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合齒魚科之分子系統分類
Molecular systematics of Lizardfishes
(Aulopiformes: Synodontidae)

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Molecular Systematics of Lizardfishes
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本論文係王世仔君(R05241204)在國立臺灣大學海洋研究所所完成之碩士學位論文，於民國 107 年 7 月 23 日承下列考試委員審查通過及口試及格，特此證明

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摘要

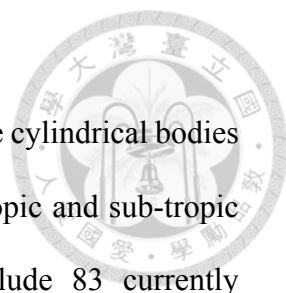


合齒魚科 (Synodontidae) 包含四個屬與八十三個有效種，其下可再分為兩個亞科：鐮齒魚亞科 (Harpadontinae) 內包含了鐮齒魚 (龍頭魚) 屬 (*Harpadon*) 與蛇鰻屬 (*Saurida*)；狗母魚亞科 (Synodontinae) 內則包含了狗母魚屬 (*Synodus*) 及大頭狗母魚屬 (*Trachinocephalus*)。本科魚類為底棲性掠食者，體橢圓形或延長，具有極寬的口與尖利的牙齒，多棲息於熱帶及副熱帶海域的沙泥地。自從此類群之分類於西元 1861 年被 Gill 建立以來，其地位一直存在爭議，各屬下之物種更常發生因外型相似而有誤鑑之情形，近一步分類上的修訂仍需仰賴完善的親緣關係建構。鑑此，本研究利用分子系統分類學的方法，針對合齒魚科的物種探討以下的問題：(1) 建構較完整的合齒魚科及其相對於其他仙女魚目物種的親緣關係 (2) 檢驗合齒魚科及其下四屬是否皆為單系群 (3) 在已建立的完善親緣關係下推估合齒魚的分化時間 (4) 鑑驗目前合齒魚科下各物種的種名有效性及探索其物種之多樣性。本研究中建立了兩種型態的資料矩陣，一為包含了四個核基因 (*RH*, *RAG1*, *ZIC1* 和 *ENCI*) 與三個粒線體基因 (*COI*, *12S* 和 *16S*) 的多基因資料矩陣，用以建構合齒魚科及其相對於仙女魚目物種間之親緣關係；另一種則為搭配種類界定軟體 (ABGD 與 bPTP) 用以進行物種界定的粒線體 *COI* 基因資料矩陣，其中包含了 975 條序列 (202 條為本研究提供，773 條則由資料庫或私人資源取得) 與 52 個已知種。根據結果顯示，合齒魚科並不是一個單系群，然而其下之兩個亞科卻各自為單系群。因此，本研究結果支持將現今分類的龍頭魚亞科及狗母魚亞科提升至科別的等級。而在原先分類下的四個屬中，僅龍頭魚屬與大頭狗母魚屬為單系群，蛇鰻屬與狗母魚屬則為多系群，分別具三及四個分

支。其中龍頭魚屬與蛇鰻屬的其中兩個分支為姊妹群，而大頭狗母魚屬則與狗母魚屬中的其中兩個分支形成的單系群為姊妹群。分化時間推估顯示出狗母魚科的最近共同祖先出現於白堊紀晚期，而龍頭魚科的最近共同祖先則是出現於始新世。此外，物種界定分析的結果中，本研究定義約 87 個假定物種（演化操作單元），此數目遠高於本研究中所包含的已知種，顯示出此類群的生物多樣性可能有被低估的情形。本研究對於合齒魚的系統分類提供了一個更深入的觀點，並對於後續分類學及演化學的相關研究提供了一個完善的架構。

關鍵字： 合齒魚科、分子系統分類、親緣關係、分化時間、生命條碼、種類界定

Abstract

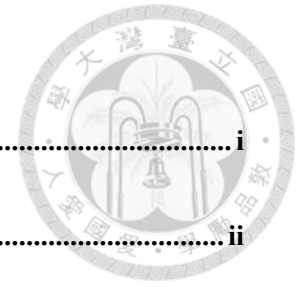


Lizardfishes are a group of benthic carnivorous fishes that have cylindrical bodies and relatively large mouths, live mostly in the sandy bottom of tropic and sub-tropic seas. Belong to the family Synodontidae, the lizardfishes include 83 currently recognized species in 4 genera, *Synodus*, *Harpadon*, *Saurida*, and *Trachinocephalus*. However, the taxonomy of the family has been controversial since it had been established by Gill (1861). A robust phylogeny of this family is required for further taxonomy revision. In this study, we aimed to: (1) reconstruct a comprehensive phylogeny of the family Synodontidae along with its aulopiform allies; (2) test the monophyly of the family and the four recognized genera; (3) estimate the divergence times of synodontids under a robust phylogeny; (4) investigate the validity of the existing species within the family with an integrated approach in taxonomy (i.e. species delimitation). To infer the phylogeny of the family, a multi-gene dataset was composed of four nuclear genes (*RH*, *RAG1*, *ZIC1* and *ENCI*) and three mitochondrial (*COI*, *12S*, *16S*) genes. The datasets used for the species delimitation analysis with two programs (ABGD and bPTP) included 975 mitochondrial *COI* gene sequences, of which 202 were newly generated in this study and 773 were retrieved from public and private sources. In the results, the Synodontidae was not monophyletic while each of the two subfamilies of the Synodontidae was resolved as a monophyletic group. Therefore, the elevation of the two subfamilies Synodontinae Gill 1861 and Harpadontinae Bleeker 1875 is suggested, i.e., from subfamily level to family level. Within the family, only two out of the four currently recognized genera are monophyletic, which are *Harpadon* and *Trachinocephalus*. The monophyletic *Harpadon* is sister to the clade composed of two of the four well-resolved *Saurida* lineages, while the monophyletic genus *Trachinocephalus* is sister to the clade composed of two of the three well-resolved

Synodus lineages. The divergence time estimations recovered that the most recent common ancestor of the family Synodontidae arose during the Late Cretaceous, while that of the family Harpadontidae occurred during the Eocene. From the species delimitation analyses, 87 putative species (OTUs) were observed out of the 52 recognized species included in the study, indicating an underestimated biodiversity of the family. This study offers an insight into the systematics of the family Synodontidae, and provides a framework for further taxonomic and evolutionary studies.

Key words: Synodontidae, molecular systematics, phylogeny, divergence time, Automatic Barcoding Gap Discovery, bPTP

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1. Introduction

The aulopiform family Synodontidae (Teleostei), known as lizardfishes, comprises 83 species in 4 genera that are classified into two subfamilies (Eschmeyer *et al.* 2018). The subfamily Synodontinae includes two genera, *Synodus* Scopoli 1777 (49 species) and *Trachinocephalus* Gill 1861 (3 species) and the subfamily Harpadontinae includes the other two genera, *Saurida* Valenciennes 1850 (24 species) and *Harpadon* Lesueur 1825 (7 species) (Eschmeyer *et al.* 2018; Froese & Pauly 2018). This family is believed to have its closest relationship to its aulopiform allies, Aulopidae and Pseudotrichonotidae, based on the most updated morphological evidence, which altogether are placed in the same aulopiform suborder, the Aulopoidei (Nelson *et al.* 2016).

Being benthic carnivorous predators, lizardfishes are mostly found over sandy or muddy bottoms in shallow to mid waters of continental shelves, with several species (e.g., *Synodus variegatus* (Lacepède 1803) and *Saurida gracilis* (Quoy & Gaimard 1824)) occurring on coral reefs (Norman 1935). Some species, for example the species from the genus *Harpadon* exhibit a benthopelagic habit and are able to live in deeper waters (Chaiyapo 2013; Ganga *et al.* 2015), with the greatest depth reported at 801m (*Harpadon erythraeus*) (Klausewitz 1983). Geographically, although the family Synodontidae can be found in tropical and subtropical marine waters throughout the world, there is little evidence to show that any of the species have a pattern of wider or global distribution. The blunt-nose lizardfish, *Trachinocephalus myops* (Forster 1801), was thought to have a nearly circum-tropical and subtropical distribution (Briggs 1960). However, recent studies (Polanco *et al.* 2016; Wang *et al.* in press, see Appendix III) based on morphological and molecular evidence, challenged this traditional point of view, and recognized three distinct species. One of the species, *T.*

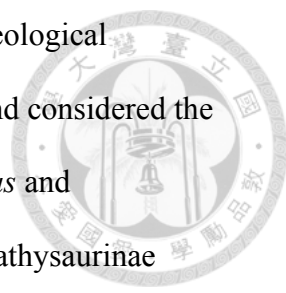
gauguini Polanco, Acero & Betancur 2016, was recently described based on the specimens collected in French Polynesian waters around the Marquesas Islands in the southern central Pacific. New evidence from the study of Wang *et al.* (in press) showed the distribution range of this species extends to Papua New Guinean waters, in the western Pacific. The other two congeneric species, *T. myops* and *T. trachinus* (Temminck & Schlegel 1846), recognized by Polanco *et al.* (2016) are distributed in the Atlantic and the Indo-West Pacific Oceans (except the Marquesas), respectively.

In their overall appearance, the lizardfishes are small to median sized fishes with elongated bodies (Nelson *et al.* 2016; Norman 1935; Russell 2002), and the species are characterized by the following combined characters: head depressed to compressed; maxilla reduced or very slender (degenerate in species within the genus *Harpadon*); large mouth with oblique gape; laterally directed eye of small to moderate size; adipose eyelid on anterior and posterior margins of eye; branchiostegal rays 8-26; pelvic fin with 8 (Synodontinae) or 9 rays (Harpadontinae); dorsal fin about mid-way on back with first two rays unbranched; dorsal adipose fin usually present over base of anal fin (except *Synodus sageneus*, with a reduced or absent adipose fin); body coloration variable, but usually brightly colored for reef species and plainly colored for deeper water species.

While the species of the family are similar in morphology, members of the two subfamilies can be distinguished from each other by the number of teeth bands on the palate (single band in Synodontinae, double bands in Harpadontinae) and relative length of the inner and outer rays of the pelvic fins (Synodontinae: inner rays of pelvic fin much longer than outer ones; Harpadontinae: inner rays of pelvic fin in almost equal length to the outer ones). The common features of the subfamily Synodontinae also include: scales along lateral line remain constant in size, dorsal fin

rays 10-15, anal fin rays 8-16, 8 pelvic fin rays and usually moderate body size (maximum length about 60 cm). Within this subfamily, the genus *Synodus* is characterized by having a snout length similar to or longer than eye diameter, while the genus *Trachinocephalus* has a relatively short snout length and higher number of anal fin rays (15-16 rays compare to 8-15 rays in *Synodus*). The species from the other subfamily, Harpadontinae, are characterized by having 9 pelvic fin rays with 9-15 dorsal and anal fin rays. The genus *Saurida* can be further distinguished by the presence of scales on procurrent and primary caudal fin rays. The genus *Harpadon* is a highly specialized group within the family with some derived characters, such as an extremely short maxilla and the absence of the ethmo-maxillary ligament, and some species lack cycloid scales on the head (Norman 1935; Chaiyapo 2013).

