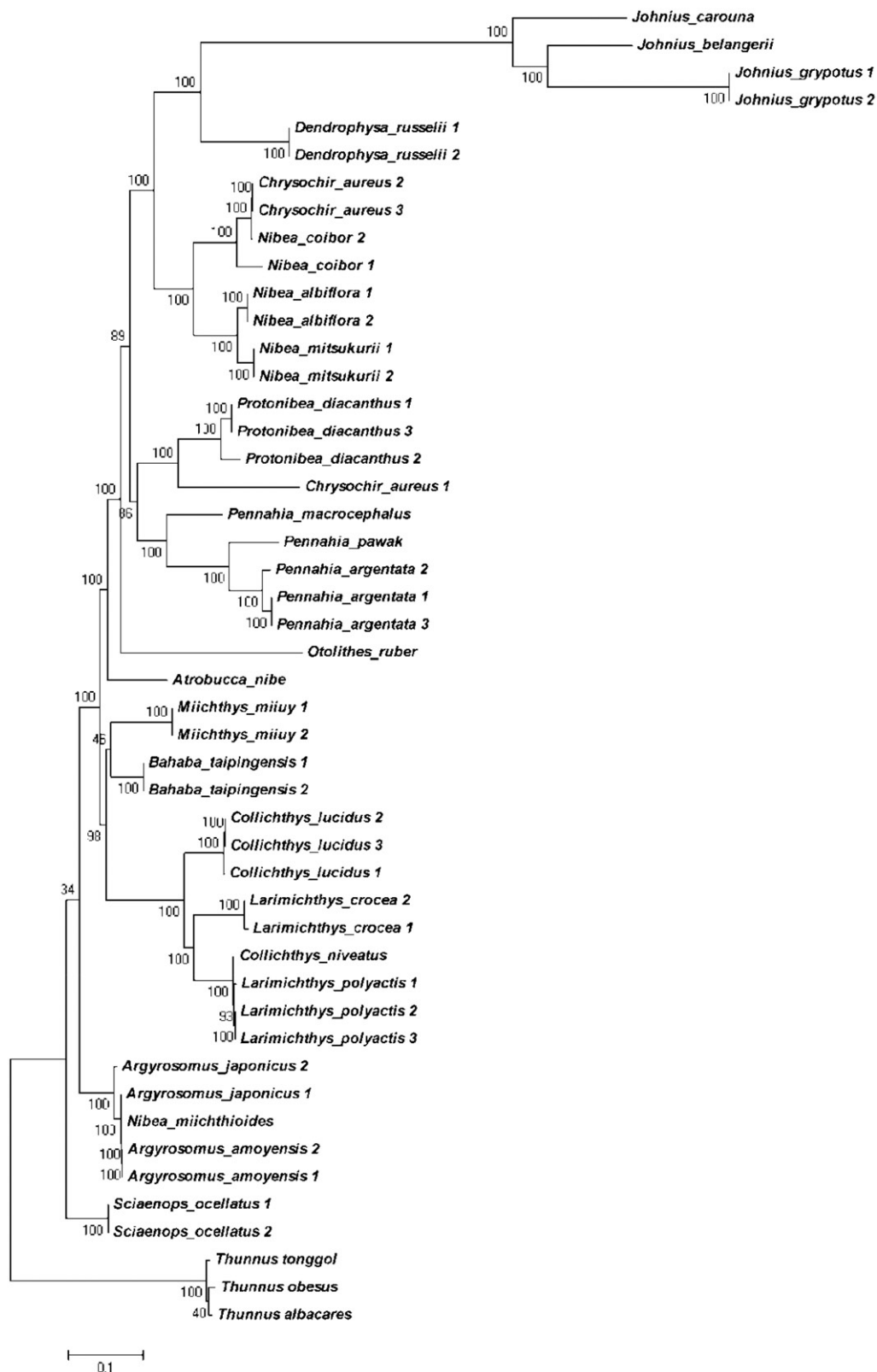


Figure 1. Phylogenetic relationship among 48 Sciaenidae sequences from GenBank based on Maximum Likelihood method.

(2017), which indicated that the taxa status of *Col. niveatus* needed more advanced study in the nearest future.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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