

REVISION OF CROAKERS (PERCIFORMES: SCIAENIDAE)  
IDENTIFICATION BY USING INTEGRATIVE APPROACHES

NORHAFIZ HANAFI BIN AHMAD SHAH

MASTER OF SCIENCE

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**July 2016**

**Main Supervisor : Seah Ying Giat, Ph. D.**

**Co-Supervisor : Lilian Wong, Ph. D.**

**School : School of Fisheries and Aquaculture Sciences**

The present study describes the meristic and morphometric, comparative analysis and molecular phylogeny of croakers in Peninsular Malaysia. Several series of sampling were carried out in the fish landing port at Terengganu and Kuala Kurau, Perak during March 2013 until December 2014 using commercial trawler. Fifteen species of croakers were caught throughout the study that is *Otolithes ruber*, *Panna microdon*, *Chrysochir aureus*, *Larimichthys terengganui*, *Nibea semifasciata*, *Pennahia anea*, *Pennahia argentata*, *Dendrophysa russelli*, *Johnius amblycephalus*, *Johnius belangerii*, *Johnius boorneensis*, *Johnius carouna*, *Johnius macrorhynchus*, *Johnius plagiotoma* and *Johnius weberi*. Fish species were examined for their meristic and morphometric differences. Comparative approach was used to show the distinct measurements between genera and species according to the morphometric parameters. The analysis divided the croaker

species into two major group which are Sciaenid- and *Johnius*-groups using SPSS version 22. Discriminant analysis suggested Sciaenid-group were significantly dissimilar through Kruskal-wallis test in lower jaw length, eye diameter, interorbital width, body depth, base dorsal 2 length and second anal spine length. While through detailed examination in *Johnius*-group, it had very high similarities in meristic counts and morphometric measurements. However, *Johnius*-group were significantly dissimilar in maxillary length, interorbital width, second anal spine length, longest dorsal 1 base length, pectoral length and gill rakers length. 16S mitochondrial rDNA genes were used to inferred the phylogenetic relationships among the croakers in this study. Analysis tree generated by MrBayes and MEGA6.0, suggested that all the genera were monophyletic. *Panna microdon* and *Otolithes ruber* formed the basal branch of the other croaker species but with low bootstrap value. *Pennahia* formed a sister group to genus *Chrysochir* and *Larimichthys*. Furthermore, *Nibea semifasciata* and *Dendrophysa russelli* were a sister group to *Johnius*, with the latter had high bootstrap value. The molecular phylogenetic positions of the sciaenids studied were identical with morphological delineation. This study has shown that 16S mitochondrial rDNA is a good marker phylogenetic analysis of the Sciaenidae. Present study will help the taxonomist and fisheries scientists to distinguish croakers species in Malaysian waters especially problematic species which has high similarity morphology respectively.

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**SEMAKAN PENGECAMAN GELAMA (PERCIFORMES: SCIAENIDAE)**

**MENGGUNAKAN PENDEKATAN BERSEPADU**

**NORHAFIZ HANAFI BIN AHMAD SHAH**

**Julai 2016**

**Penyelia Utama : Seah Ying Giat, Ph. D.**

**Penyelia Bersama : Lilian Wong, Ph. D.**

**Pusat Pengajian : Pusat Pengajian Sains Perikanan dan Akuakultur**

Kajian ini menerangkan meristik dan morfometrik, analisis perbandingan dan filogeni molekul ikan gelama di Semenanjung Malaysia. Beberapa siri persampelan telah dijalankan di pelabuhan pendaratan ikan di Terengganu dan Kuala Kurau, Perak di sepanjang bulan Mac 2013 sehingga Disember 2014 yang menggunakan pukut tunda komersial. Lima belas spesies ikan gelama telah ditangkap di sepanjang kajian ini iaitu *Otolithes ruber*, *Panna microdon*, *Chrysochir aureus*, *Larimichthys terengganui*, *Nibea semifasciata*, *Pennahia anea*, *Pennahia argentata*, *Dendrophysa russelli*, *Johnius amblycephalus*, *Johnius belangerii*, *Johnius boorneensis*, *Johnius carouna*, *Johnius macrorhynchus*, *Johnius plagiostoma* dan *Johnius weberi*. Spesies ikan telah diperiksa dari segi perbezaan meristik dan morfometrik. Pendekatan perbandingan telah digunakan untuk menunjukkan pengukuran nyata di antara genus dan spesies mengikut parameter morphometrik.

Analisis ini telah membahagikan spesies ikan gelama kepada dua kumpulan utama iaitu kumpulan Sciaenid dan *Johnius* menggunakan SPSS version 22. Analisis diskriminasi mencadangkan kumpulan Sciaenid berbeza signifikan melalui ujian Kruskal-wallis secara ketara pada panjang rahang bawah, diameter mata, jarak antara orbit, kedalaman badan, panjang spina anal kedua. Sementara, melalui pemeriksaan terperinci dalam kumpulan *Johnius*, ia mempunyai persamaan yang sangat tinggi dalam ukuran meristik dan morphometrik. Walau bagaimanapun, tujuh spesies *Johnius* adalah berbeza secara panjang maksila, jarak antara orbit, panjang spina anal kedua, panjang tapak dorsal 1 terpanjang, panjang pektoral, dan panjang raker insang. Jujukan 16S mitokondria rDNA telah digunakan untuk menyimpulkan hubungan filogenetik di antara ikan gelama. Menurut pokok analisis yang dihasilkan oleh MrBayes dan MEGA6.0, mencadangkan bahawa semua genera adalah monofiletik. *Panna microdon* dan *Otolithes ruber* membentuk cabang asas kepada spesies ikan gelama lain tetapi dengan nilai butstrap yang rendah. *Pennahia* membentuk satu kumpulan beradik kepada *Chrysochir* dan *Larimichthys*. Tambahan pula, *Nibeaa semifasciata* dan *Dendrophysa russelli* adalah kumpulan beradik kepada *Johnius*, dengan mempunyai nilai bootstrap tinggi. Kedudukan filogenetik molekul ikan gelama yang dikaji adalah selari dengan penggambaran morfologi. Kajian ini telah menunjukkan bahawa 16S mitokondria rDNA merupakan penanda analisis filogenetik yang bagus kepada famili Sciaenidae. Kajian ini akan membantu ahli taksonomi dan saintis perikanan untuk membezakan spesies gelama di perairan Malaysia.