Regan (1911) included the lizardfishes in the family Synodontidae under the order “Iniomi”. Within the same order, Gosline *et al.* (1966) followed Regan’s classification but further suggested a division of the Synodontidae into two distinct families, Synodontidae and Harpadontidae (Fig. 1). Gosline *et al.* (1966) proposed a closer relationship of these two families with eight other “aulopiform”-like taxa (Aulopidae, Bathysauridae, Bathypteroidae, Ipnopidae, Chlorophthalmidae, Notosudidae, Myctophidae, and Neoscopelidae), and grouped them together as the superfamily Myctophoidea. Later, Rosen (1973) established the order Aulopiformes in which two suborders (Aulopoidei and Alepisauroidi) were recognized based on the presence of an elongated uncinat process on the second epibranchial located within the gill arches, and excluded the two myctophiform families (Myctophidae and Neoscopelidae) from the Aulopiformes (Fig. 1). Under the suborder Alepisauroidi, Rosen (1973) proposed a new superfamily Synodontoidea comprising the Synodontidae and Harpadontidae, Giganturidae and two fossil genera, †*Sardinius* and



†*Volcichthys* (Rosen 1973) (Fig. 1). Sulak (1977) examined the osteological characteristics of the benthic "Myctophiforms" (= Aulopiformes) and considered the family Synodontidae to be three subfamilies: Synodontinae (*Synodus* and *Trachinocephalus*), Harpadontinae (*Harpadon* and *Saurida*), and Bathysaurinae (*Bathysaurus*) (Fig. 1). R. K. Johnson (1982) studied the distribution of selected characters among iniomes and the phylogeny inferred in his study confirmed Sulak's (1977) placement of bathysaurids within the synodontid + harpadontid lineage, and gave family status to the three previously recognized synodontid subfamilies, under the superfamily Synodontoidea. Later, Okiyama (1984) reviewed R.K. Johnson's (1982) hypothesis of Synodontoidea by considering evidence from aulopiform larvae. He noted that *Bathysaurus* larvae are highly specialized and the larval morphology did not support a close relationship between bathysaurids and the other two families in Synodontoidea (Synodontidae and Harpadontidae). Baldwin & Johnson (1996) re-investigated the relationships among aulopiform genera based on a cladistic analysis of 118 morphological characters, and suggested four aulopiform suborders (Fig.1). The suborder Synodontoidei included three families: Aulopidae (*Aulopus*), Pseudotrichonotidae (*Pseudotrichonotus*), and Synodontidae (*Harpadon*, *Saurida*, *Synodus*, and *Trachinocephalus*) (Fig. 1). Sato & Nakabo (2002) extended the classification as defined in Baldwin & Johnson (1996) with an addition of the family Paraulopidae in the Synodontoidei (Fig. 1). Davis (2010) combined the morphological and molecular evidences to examine the evolutionary relationships of the Aulopiformes, and confirmed the monophyly of the Synodontidae under the suborder Aulopoidei (= Synodontoidei); the other two families within the suborder are Aulopidae and Pseudotrichonotidae (Fig.1, Fig. 2b). Following Davis's (2010) phylogenetic hypothesis, Nelson (2016) recognized the "monophyletic" Synodontidae

to be a valid family that includes two subfamilies: Synodontinae (*Synodus* + *Trachinocephalus*) and Harpadontinae (*Saurida* + *Harpadon*) under the suborder Aulopoidei (Nelson 2016). This suborder was placed with two other suborders (Paraulopoidei and Alepisauroidae) within the currently recognized Aulopiformes whose monophyly was supported by several synapomorphic characters, for example, the presence of an enlarged uncinat process on second epibranchial and the absence of swim bladder (Marshall 1954; Gosline *et al.* 1966; Rosen 1973; Sulak 1977; Johnson 1982; Rosen 1985; Baldwin & Johnson 1996; Sato & Nakabo 2002; Davis 2010; Chaiyapo 2013).

Although the closer affinity between the two synodontid subfamilies has been mentioned from previous studies of aulopiform interrelationships (Rao 1977; Hartel & Stiassny 1986; Baldwin & Johnson 1996; Davis 2010), few studies have really tested the monophyly of the family, subfamilies, and included genera; and none have focused on the detailed relationships within the family Synodontidae with relevant taxonomic sampling. Rao (1977) investigated the systematics and examined the osteology of Indian lizardfishes and suggested a similar pattern in osteology among the four genera (*Synodus*, *Trachinocephalus*, *Harpadon* and *Saurida*). He noted a resemblance between *Saurida* and *Harpadon* in respect of the absence of the orbitosphenoid as well as the laminar expansion in the lowest radial in the pectoral girdle. In addition, Rao also made an osteological comparison among *Saurida*, *Synodus* and *Trachinocephalus*, and found a closer relationship between *Synodus* and *Saurida* based on the characters of vertebral column (Rao 1977). Hartel & Stiassny (1986) also mentioned the anatomical relationships of Aulopiformes in their study of larval *Parasudis* (Chlorophthalmidae). Their results indicated a closer relationship of *Saurida*, *Harpadon* and *Bathysaurus* within the Synodontidae, based on the absence

of a “rostral cartilage”. Recently, Chaiyapo (2013) examined 18 synodontid species and redefined the family into three monophyletic genera based on the osteological and morphological characters. In this schema, the previously defined genus *Trachinocephalus* has the closest relationship with *Synodus saurus* and it was proposed that *Trachinocephalus* should be synonymized under *Synodus*, supported by four synapomorphies, including the presence of tiny spines on the supraorbital and the posterior portion of the posterior process of the pelvic girdle extremely long (Chaiyapo 2013). However, the phylogenetic hypotheses described above (Rao 1977; Hartel & Stiassny 1986; Chaiyapo 2013) included less than one third of the recognized species from the family, and no reliable phylogeny illustrating the evolutionary relationships at inter- and intra-generic levels of the family is presently available.

The taxonomy at the species level within the family also is problematic. Some distinctive species were reported to be recognized as the same taxon under previous classification with improper symplesiomorphic characters. For instance, *Saurida undosquamis* was regarded as a widely distributed species characterized by having dark dots on the upper margin of the caudal fin (Matsubara 1951; Tomiyama & Abe 1958; Machida 1984). However, subsequent studies indicated that *S. undosquamis* was actually a species complex and exhibited two morpho-lineages around Japan (Yamada & Ikemoto 1979; Yamada 2000). Further genetic evidence confirmed the separation of these two lineages (Yamaoka *et al.* 1989). A subsequent study done by Inoue and Nakabo (2006) recognized four species within this species complex (*S. undosquamis*, *S. umeyoshii*, *S. macrolepis*, and *S. longimanus*) with the morphological evidence.

Recently developed molecular approaches have provided a new perspective into the systematics of fishes at all taxonomic levels (Mayden & Chen 2010; Near *et al.* 2012). Based on DNA sequence variation among species, the molecular approaches can provide valuable information to improve the accuracy of species identification and are also useful for the reconstruction of evolutionary relationships of the targeting taxa (Mayden & Chen 2010; Lo *et al.* 2017). Mitochondrial DNA (mtDNA) has been widely used in phylogenetic studies in intra- and inter-specific levels (Bargelloni *et al.* 2000; Bowen *et al.* 2001; Lessios & Robertson 2006) with advantages of quick amplification, generally variable in species level, and facilitates comparison with published sequences (DiBattista *et al.* 2013). However, mtDNA also has disadvantages. As an inherited symbiont, mtDNA is assumed to be involved in maternal inheritance and has a rapid evolution rate, leading to a lower resolution of phylogeny at intergeneric or higher levels (Schwartz & Vissing 2002; Hurst & Jiggins 2005). Therefore, a robust phylogeny needs to be built up based on both nuclear and mitochondrial genomes to infer robust evolutionary relationships.

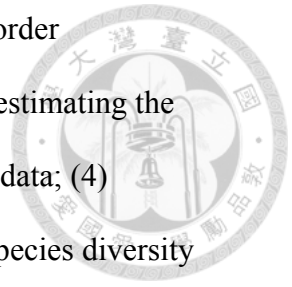
Davis (2010) inferred the first phylogeny of the Aulopiformes based on evidence both from morphological and molecular characters. His molecular dataset comprised data from four nuclear genes (*RAG1*, *ZIC1*, *ENC1*, *PLAGL2*; see material and methods for gene's full name) and one mitochondrial gene (*COI*). In this study, two distinctive patterns of the synodontid phylogeny were observed from the analyses based on different datasets (Fig. 2). The Bayesian reconstruction from the dataset of five genes recovered Synodontidae as a non-monophyletic group. The result showed that subfamily Harpadontinae was nested within the clade comprising the Pseudotrichonotidae and Aulopidae, and the whole clade was sister to the subfamily Synodontinae (Fig. 2a). However, when a total evidence approach (i.e., DNA +

morphology) was performed, Synodontidae became monophyletic and the sister group to the clade comprised the family Pseudotrichonotidae and Aulopidae (Fig. 2b). Although Davis (2010) proposed the monophyly of the family based on the total evidence, only 6 out of 83 synodontid species were sampled in his study. To obtain a comprehensive phylogeny of the family, an analysis based on boarder taxon sampling as well as more representative molecular markers is still necessary.

In terms of the timing of evolutionary origins of the synodontid lineages, although the divergence times of the aulopiform species as a whole have been estimated by Davis & Fielitz (2010), the detailed results within the Synodontidae remains unclear. Davis & Fielitz (2010) dated the origin of the major aulopiform lineages back to the Early Cretaceous, while most of the extant families were present by the late Cretaceous to the Eocene. As most of the synodontids were regarded as coral reef or shelf-inhabiting benthic species, the origins of this group was hypothesized to be related to the tremendous coral reef diversity which arose during the Late Jurassic and Early Cretaceous, as proposed by Veron (1995). In addition, the Synodontidae is one of the few exceptions that have separate sexes, a primitive character of reproduction within the order Aulopiformes, thus implicating an origin earlier than other aulopiform allies (Davis 2010). Within the family, previous osteological study also suggested a prior existence of the genus *Saurida* based on the intermediate characters between Aulopidae and Synodontidae (Sulak 1977). However, these evolutionary inferences could not be validated without a robust time calibrated phylogeny of the family.

In this study, four main objectives were addressed: (1) reconstructing a robust phylogeny of the family Synodontidae and its aulopiform allies with a seven-gene dataset to test monophyly of the family and the four recognized genera; (2) examining

the phylogenetic position(s) of the family Synodontidae within the order Aulopiformes based on the inferred phylogenetic relationships; (3) estimating the divergence times of synodontid lineages using molecular and fossil data; (4) investigating the validity of the existing species and exploring the species diversity within the family with an integrated approach in taxonomy (i.e., species delimitation) with *COI* gene sequences.



2. Materials and methods

2.1 Sample collection



In total of 975 samples from 52 out of 83 morphologically recognized species among the four genera were analyzed in this study, of which 96 samples were collected by Prof. Wei-Jen Chen's research team, two samples were available from Academia Sinica ASIZ museum, Taipei, Taiwan, and 104 samples were provided by collaborators (Dr. Hsuan-Ching Ho, Dr. Barry Russell and his colleagues). The samples were collected from 52 collection sites either from local fish markets or wild populations in Taiwan, Japan, Hong Kong, Singapore, Malaysia, Philippines, South China Sea, Vietnam, Indonesia, Thailand, Myanmar, Dubai, India, Australia, Papua New Guinea, and New Caledonia (Table 1). The examined specimens from the South China Sea, Papua New Guinea and New Caledonia were collected during seven exploratory cruises (Campaigns: Madang, Kavieng 2014, Kanacono, Papua Niugini, Madeep, DongSha 2014 and ZhongSha 2015) conducted between 2012 and 2016 under the *Tropical Deep-Sea Benthos* program and its joint bilateral cooperation research project entitled “Taiwan France marine diversity exploration and evolution of deep-sea fauna (TFDeepEvo)” with the French research vessel *ALIS* and the Taiwanese research vessel *ORI*. Before fixation of the collected specimens in formalin, a small piece of muscle tissue or fin was cut from each specimen and preserved in 95% ethanol and stored in the -20°C freezer at the Marine Biodiversity and Phylogenomics laboratory of the Institute of Oceanography, National Taiwan University, for later molecular analysis. Collected specimens were photographed and identified to species using morphological keys in taxonomic references, notably in “FAO species identification guide for fishery purposes: the living marine resources of the Western Central Pacific” (Russell 2002) and “Fishes of Japan” (Nakabo 2002)

with further checking against photos available on FishBase (<http://www.fishbase.org>). Methods for obtaining morphological data from the examined specimens for identification and/or comparison purposes followed Anderson et al. (1966). All measurements were taken in a straight line, made with a dial caliper and recorded to the nearest 0.1 mm. For the specimen that could not be identified to species level (especially juvenile specimens), an assignment at the genus level was made first, and then further checked with the *COI* gene sequence. The collected specimens were deposited in the following places: Ichthyologic collections of the National Taiwan University Museums, Taipei (NTUM); National Museum of Marine Biology and Aquarium, Pingtung (NMMBA); Faculty of Agriculture, Kyoto University, Japan (FAKU); Museum and Art Gallery of the Northern Territory, Australia (MAGNT); Division of Fisheries Science, Miyazaki University, Japan (MUFS); and Kagoshima University Museum, Japan (KAUM) (Table. 1).

2.2 DNA extraction, PCR amplification and sequencing

Whole genomic DNA was extracted from the tissue samples using an automatic extractor: LabTurbo 48 Compact System (TAIGEN BIOSCIENCE CORPORATION) with the pretreatment followed the manufacturer protocol using LabTurbo DNA Mini Kit LGD 480–500 (TAIGEN BIOSCIENCE CORPORATION). Four nuclear genes (Rhodopsin gene [*RH*], Recombination activating gene 1 [*RAG1*], gene encoding Zinc finger protein family member 1 [*ZIC1*], and gene encoding Ectodermal-neural cortex 1 [*ENC1*]) and three mitochondrial genes (Cytochrome oxidase subunit I gene [*COI*], two subunit of mitochondrial ribosomal RNA genes [*12S*] and [*16S*]) were used in this study for reconstructing the high level phylogeny of the Synodontidae and its aulopiform allies. These genes were selected for their ability to provide valuable

phylogenetic information according to the previous studies (Kocher *et al.* 1989; Chen *et al.* 2003; Ward *et al.* 2005; Chen *et al.* 2008; Davis 2010; Li *et al.* 2007; Chen *et al.* 2014; Lo *et al.* 2015). Primers used in this study were listed in Table 2.

The target sequences were amplified using polymerase chain reaction (PCR). Temperature cycling profiles for amplification consisted of an initial denaturation stage (95°C, 60 seconds for *COI*, *12S*, *16S* and 4 minutes for *RH*, *RAG1*, *ZIC1*, *ENC1*) followed by 35 cycles, each with a denaturation step (95°C, 30 seconds for *COI*, *12S*, *16S* and 40 seconds for *RH*, *RAG1*, *ZIC1*, *ENC1*), an annealing step (51°C, 30 seconds for *COI*; 55°C, 40 seconds for *12S*, *16S* and *RH*; 53°C, 40 seconds for *RAG1*; 57°C, 40 seconds for *zic1*, 54°C, 40 seconds for *ENC1*) and an elongation step (72°C, 40 seconds for *COI*, *12S*, *16S*, 75 seconds for *RH*, *zic1*, *ENC1*, and 90 seconds for *RAG1*) before a final extension stage (72°C, 7 minutes). The PCR products were purified using the AMPure magnetic bead cleanup protocol (Agencourt Bioscience Corp). Purified amplicons were then sequenced by Sanger sequencing using dye-labeled terminators. Sequence determinations from Sanger reaction products were generated on ABI 3730 analyzers (Applied Biosystems) at the Genomics BioSci & Tech (Taipei) and at the Center of Biotechnology (National Taiwan University). *COI*, *12S*, *16S* genes were sequenced only from 3' ends due to the relatively short length (<750 bp.), while *RH*, *RAG1*, *zic1*, *ENC1* genes were sequenced from both 5' and 3' ends (forward and reverse sequencing).

2.3 Analytical methods

2.3.1 Sequence editing

The obtained DNA chromatograms were edited and assembled using CodonCode Aligner 7.1.2 (CodonCode Corporation, Dedham, MA, USA). Some problematic

bases with low qualities were checked manually by eyes and discarded if they were unable to make the base calls. In addition, the nucleotide sites in nuclear gene sequences appearing to be heterozygote were recorded into degenerate base symbols (W for A or T; S for G or C; M for A or C; K for G or T; R for A or G; and Y for C or T). The edited sequences of each protein-coding gene (*COI*, *RH*, *RAG1*, *ZIC1*, and *ENC1*) were organized and aligned by eyes based on the inferred amino acid translation with Sequence Alignment Editor (Se-Al) v2.0a11 (Rambaut 1996). For the RNA-coding gene sequences (*12S* and *16S*), a preliminary alignment was conducted using the automatic multiple-alignment program MUSCLE (Edgar 2004), then modified manually by eye based on the codon position and the loop region with Se-Al.

Except the sequences newly obtained through the lab work, mounts of reference sequences were also included in this study (see below for detail). For the higher-level phylogenetic analysis, three nuclear genes (*RAG1*, *ZIC1*, *ENC1*) and one mitochondrial gene (*COI*) from 15 aulopiform taxa plus one outgroup taxa from Ateleopodidae were retrieved from the published data by Davis (2010) (Table 3). For the species validation and delimitation, 651 *COI* gene sequences of the Synodontidae were retrieved from the GenBank (NCBI, Nation Center for Biotechnology Information, Benson *et al.* 2000) and BOLD system (The Barcode of Life Data Systems, Ratnasingham & Hebert 2007) (see Table 4). In addition, 122 unpublished *COI* sequences of Synodontidae provided by Dr. Barry Russell were also included in the analysis (Table 5). To the optimize the dataset, some problematic sequences that are either misidentified or contaminated (i.e., sequences belong to non-synodontid fishes confirmed by the BLAST search or by the result of my preliminary phylogenetic analysis) were removed from the analyses.

2.3.2 Phylogenetic reconstruction and divergence time estimation

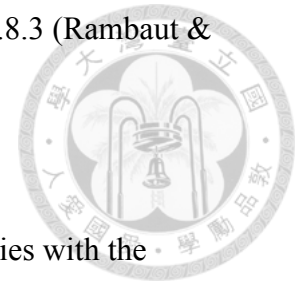
From the aligned sequences, two types (in terms of gene composition) of datasets were generated. First, the combined gene dataset was compiled from the data from four nuclear genes (*RH*, *RAG1*, *ZIC1* and *ENCI*) and three mitochondrial (*COI*, *12S*, *16S*) gene sequences that was used for the higher-level phylogenetic analysis. Within the multi-gene dataset, the taxon sampling of synodontids was based on the preliminary result of *COI* gene tree (data not shown), one or two representative species were selected from each major clade. Eventually, 29 individuals from four synodontid genera were chosen. For other aulopiform allies, 23 taxa were included to represent 13 out of 14 recognized families. Additionally, two taxa from Ateleopodidae (*Ateleopus japonicus* and *Ijimaia antillarum*) were used as outgroups to root the inferred phylogenetic trees based on previous phylogenetic results (Chen *et al.* 2014; Davis 2010) (Table 3). Second, two separate *COI* gene datasets for each subfamily, Synodontinae and Harpadontinae, were compiled for evaluating the validity of synodontid species through the phylogenetic and species delimitation analyses: the dataset of the Synodontinae contained 396 individuals from the genera *Synodus* (312) and *Trachinocephalus* (84); the dataset of the Harpadontinae contained 580 individuals from the genera *Saurida* (505) and *Harpadon* (75). *Hime japonica* (individual no.: WJC480; Aulopidae) was chosen as out groups for both *COI* datasets based on the result of higher-level phylogenetic analysis (Table 1, 4, and 5).

To infer the phylogeny of the family Synodontidae, a partitioned maximum-likelihood (ML) method as implemented in the program RAxML version 8.0.24 (Stamatakis 2014) was carried out with GTR+G nucleotide substitution model. For the combined gene dataset, fifteen partitions were assigned with respect to codon

positions of each protein-coding genes (five genes). For the *COI* datasets, three partitions were set with respect to codon positions of the gene. In each analysis, nodal support was assessed by bootstrapping (Felsenstein 1985) with the ML criterion based on 100 pseudo-replicates. The phylogenetic trees were viewed and edited with FigTree v1.4.0 (Rambaut 2012).

The divergence time estimation as well as the phylogenetic inference under Bayesian criteria of the family were performed in BEAST v.1.47 (Drummond & Rambaut 2007) with an input of the combined gene dataset. For each codon position, the best-fit model was assigned by the suggestion of prior test in the program PartitionFinder v. 1.1.0 (Lanfear *et al.* 2012), with mean substitution rate estimated under a relaxed uncorrelated lognormal clock (Drummond *et al.* 2006). Based on the result of the high-level phylogeny analysis in this study, the monophyly of the taxon “Aulopiformes” and the “*Pseudotrichonotus* + Aulopidae + Harpadontinae” clade were assumed, and the two taxa from Ateleopodidae were set as the monophyletic outgroup. Rosen and Patterson (1969) found that the osteology of *Aulopus* is highly similar to the Cretaceous genus †*Nematonotus*, and the fossil genus was later placed in the family Aulopidae by Rosen (1973). Based on this systematic placement, the age of the most recent common ancestor (MRCA) of the clade *Pseudotrichonotus* + Aulopidae + Harpadontinae was dated to a time range of 93-96 Ma based on the result of ML tree. The MCMC run was conducted for 50 million generations with the sampling every 5000 generations. Tracer v.1.6 (Rambaut *et al.* 2007) were used to check the convergence of the run parameter, and the effective sample sizes (ESSs) of the posterior, prior, likelihood, and treeModel.rootHeight were all greater than 200. The first 10% of samples were discarded as burn-in, and the maximum clade credibility tree with mean divergence time and 95% credibility intervals (CIs) were

generated from the combined tree samples from TreeAnnotator v.1.8.3 (Rambaut & Drummond 2012).



2.3.3 Species delimitation

DNA barcoding has been a useful tool for identifying the species with the advantages of short fragments and conserved at intraspecific level in last decade (Ivanova *et al.* 2007; Ward *et al.* 2009). In this study, the *COI* gene marker was chosen for the molecular analyses for delimiting species by two following programs.

Automatic Barcode Gap Discovery, (ABGD, Puillandre *et al.* 2012) is an exploratory tool based on pairwise distances to automatically detect the significance between intra- and inter-specific variation (barcode gap). The function of this analysis is to calculate the number of operational taxonomic units (OTUs) of the target group based on the barcode gaps. This grouping can help to redefine groups, especially for some putative species. The analysis was performed at the web interface (<http://www.wabi.snv.jussieu.fr/public/abgd/>) using a default value of relative gap width (X) as 1.5, intraspecific divergence (P) value from 0.001 to 0.1 with 20 steps and K80 model (Kimura 1980).

Bayesian based Poisson Tree Process (bPTP, Zhang *et al.* 2013) is another exploratory tool based on the phylogenetic tree inferred from molecular sequences under Bayesian criteria. This model outperforms the similar GMYC with simpler procedure and generates a more reliable result. The bPTP analysis is based on an input of phylogenetic tree, and number of mutations are modeled as speciation or branching events. In this study, we use the same *COI* trees in the phylogenetic inference as the input trees. The analyses were performed at the web interface (<http://species.h-its.org/ptp/>) using a default value of 500,000 MCMC generations and the default parameters.

Congruent results between the two analyses were considered as a robust support of the OTU (i.e., inferred potential species) (Carstens *et al.* 2013; Hung *et al.* 2017; Lo *et al.* 2017), while other species delimitation criteria were used for the final validation, especially when inconsistent results were observed between ABGD and bPTP. Considering the biological species concept, species are defined as separately evolving metapopulation lineages with reproductive isolation to each other (Mayr 1942; Dobzhansky & Dobzhansky 1970). However, the absence of interbreeding between heterospecific organisms can only be tested where sympatric distribution occurs. Furthermore, it is suggested that the phylogenetic perspective cannot properly solve the “species problem” without the consideration of sorting processes at microevolutionary scale, such as reproductive isolation (Avise & Wollenberg 1997). In case of overestimating species diversity, the inconsistent putative species clusters were assessed following the methodology suggested by Kekkonen & Hebert (2014), which considered only sympatric sister-clusters as distinct lineages and merged the allopatric species. In this study, the determination of the sympatry of the inferred sister OTUs is based on previously described geographical regions, such as the Greater Caribbean (GC), Brazilian provinces (BP), tropical East Atlantic (TEA), East China Sea (ECS), South China Sea + Coral Triangle (SCS + CT), Sahul Shelf and Australia (SAS) and Indian Ocean (IO) (Luiz *et al.* 2012, Hung *et al.* 2017; Lo *et al.* 2017). Final validation of the putative species was reconfirmed with reciprocal monophyly of the *COI* trees and morphological characters of specimens or available photos to minimize the bias of these two analyses (ABGD and bPTP).

3. Results

3.1 Characteristics of sequence data

3.1.1 Multi-gene dataset

The dataset included newly generated sequences of 4 nuclear genes (*RH*, *RAG1*, *ZIC1*, *ENC1*) and 3 mitochondrial genes (*COI*, *12S*, *16S*) obtained from 32 individuals compiled with three nuclear genes (*RAG1*, *ZIC1*, *ENC1*) and one mitochondrial gene (*COI*) from 22 taxa published by Davis (2010). In total, the dataset represented 54 taxa, including 29 taxa from the family Synodontidae, 23 taxa from other Aulopiform families, and two outgroups from the family Ateleopodidae (Ateleopodiformes). All of the four synodontid genera were included in the analysis, with 10 taxa from *Synodus*, 3 from *Trachinocephalus*, 12 from *Saurida*, and 4 from *Harpadon* (Table 3). The other aulopiform representatives included 13 out of 14 other families: Aulopidae, Pseudotrichonotidae, Paraulopidae, Giganturidae, Bathysauridae, Bathysauroididae, Ipnopidae, Chlorophthalmidae, Notosudidae, Scopelarchidae, Evermannellidae, Sudidae, Alepisauridae, Paralepididae (Table 3). The family Bathysauropsidae is not included due to the shortage of sequence data. The final trimmed matrix comprised 5591 aligned base-pairs and none of insertion, deletion and stop codon were found along the protein coding gene sequences, but some were observed in the RNA sequences (*12S* and *16S*) at the loop region. The sequence characteristics of each gene (codon) were summarized in Table 6. The third codon position of each protein coding gene showed significant difference in the base frequencies homogeneity analysis (Table 6).



3.1.2 *COI* gene dataset

The high level phylogenetic analysis (Fig. 3) confirmed the two subfamilies were two independent monophyletic groups. Therefore, the synodontid *COI* gene sequences were separated into two datasets with respect to each subfamily

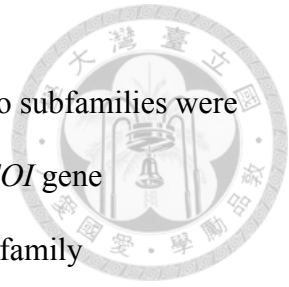
(Synodontinae: *Synodus* + *Trachinocephalus*; Harpadontinae: *Harpadon* + *Saurida*).

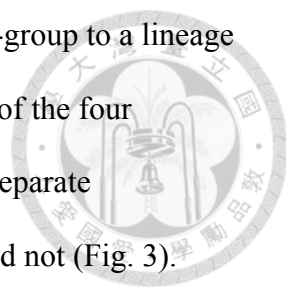
For a more comprehensive investigation with good species coverage, the dataset included not only the sequences that were newly generated in this study, but also the reference sequences from public databases (GenBank and BOLD, Table 4) and private resources (Table 5). In total, the two *COI* datasets included 975 taxa from 52 of 83 morphologically recognized species among the four genera (Table 1, 4, and 5). The dataset of Synodontinae included 395 *COI* sequences (*Synodus*: 312, *Trachinocephalus*: 83), comprising 707 aligned base-pairs with 301 variable sites (271 sites are parsimony informative). The dataset of Harpadontinae included 580 *COI* sequences (*Saurida*: 505, *Harpadon*: 75), comprising 684 aligned base-pairs with 291 variable sites (255 are parsimony informative). The sequence characteristics of both datasets are summarized in Table 7. For both datasets, most of the third codon positions are parsimony informative, and the frequencies homogeneity test showed significant differences of the bases at the third codon position (Table 7).

3.2 Phylogenetic inferences

3.2.1 Combined gene tree

From the result of partitioned maximum-likelihood analysis, the family Synodontidae was not resolved as a monophyletic group. Although two subfamilies (Synodontinae and Harpadontinae) formed two highly supported clades, they were not sister to each other (Fig. 3). Instead, the Synodontinae appeared to be the first-evolved





lineage in the Aulopiformes while the Harpadontinae was the sister-group to a lineage of the family Aulopidae (*Aulopus*) (Fig. 3). At the genus level, two of the four synodontid genera (*Trachinocephalus* and *Harpadon*) formed two separate well-supported clades while the other two (*Synodus* and *Saurida*) did not (Fig. 3). Within the “*Synodus*” and “*Saurida*”, three and four main lineages could be defined according to the bootstrap support values (BP) and Bayesian posterior probabilities (PP) (Fig. 3). Within the genus “*Synodus*”, the first and second lineages (*S. foetens* and *S. intermedius*) formed a strongly supported clade with *Trachinocephalus* (Fig. 3). Notably, these two species were all common in the western Atlantic. The third lineage comprised common species in the Indo-West Pacific region including *S. oculus*, *S. macrops*, *S. kaianus*, *S. “kaianus”* (= *Synodus* sp. II), *Synodus* n. sp. (Papua New Guinea, Russell), *S. dermatogenys*, and *S. variegatus* (Fig. 3). Within the genus “*Saurida*”, four distinct lineages were observed. However, the distribution of the four lineages only weakly accorded with geographical variance, with most of the species occurring in the Indo West-Pacific region. The first lineage included *Saurida* sp. and *S. gracilis*, and was sister to the remaining lineages of Harpadontinae, with the highest bootstrap and Bayesian supports. The second lineage only included *S. longimanus*, and only had a weakly supported sister group relationship with the remaining lineages of Harpadontinae except the first lineage of Saurida. The third lineage included *S. eso*, *Saurida* aff. *tumbil*, *S. tumbil* and *S. micropectoralis*. The fourth lineage comprised *Saurida umeyoshii*, *S. undosquamis*, *Saurida “undosquamis”* (= *macrolepis*), *S. grandisquamis*, and *S. lessepsianus* (Fig. 3).

3.2.2 Divergence time estimation

From the inferred time tree based on Bayesian divergence time analysis, the reconstructed phylogeny was identical to the topology of the combined gene tree under ML criteria, thus reconfirming the phylogenetic relationships of the family, especially the monophyly of the two subfamilies, Synodontinae and Harpadontinae (Fig. 4). The origin of the Aulopiformes was estimated to be at the mean age of 117 Ma (95%HPD: 105-132), which overlapped with the time range estimation of a previous study (95%HPD: 127-156) by Davis (2010). The origin of the Synodontinae clade was estimated to be at 68 Ma (95%HPD: 58-79), while the Harpadontinae clade was estimated to have a more recent occurrence at around 50 Ma (95%HPD: 42-58).

3.2.3 *COI* gene tree

Figure 5 and 6 illustrated the phylogenetic trees of the two subfamilies based on the two separated *COI* gene datasets. Despite the low bootstrap supports, the relationships among genera in both *COI* gene trees were consistent with the results of the combined gene tree (Fig. 3, 5, 6). Within each genus, most of the nodes that indicated species level were supported by high bootstrap value. Therefore, the trees revealed the grouping of recognized species. However, many doubtful clades were observed in the sequences retrieved from other sources, with two or more ‘species’ names showing in one monophyletic group (Fig. 5, 6). This situation was likely due to high levels of misidentification, especially for sources such as GenBank and BOLD. To infer the “true” species name of each monophyletic clade, the identity of the species was reconfirmed by examining the deposited specimens in NTUM and NMMBA collections or validated by the clade that included samples collected from type locality.

Within the subfamily Synodontinae, the genus *Trachinocephalus* was clearly a monophyletic group, with the bootstrap support value of 100 (Fig. 5). However, the results showed the presence of at least six lineages for this genus. The known widespread species *Trachinocephalus myops* is polyphyletic, with three genetically and geographically distinct lineages, and the Red Sea lineage (*T. myops* III) is sister to the Indo-West Pacific distributed *T. trachinus* (Fig. 5). The genus *Synodus* is not monophyletic regarded to the monophyletic genus *Trachinocephalus*. Within the genus, 40 well-supported clades or lineages (bootstrap value > 80) were observed (Fig. 5). The offshore lizardfish, *Synodus poeyi*, contains two distinct lineages, one in the Caribbean Sea, the other in Gulf of Mexico. *Synodus variegatus* and *Synodus dermatogenys* were polyphyletic and can be divided into four and two lineages, respectively (Fig. 5).

In the subfamily Harpadontinae, the genus *Harpadon* also formed a well-supported monophyletic group (BP= 99; Fig. 6). With five recognized species from this genus included in the analysis, three main clades were observed. The first contained species *H. nudus* and *H. squamosus*; while the second comprised *H. translucens* and *H. microchir*. Additionally, the *H. microchir* clade was further divided into two genetically and geographically different lineages: one from Papua New Guinea; the other from Taiwan and Japan (Fig. 6). The remaining clade, *H. nehereus*, was well-supported (BP= 100). The genus *Saurida* was recovered as polyphyletic. From the *COI* tree, 37 well-supported monophyletic clades (BP > 80) out of 18 recognized species were found (Fig. 6). Most of the morphospecies were monophyletic with some exceptions. In addition, *S. nebulosa*, *S. brasiliensis*, and *S. longimanus* each included two lineages which are both genetically and geographically different (Fig. 6).



3.3 Species delimitation

Two analytic programs were used for the species delimitation among the collected *COI* sequences from the Synodontidae (two datasets for two subfamilies). For the subfamily Synodontinae, the ABGD analysis was conducted by partitioning all the individuals with prior maximal distance (P)= 0.0359, and resulted in 48 OTUs (putative species). However, 56 entities were observed through the bPTP analysis, which was based on a maximum likelihood partition. For the subfamily Harpadontinae, ABGD analysis was conducted by partitioning all the individuals with prior maximal distance (P)= 0.0359, and resulted in 40 entities, while bPTP analysis indicated 59 entities with a maximum likelihood partition. The conflict between the results of the two analyses are discussed below and will be further addressed in the discussion.

Within the genus *Synodus*, 42 OTUs were defined by ABGD while bPTP suggested 48 putative species groups. ABGD grouped *S. saurus*, distributed in Bahamas and Mediterranean waters, together as one OTU, while bPTP considered them as two different OTUs (Fig. 5). Similarly, *S. kaianus* was divided into two OTUs by bPTP, with one lineage distributed in Papua New Guinea and the other distributed in Tosa Bay, Japan and South China Sea; however, the ABGD grouped all the lineages together as a single OTU. Likewise, for *Synodus* sp. (PNG3123) bPTP showed one lineage from Papua New Guinea and the other lineage from North West Australia (Fig. 5). In some cases, two or three different species names were found within a certain OTU. This is likely the result of species misidentification among some morphologically similar species (e.g., *S. microcephalus* and *S. macrops*) (Fig. 5).

For the genus *Trachinocephalus*, six OTUs were determined by ABGD while eight by bPTP mainly because of the widely distributed species *T. myops* (Fig. 5). Despite the three lineages reported by bPTP relative to the minor geographic difference around the America, ABGD assumed all the allopatric lineages as the same species (*T. myops* II; Fig. 5).

Under the genus *Saurida*, 35 OTUs were defined by ABGD in contrast to 54 OTUs considered by bPTP (Fig. 6). The *Saurida* sp. I clade included *Saurida nebulosa* JQ350326, ABGD grouped all 14 species together as one OTU, but five OTUs were detected by bPTP (Fig. 6). Similarly, the *Saurida* sp. II clade that contained *Saurida* sp. SYN192, only one group was detected by ABGD for all 10 individuals, while 6 OTUs were detected by bPTP. In some cases, bPTP tended to differentiate species that shared almost identical sequences, such as *Saurida* sp. HM382761 and PNG3124. Although bPTP usually recognized more groups than ABGD, it can more accurately represent the grouping in some conditions. For example, ABGD considered *S. umeyoshii* and *Saurida* n. sp. 'meesha' as one distinct group, while bPTP recognized they were two different groups (Fig. 6). Considering the paraphyletic relationship among these two groups in the COI tree as well as the existence of morphological differences, two species were assigned in final decision. The low resolution of ABGD result in this case may contribute to the insufficient variance between the sequences among inter- and intra- specific levels.

Within the genus *Harpadon*, both ABGD and bPTP recognized 5 OTUs out of the 5 recognized species (Fig. 6). Notably, *H. nudus* and *H. squamosus* were regarded as one identical species in both analyses. While both analyses detected two lineages within the species *H. microchir*, one occurred in Papua New Guinean water, and the other was found in Japan and Taiwan (Fig. 6).

Generally, the results showed a higher number of OTUs than the recognized species among the four genera despite the minor discordance of the two analytic programs. These results not only reveal a hidden biodiversity in the family but also indicate some potential new species in the Synodontidae. Further investigation based on morphology is necessary to support these findings (see discussion for more detail).

4. Discussion

4.1 High level phylogeny

4.1.1 Phylogenetic position(s) of the Synodontidae within the Aulopiformes



Currently, the monophyly of Aulopiformes is supported by nine morphological synapomorphies (Baldwin & Johnson 1996; Sato & Nakabo 2002; Davis 2010) including 1) presence of an enlarged uncinat process on second epibranchial (Rosen 1973); 2) absence of cartilaginous condyle on third pharyngobranchial (G. D. Johnson 1992); 3) epipleural bones extending to second or first vertebra (Patterson & Johnson 1995); 4) absence of swim bladder (Marshall 1954); 5) presence of peritoneal pigment in larvae (R. K. Johnson 1982); 6) medial processes of pelvic girdle joined medially by cartilage (Baldwin & Johnson 1996); 7) presence of fifth epibranchial (Baldwin & Johnson 1996); 8) one or more epipleurals displaced dorsally into horizontal septum (Patterson & Johnson 1995); 9) palatine not expanded laterally (Sato & Nakabo 2002). Davis (2010) further demonstrated the monophyly of the Aulopiformes based on a combination of molecular and morphologic evidences with thorough sampling of representatives from major euteleostei lineages and extensive aulopiform families. However, the phylogenetic position and taxonomic statues of the synodontids have long been controversial within the Aulopiformes (Gosline *et al.* 1966; Rosen 1973, 1985; Sulak 1977; Johnson 1982; Baldwin & Johnson 1996; Sato & Nakabo 2002; Davis 2010; Chaiyapo 2013) (Fig. 1). Within the order, the family Synodontidae has the closest relationship with the Aulopidae and Pseudotrichonotidae as supported by shared synapomorphies such as the elongated and widely separated posterior pelvic processes (Baldwin & Johnson 1996). The two subfamilies of the Synodontidae were usually assigned into one group based on the structural characters such as a strong premaxilla dominated upper jaw; reduced or absence of supramaxillae; a modified gill

raker with cluster of short gill teeth; a pointed snout; a high number of branchiostegal rays (12-26), and a dioecious mode of reproduction (Sulak 1977). However, some of these synapomorphies are also found in other aulopiform species. For example, the strong premaxilla can also be observed in the genus *Bathysaurus*, and dioecious reproduction occurs in *Pseudochronotus*, *Aulopus* and *Paraulopus* (Sulak 1977; Davis 2010).

From the high-level phylogenetic analysis in this study (Fig. 3), the family Synodontidae was not resolved as a monophyletic group that corresponds to previous classifications proposed by Gosline *et al.* (1966), Rosen (1973), and R. K. Johnson (1982). In addition, the result showed that Harpadontinae has a closer relationship to the family Aulopidae, a result also observed by Sulak (1977). Considering that the classification of species should reflect their actual evolutionary relationships (Henning 1956), the placement of the two subfamilies under the same family Synodontidae might no longer be appropriate. We herein suggest an elevation of the two subfamilies into two independent families within the Aulopiformes, Synodontidae and Harpadontidae, and this classification will be followed in the rest of the discussion.

To distinguish the two newly proposed families, despite the common characters, there are still some apparent morphological variations that can be observed. The most obvious dissimilarity is the number and relative length of the pelvic fin rays (species within the Synodontidae have eight pelvic fin rays, with the inner one much longer than the outer; while species within the Harpadontidae have nine pelvic fin rays of almost equal length.) Other morphological differences can also be found, such as the presence of toothed vomer and supramaxillae in Harpadontidae but the absence in Synodontidae. According to Chaiyapo (2013), both families were unambiguously

supported by several synapomorphic characters. The family Synodontidae was supported by 16 synapomorphic characters, such as the rostral cartilage enlarged and loosely attached with the ethmoid, and the lowermost actinost expanded. While species within the Harpadontidae shared 11 synapomorphies, including teeth on the ectopterygoid, and the presence of a gap between the fourth basibranchial and fifth ceratobranchial (Chaiyapo 2013). This morphological differentiation of the two groups further supports the validation of two independent synodontid-like fish families proposed according to the result of the high-level phylogeny analysis in this study.

Another additional finding in this study is that the family Aulopidae is also non-monophyletic (Fig. 3). At least two independent lineages exist in this family, *Hime* and *Aulopus*. *Hime* was first published to describe the Pacific aulopids and was often regarded as a junior synonym of *Aulopus* (Starks 1924; Sulak 1977; Thompson 1998, 2002; Prokofiev 2008; Nelson *et al.* 2016). Although the genus *Hime* was resurrected by Parin & Kotlyar (1989), subsequent studies found no evidence in either morphology nor genetics that support the validity of this genus, and synonymized *Hime* in the genus *Aulopus* (Baldwin & Johnson 1996; Davis 2010). However, with the enhanced molecular markers, our high-level phylogeny found a distinct pattern of genetic variation between these two genera (Fig. 3), which support *Hime* as a valid genus of the Aulopidae (Randall 2007; Fricke *et al.* 2011; Gomon *et al.* 2013; Gomon & Struthers 2015). Further systematic investigations by including more aulopid taxa, notably, the species from the remaining genera, *Latropiscis* and *Leptaulopus*, are still necessary.

4.1.2 Phylogeny of the synodontid-like fishes

A reliable phylogeny of the family Synodontidae was reconstructed in this study through the “top-down” and “bottom-up” processes. At first, the bottom-up process was conducted through the preliminary phylogenetic inference of collected *COI* sequences. This analysis benefits in grouping of numerous unknown or misidentified species and shows the basic relationships of each major clade. Subsequently, 29 taxa were selected to represent the major groups of the synodontids in the top-down process considering the result of *COI* tree. Finally, the top-down process was accomplished by obtaining the high-level phylogeny of the Aulopiformes which was inferred based on seven informative genetic markers. Nonetheless, the result of the top-down process also contributed to the further division of the *COI* dataset based on two subfamilies. The combination of the bidirectional process can exclude the bias caused by misidentifications or over-concentration sampling in some specific groups and offer a profound insight into the phylogeny of the family.

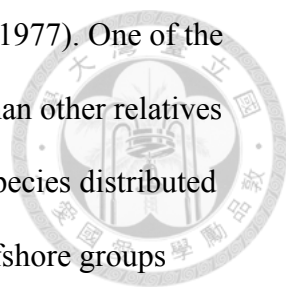
The phylogeny based on the *COI* gene sequences, however, failed to resolve most of the intra-generic relationships among synodontid species. This condition may regard as soft polytomy that was led by fast species radiation (Pavlicev & Mayer 2009), which indicates a faster evolution of *COI* gene rather than the phenotypic traits. Fortunately, this problem can be solved with more input of phylogenetic information, such as increased molecular markers or enhanced taxon sampling. Thus, the discussion of phylogeny inference of the family Synodontidae here is based mainly on the multi-gene tree, and the *COI* gene trees were used for defining the monophyly at the species level.

This is the first study that provides a molecular phylogenetic investigation focusing on the synodontid-like fishes. Although the dataset did not include all of the

existing species of this group due to the limitation of sample collection, the general phylogeny can still be inferred based on the chosen representatives. From the phylogenetic result (Fig. 3), the lizardfishes were not monophyletic as expected from previous taxonomic classifications (Sulak 1977; Baldwin & Johnson 1996; Sato & Nakabo 2002; Davis 2010). Instead, the two subfamilies are both monophyletic and independent to each other. The overall phylogeny of synodontids as well as its aulopiform allies reconstructed in this study is similar to that of Davis (2010) based on five genetic markers. However, his phylogeny based on total evidence approach is likely to be influenced by the morphologic characters, which showed monophyly of the Synodontidae (Fig. 2b).

The inter-generic relationships within the lizardfishes were also investigated in this study. The monophyly of *Trachinocephalus* and *Harpadon* was confirmed. Although both *Synodus* and *Saurida* were found paraphyletic and enclosed three and four lineages respectively, this division within the genus has never been noted in previous systematic studies (Gosline *et al.* 1966; Rosen 1973; Johnson 1982; Sulak 1977; Rao 1977; Baldwin & Johnson 1996; Sato & Nakabo 2002; Davis 2010). Notably, the second lineage of *Saurida* contained only one species, *S. longimanus*, and showed a polytomous pattern in respect of other harpadontid lineages except the first lineage of *Saurida*. This result may be a soft polytomy caused by the failure in amplifying the nuclear genes of certain taxa in the dataset (Table 3). To fully resolve the inter-generic relationships of lizardfishes, an investigation with a more comprehensive molecular dataset is necessary.

The two monophyletic genera from each family were highly specialized in morphology and habitat. The genus *Harpadon*, so called “Bombay duck”, is characterized by a greatly specialized appearance (e.g., a large gape with extremely



short snout and elongated jaw) and lives in a pelagic habitat (Sulak 1977). One of the species, *H. erythraeus*, was reported to have a deeper distribution than other relatives (Klausewitz 1983). Previous studies suggested that the *Harpadon* species distributed in the Indo-West Pacific region could be separated into inshore / offshore groups based on phenotypic and osteological differences. *H. erythraeus*, *H. squamosus*, and *H. microchir* were offshore species while *H. translucens* and *H. nehereus* were inshore species (Ganga *et al.* 2015; Johnson *et al.* 1997). Although this study failed to recover this relationship due to the lack of sampling of *H. erythraeus* and *H. squamosus*, the combined gene tree supported the monophyly of *H. nehereus* along with a supported sister-group relationship with other *Harpadon* species (Fig. 3). Another specialized group is the genus *Trachinocephalus* (blunt-nose lizard fish). Unlike *Synodus*, species of this genus have a reduced snout length with nearly blunt head, and a higher number of anal fin rays (Polanco & Acero 2016). These morphological characters supported the result of phylogenetic analysis that showed this genus as an independent monophyletic group, although the validity of the genus has been debated based on both molecular and morphological evidences in recent years (Davis 2010; Chaiyapo 2013; Polanco & Acero 2016).

4.2 Evolutionary history of the synodontid-like fishes

The fossil-calibrated time tree showed different divergence times of the two synodontid-like fish families (Fig. 4). The divergence time of the Synodontidae was estimated to be during the Late Cretaceous (68 Ma), while the origin of Harpadontidae was during the Eocene (50 Ma). The divergence time estimation of Aulopiformes inferred by Davis & Fielitz (2010) showed that most extant aulopiform

families appeared by the Late Cretaceous to the Eocene, which corresponds well with the present result.

From the perspectives of evolutionary history, the synodontid-like fishes share the most primitive characters with the stem species of Aulopiformes, including a round, laterally directed eye and a dioecious reproduction strategy (i.e. separate sexes) (Sulak 1977; Baldwin & Johnson 1996; Davis & Fielitz 2010). Sulak (1977) suggested that *Saurida* is the most primitive member of the previously defined Synodontidae, with many transitional characters between the aulopid and synodontid, such as an *Aulopus*-like vomer and a long, well-toothed palate similar to synodontids. Based on the same study, Sulak further suggested that the order of occurrence of the four synodontid-like fish genera could also be inferred based on the existence of supramaxilla (two supramaxillae in *Saurida*, one vestigial supramaxilla in *Harpadon*, and none in *Synodus* and *Trachinocephalus*) (Sulak 1977). However, the divergence time estimation as well as the evolutionary relationships inferred in the present study failed to support this assumption. The origin of the Synodontidae was estimated to have evolved earlier than the Harpadontidae clade, and the existence of supramaxillae is likely to be an independent evolution. In addition, the presence of the toothed vomer not only occurred in Harpadontidae but also is found in other aulopiformes such as species in the Aulopidae and Bathysauridae, indicating a closer relationship among these families (Sulak 1977). Despite the disagreement of the origin of the previously described Synodontidae, the Sulak's study did provide evidence of the closer relationship between the Harpadontidae and Aulopidae. Furthermore, since the two families diverged in different evolutionary lineages and in different geological times, the shared common characters of the synodontid-like fishes such as round eyes or separate sexes should be regarded as homoplastic characters.



4.3 Species diversity exploration

4.3.1 Species delimitation

Two programs were applied to help to delimitate species, ABGD and bPTP. As both analytical approaches using single locus data for computation, they can provide a relatively fast and valuable perspective into species boundaries (Kekkonen & Hebert 2014; Leavitt *et al.* 2015). Several disagreements between the results from ABGD and bPTP analysis were observed in this study. This incongruity could be attributed to the difference between the algorithms applied for species delimitation in the two analytical software. With an input of sequence alignment file, ABGD sorts sequences into hypothetical species (OTUs) based on the detected barcode gap using the recursive approach (Puillandre *et al.* 2012). The analysis of bPTP needs an input file of an inferred phylogenetic tree, and then the inference of putative species boundaries is made based on a Bayesian implemented Poisson tree processes model. This model considers the number of mutations as speciation or branching events and can infer species boundaries with the phylogenetic species concept (Zhang *et al.* 2013). However, these two methods were based on single locus data and can only provide a preliminary assessment for species delimitation (Fujisawa & Barraclough 2013; Leavitt *et al.* 2015). The validation of certain species should also consider other criteria such as geographic distribution or morphological difference (Carstens *et al.* 2013; Kekkonen & Hebert 2014; Leavitt *et al.* 2015; Lo *et al.* 2017; Hung *et al.* 2017). In this study, further validation for discordant clusters were made with consideration of combined evidence from monophyletic groups of *COI* gene tree, geographic distribution and morphology (if possible). Cases of species delimitation are discussed below.

Generally, bPTP tended to differentiate the sister clusters with the geographical differences while ABGD did not. For example, *Synodus saurus* JX519385 (Bahamas) and other *S. saurus* individuals (Israel); *Synodus kaianus* (Papua New Guinea) and other *S. kaianus* individuals (Tosabay and South China Sea); *Synodus macrops* SYN65 (Myanmar) and other individuals (western Indian Ocean region) (Fig. 5); *Trachinocephalus myops* II from the Caribbean Sea, North America and South America (Fig. 5); *Saurida normani* from Gulf of Mexico and Caribbean Sea (Fig. 6). For most of the cases mentioned above, further examination of morphology was not possible due to the non-availability of specimens. Because of the short genetic distance ($P < 3.59\%$) and the lack of sympatric occurrence, the emergence of those sister clusters into single inferred species for certain OUT groups is tentatively suggested.

In some other cases, bPTP seemed to overestimate the number of OTUs for the species that shared almost identical sequences. For example, *Saurida* sp. HM382761 and PNG3124, there was nearly no barcode gap between these two taxa in ABGD result, but they were considered as two different OTUs by bPTP due to the strict criterion for reciprocal monophyly (Fig. 6). Similar situations were found in the *Saurida* sp. I clade which contained JQ305025 *Saurida nebulosa*, and *Saurida* sp. II clade which included SYN192 *Saurida* sp., the *Saurida tumbil* clade, and the *Saurida undosquamis* clade. For the putative species described above, the separation made by bPTP is overestimated, and the final decision of the species delimitation basically followed the result of ABGD (Fig. 6).

For *Saurida umeyoshii* and *Saurida* n. sp. ‘meesha’ (India), ABGD did not differentiate these two taxa as bPTP did. Based on the *COI* gene tree and morphological evidence, these two morphologically differentiated taxa formed two

separate monophyletic groups, indicating a validity of two distinct species. The failure in ABGD in this case can likely be attributed to the little interspecific genetic variance between the two species (Puillandre *et al.* 2012).



4.3.2 Species diversity of the synodontid-like fishes

As a result of this study, 87 final inferred species were observed from the 52 recognized synodontid species in the *COI* dataset, revealing an underestimated biodiversity of the synodontid-like fish families. The inferred species clusters included some questionable taxa that are either undescribed or simply not well identified, and some independent evolutionary lineages were observed within a certain species. For the sequences downloaded from GenBank or BOLD, further morphological examination was restricted due to the limitation of accessing the specimens.

According to both species delimitation analyses, several recognized synodontid species were found to have two or more independent evolutionary lineages that are both genetically and geographically different. For instance, the lineage of *Synodus poeyi* distributed in the Caribbean Sea was separated from the lineage distributed in the Atlantic Ocean and Gulf of Mexico (Fig. 5). The two lineages of *S. poeyi* was noted by Frable *et al.* (2013). Within their study, the lineage occurring in the Caribbean Sea was regarded as a deeper water lineage. *Saurida nebulosa* contains two distinct species, one distributed in French Polynesia (FP), and the other was found in the waters around the Indonesia and Torres Strait (Fig. 6). Two inferred species were found in *Saurida brasiliensis*, one occurring in the Gulf of Mexico, the other observed in Belize and Panama. For *Saurida longimanus*, a distinct lineage in Red Sea was detected, apart from the other lineage that is distributed in Thailand and India.

Another interesting case was *Harpadon microchir*, which had a discrete lineage in Papua New Guinea, compare to other individuals occurring in Taiwan and Japan. Although the species within these two lineages all present the features of *H. microchir* (posterior tip of the pectoral fin does not reach the origin of pelvic fin) (Nakabo 2002), a detailed examination in morphology is still required for the validation of these two species. The speciation led by allopatric distribution is not a rare case for the family. Within the genus *Saurida*, one species, *Saurida lessepsianus*, even experienced speciation in the Red Sea during the isolation caused by last glacial maximum and finally invaded back into the Mediterranean Sea through the process of “lessepsianus migration” according to the recent report (Tikochinski *et al.* 2016).

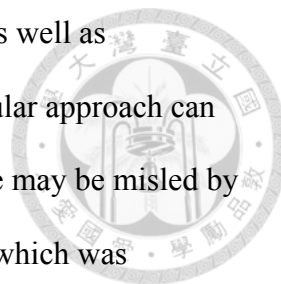
The genus *Trachinocephalus* was previously regarded as a monotypic genus containing only *Trachinocephalus myops* (Forster 1801), a species with nearly circum-tropical and subtropical distributions (Norman 1935; Briggs 1960; Anderson *et al.* 1966). With little difference in morphology, *T. trachinus* (Temminck & Schlegel 1846) was regarded as a junior synonym of *T. myops* in Pacific region (Sulak 1989). According to the taxonomic revision of the genus based on morphological and molecular evidences from Polanco and Acero (2016), *T. trachinus* is regarded as a valid species. With a boarder taxon sampling, the phylogenetic reconstruction in this study further reconfirmed *T. myops*, *T. trachinus* and the newly described *T. gauguini* as three valid species under the genus *Trachinocephalus* (Fig. 5). In addition, the species delimitation result in the present study revealed three genetically and geographically different lineages of *T. myops*, indicating the presence of potential new species (Fig. 5).

My results also challenged the validity of an extant species in the genus *Harpadon*. *Harpadon nudus* is a newly described species by Ganga *et al.* (2015).

Compared with other congeneric species, *H. nudus* was described as having a slenderer body and shorter pectoral and pelvic fins with nearly no scales on its body. However, our species delimitation analyses indicated a conspecific relationship of *H. nudus* and *H. squamosus* (Fig. 6). Furthermore, only slightly differences were found among the *COI* sequences between these two species (overall mean p-distance= 0.9% $\pm$ 0.2%). Although Ganga *et al.* (2015) did provide the molecular evidence with the UPGMA tree compare with two of the congeners (*H. microchir* and *H. nehereus*), the genetic comparison in these two closely related species was not correctly made in the study. While dealing with species delineation, it is essential to consider an integrated view based on the evidences from both traditional taxonomy and molecular approaches. However, the molecular analysis should be conducted with caution, especially when examining the genetic variance among close related species. All of the closest related species within the extant dataset (e.g. GenBank or BOLD) should be involved in the analysis. In this case, the validity of the newly proposed species is still unreliable, requiring further morphological examination for confirmation.

Despite the fact that many new synodontid species have been proposed in recent years (Frable *et al.* 2013; Ganga *et al.* 2015; Russell 2015; Allen 2017), rather less attention has been paid to a comprehensive taxonomic revision of the family. Moreover, the observed number of putative species clusters within the species delimitation analysis in this study is still higher than that of the recognized species, indicating the taxonomy of the family is far from fully described and understood. According to this study, the name “*Saurida undosquamis*”, has been confused with other species such as *S. gracilis*, *S. grandisquamis*, *S. macrolepis*, *S. lessepsianus*, *S. elongata* and *S. wanieso* (Fig. 6; Table 4), which indicates a high frequency of misidentification. In this study, the “true” species was identified by the cluster that

contained species from the type locality (north-western Australia) as well as reconfirmation based on morphology (Fig. 6). In this case, a molecular approach can provide a better insight into some widespread species that otherwise may be misled by some symplesiomorphic characters. In addition, *S. grandisquamis*, which was previously synonymized with *S. undosquamis* by Inoue and Nakabo (2006), is independently evolved from *S. undosquamis* based on the molecular phylogeny inferred in this study (Fig. 6). Several inferred species clades within both *COI* trees still remained unidentified, indicating the taxonomic problems of the synodontid-like fishes need further resolution (Fig. 5 & 6).



5. Conclusion

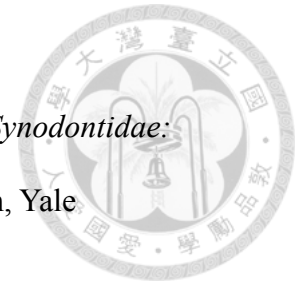
This study investigated the molecular systematics of the synodontid-like fish species and provided the first reliable phylogeny, based on the combination of the mitochondrial and nuclear gene markers. Species diversity was also evaluated based on the comprehensive *COI* datasets, especially for the species distributed in the Indo-West Pacific region.

From the results of high-level phylogeny, the synodontid-like fish were not resolved as monophyletic. Instead, the two previously defined subfamilies Synodontinae (*Synodus* and *Trachinocephalus*) and Harpadontinae (*Saurida* and *Harpadon*) were both monophyletic with the highest bootstrap support. Consequently, elevation to familiar level taxonomic status is proposed for these two subfamilies, supported by evidence from both morphology and molecular approaches. The divergence times of the two newly defined families were also estimated in the study. Synodontidae seemed to have an earlier occurrence during the late Cretaceous, while the origin of Harpadontidae was estimated in the Eocene.

From the species diversity exploration based on the *COI* datasets, a higher number of inferred species was obtained, compared to that of the recognized species included in the study. This result indicates the presence of numbers of potential new species, and further taxonomic revision of the families is required.

Although the analyses did not include all of the recognized synodontid-like fish species due to limitations of sample collection, the present study provides a framework for further taxonomic, phylogenetic and biogeographic studies. More investigations are required in order to validate and expand on the discoveries from this study, especially for some “cryptic” or undescribed species that await formal descriptions within the established phylogeny in this study.

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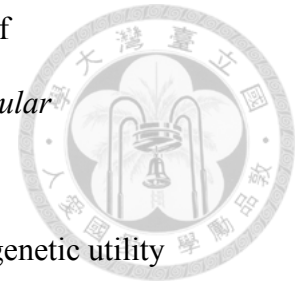


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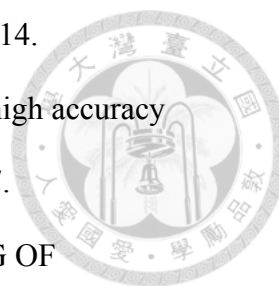
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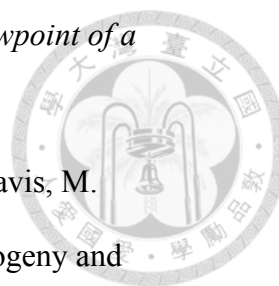
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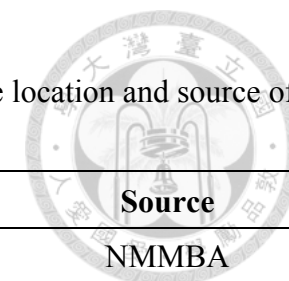


Table 1. Species list of *COI* sequences published in this study, including the species name, sample ID, voucher ID, sample location and source of each sequences. The sources of voucher specimens were shown in Remark. NA: No data available.

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Harpadon nehereus</i>	SYN220	NMMBA23626	Pingtung, Taiwan	This study	NMMBA
<i>Harpadon nehereus</i>	SYN248	NA	Vietnam	This study	NTUM
<i>Harpadon</i> aff. <i>microchir</i>	PNG1197	NTUM10971	Papua New Guinea (CP4044)	This study	NTUM
<i>Harpadon</i> aff. <i>microchir</i>	PNG0814	NTUM13166	Papua New Guinea (CP3991)	This study	NTUM
<i>Harpadon</i> aff. <i>microchir</i>	PNG0976	PNG0976	Papua New Guinea (CP4022)	This study	NTUM
<i>Harpadon microchir</i>	SYN297	FAKU 144057	Kanaya, Chiba, Tokyo Bay, Japan	This study	FAKU
<i>Harpadon microchir</i>	WJC431	WJC-XXX	NE Taiwan	This study	NTUM
<i>Harpadon microchir</i>	WJC5241	WJCXXXXIV	NE Taiwan	This study	NTUM
<i>Harpadon nehereus</i>	SYN4	S.17242-001	Dubai, UAE	This study	MAGNT
<i>Harpadon nehereus</i>	SYN5	S.17242-002	Dubai, UAE	This study	MAGNT
<i>Harpadon nehereus</i>	SYN6	S.17242-003	Dubai, UAE	This study	MAGNT
<i>Harpadon nehereus</i>	SYN1	S.17173-001	Singapore	This study	MAGNT
<i>Harpadon nehereus</i>	SYN2	S.17173-001	Singapore	This study	MAGNT
<i>Harpadon nehereus</i>	SYN3	S.17173-001	Singapore	This study	MAGNT
<i>Harpadon nehereus</i>	SYN176	NMMBA12075	W Taiwan	This study	NMMBA
<i>Harpadon nehereus</i>	WJC1084	NTUM12685	Pacific, Taiwan	This study	NTUM
<i>Harpadon nehereus</i>	WJC1085	NTUM12686	Pacific, Taiwan	This study	NTUM

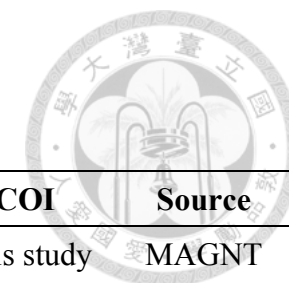


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Harpadon translucens</i>	SYN28	S.17520-007	Kakadu NT	This study	MAGNT
<i>Saurida</i> aff. <i>tumbil</i>	SYN13	S.17301-001	Abu Dhabi, UAE	This study	MAGNT
<i>Saurida</i> aff. <i>tumbil</i>	SYN12	NA	Dubai, UAE	This study	NTUM
<i>Saurida</i> aff. <i>tumbil</i>	SYN9	NA	Dubai, UAE	This study	NTUM
<i>Saurida elongata</i>	SYN254	FAKU 205087	Minoshima, Wakayama Pref., Pacific	This study	FAKU
<i>Saurida elongata</i>	SYN267	FAKU 205101	Minoshima, Wakayama Pref., Pacific	This study	FAKU
<i>Saurida elongata</i>	SYN260	FAKU 205093	Naryu, Maizuru, Kyoto Pref., Sea of Japan	This study	FAKU
<i>Saurida elongata</i>	SYN17	S.17446-004	Thailand	This study	MAGNT
<i>Saurida elongata</i>	SYN273	NTUM14486	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Saurida elongata</i>	SYN274	NTUM14486	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Saurida eso</i>	SYN258	FAKU 205091	Hiizaki, Wakayama Pref., Pacific	This study	FAKU
<i>Saurida eso</i>	SYN259	FAKU 205092	Minoshima, Wakayama Pref., Pacific	This study	FAKU
<i>Saurida eso</i>	SYN45	S.18017-002	Hong Kong	This study	MAGNT
<i>Saurida eso</i>	SYN86	MUFS 27245	Miyazaki, Japan	This study	MUFS
<i>Saurida eso</i>	SYN227	NMMBA23576	Mazu, Taiwan	This study	NMMBA
<i>Saurida eso</i>	WJC6525	WJC-XXXXI	Anping, Tainan, Taiwan	This study	NTUM
<i>Saurida eso</i>	WJC1693	NTUM12714	HCMC Vietnam	This study	NTUM

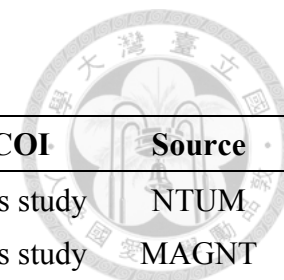


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Saurida eso</i>	SYN243	NA	Vietnam	This study	NTUM
<i>Saurida gracilis</i>	SYN67	KD83	New Ireland, PNG	This study	MAGNT
<i>Saurida gracilis</i>	SYN171	NMMBA16593	Pingtung, Taiwan	This study	NMMBA
<i>Saurida gracilis</i>	PNG0450	NTUM10215	Madang Bay	This study	NTUM
<i>Saurida gracilis</i>	WJC2244	NTUM13168	Dongsha Islands, Taiwan	This study	NTUM
<i>Saurida grandisquamis</i>	NC06	CP4654	New Caledonia (CP4654)	This study	NTUM
<i>Saurida grandisquamis</i>	NC07	CP4654	New Caledonia (CP4654)	This study	NTUM
<i>Saurida grandisquamis</i>	NC08	CP4654	New Caledonia (CP4654)	This study	NTUM
<i>Saurida grandisquamis</i>	NC09	CP4654	New Caledonia (CP4654)	This study	NTUM
<i>Saurida grandisquamis</i>	NC38	CP4655	New Caledonia (CP4655)	This study	NTUM
<i>Saurida grandisquamis</i>	NC39	CP4655	New Caledonia (CP4655)	This study	NTUM
<i>Saurida grandisquamis</i>	NC40	CP4655	New Caledonia (CP4655)	This study	NTUM
<i>Saurida grandisquamis</i>	NC41	CP4655	New Caledonia (CP4655)	This study	NTUM
<i>Saurida grandisquamis</i>	NC42	CP4655	New Caledonia (CP4655)	This study	NTUM
<i>Saurida isarankurai</i>	SYN201	NMMBA23629	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida isarankurai</i>	WJC6705	WJC-IX	NE Taiwan	This study	NTUM
<i>Saurida isarankurai</i>	WJC6706	WJC-IX	NE Taiwan	This study	NTUM
<i>Saurida lessepsianus</i>	SYN7	S.17242-004	Dubai, UAE	This study	MAGNT

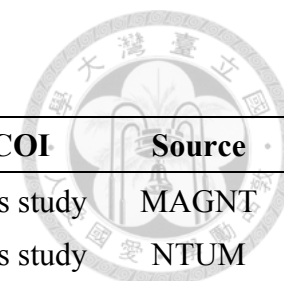


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Saurida lessepsianus</i>	SYN60	S.18029-002	Ranong, Thailand	This study	MAGNT
<i>Saurida lessepsianus</i>	SYN306	NTUM XXXX	Ranong, Thailand	This study	NTUM
<i>Saurida longimanus</i>	SYN8	S.17242-005	Dubai, UAE	This study	MAGNT
<i>Saurida longimanus</i>	SYN19	S.17446-002	Thailand	This study	MAGNT
<i>Saurida longimanus</i>	SYN20	S.17446-002	Thailand	This study	MAGNT
<i>Saurida macrolepis</i>	ASIZP900251	ASIZP61867	Taiwan	This study	ASIZ Museum
<i>Saurida macrolepis</i>	SYN271	FAKU 205105	Hiizaki, Wakayama Pref., Pacific	This study	FAKU
<i>Saurida macrolepis</i>	SYN269	FAKU 205103	northern part of Kii Channel, Wakayama Pref., Pacific	This study	FAKU
<i>Saurida macrolepis</i>	SYN38	S.18015-004	Hong Kong	This study	MAGNT
<i>Saurida macrolepis</i>	SYN39	S.18015-004	Hong Kong	This study	MAGNT
<i>Saurida macrolepis</i>	SYN16	S.17447-002	Thailand	This study	MAGNT
<i>Saurida macrolepis</i>	SYN24	S.17449-002	Thailand	This study	MAGNT
<i>Saurida macrolepis</i>	SYN93	MUFS 33026	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN94	MUFS 33027	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN95	MUFS 33028	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN96	MUFS 33029	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN98	MUFS 33032	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN99	MUFS 33033	Kagoshima, Japan	This study	MUFS

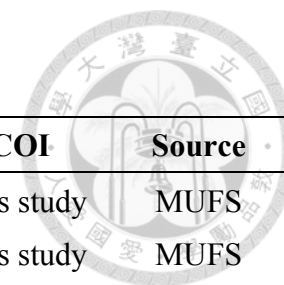


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Saurida macrolepis</i>	SYN100	MUFS 33034	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN101	MUFS 33035	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN102	MUFS 33036	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN103	MUFS 33037	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN104	MUFS 33038	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN105	MUFS 33039	Kagoshima, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN83	MUFS 25195	Miyazaki, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN87	MUFS 27659	Miyazaki, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN90	MUFS 32653	Miyazaki, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN92	MUFS 32911	Miyazaki, Japan	This study	MUFS
<i>Saurida macrolepis</i>	SYN106	MUFS 33721	Mutra, Oman	This study	MUFS
<i>Saurida macrolepis</i>	SYN301	NTUM XXXX	Pran Buri, Thailand	This study	NTUM
<i>Saurida macrolepis</i>	SYN283	NTUM14372	Tosa Bay, Iburi fishing port, Japan	This study	NTUM
<i>Saurida macrolepis</i>	SYN284	NTUM14372	Tosa Bay, Iburi fishing port, Japan	This study	NTUM
<i>Saurida macrolepis</i>	SYN289	NTUM14375	Tosa Bay, Saga fishing port, Japan	This study	NTUM
<i>Saurida macrolepis</i>	SYN290	NTUM14375	Tosa Bay, Saga fishing port, Japan	This study	NTUM
<i>Saurida macrolepis</i>	SYN293	NTUM14376	Tosa Bay, Saga fishing port, Japan	This study	NTUM
<i>Saurida macrolepis</i>	SYN294	NTUM14376	Tosa Bay, Saga fishing port, Japan	This study	NTUM

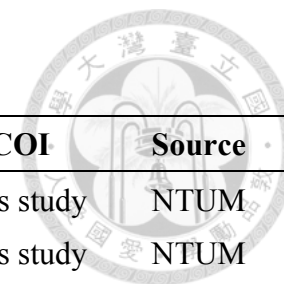


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Saurida macrolepis</i>	SYN296	NTUM14376	Tosa Bay, Saga fishing port, Japan	This study	NTUM
<i>Saurida macrolepis</i>	WJC1691	NA	Don Son Town Vietnam	This study	NTUM
<i>Saurida macrolepis</i>	WJC4399	NTUM13220	NE Taiwan	This study	NTUM
<i>Saurida macrolepis</i>	WJC1692	NA	Van Don Vietnam	This study	NTUM
<i>Saurida macrolepis</i>	SYN245	NA	Vietnam	This study	NTUM
<i>Saurida macrolepis</i>	WJC1781	NTUM13169	Xincun Harbor, HaiNan	This study	NTUM
<i>Saurida micropectoralis</i>	SYN62	S.18107-001	Pontian Kecil, Malaysia	This study	MAGNT
<i>Saurida micropectoralis</i>	SYN58	S.18029-001	Ranong, Thailand	This study	MAGNT
<i>Saurida micropectoralis</i>	SYN21	S.17446-003	Thailand	This study	MAGNT
<i>Saurida micropectoralis</i>	SYN15	S.17447-001	Thailand	This study	MAGNT
<i>Saurida micropectoralis</i>	SYN23	S.17448-001	Thailand	This study	MAGNT
<i>Saurida micropectoralis</i>	SYN204	NMMBA23630	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida micropectoralis</i>	SYN194	NMMBA23633	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida micropectoralis</i>	SYN303	NTUM XXXX	Pran Buri, Thailand	This study	NTUM
<i>Saurida micropectoralis</i>	SYN309	NTUM XXXX	Ranong, Thailand	This study	NTUM
<i>Saurida micropectoralis</i>	WJC6522	WJC-XXXXI	Anping, Tainan, Taiwan	This study	NTUM
<i>Saurida micropectoralis</i>	WJC6523	WJC-XXXXI	Anping, Tainan, Taiwan	This study	NTUM
<i>Saurida micropectoralis</i>	WJC6524	WJC-XXXXI	Anping, Tainan, Taiwan	This study	NTUM

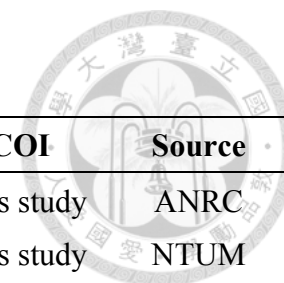


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Saurida micropectoralis</i>	SYN315	VZ13	India	This study	ANRC
<i>Saurida micropectoralis</i>	WJC453	NTUM13167	Pacific/West.Tw Taiwan	This study	NTUM
<i>Saurida micropectoralis</i>	SYN244	NA	Vietnam	This study	NTUM
<i>Saurida</i> sp.	SYN209	NMMBA23618	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida</i> sp.	SYN198	NMMBA23619	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida</i> sp.	SYN199	NMMBA23619	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida</i> sp.	SYN219	NMMBA23634	Pingtung, Taiwan	This study	NMMBA
<i>Saurida</i> sp.	SYN213	NMMBA23635	Pingtung, Taiwan	This study	NMMBA
<i>Saurida</i> sp.	SYN108	KAUM-I.62984	Panay I, Philippines	This study	KAUM
<i>Saurida</i> sp.	SYN18	S.17446-005	Thailand	This study	MAGNT
<i>Saurida</i> sp.	SYN192	NMMBA23631	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida</i> sp.	SYN193	NMMBA23631	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida</i> sp.	SYN214	NMMBA23634	Pingtung, Taiwan	This study	NMMBA
<i>Saurida tumbil</i>	SYN14	S.17301-001	Abu Dhabi, UAE	This study	MAGNT
<i>Saurida tumbil</i>	SYN36	S.18015-003	Hong Kong	This study	MAGNT
<i>Saurida tumbil</i>	SYN37	S.18015-003	Hong Kong	This study	MAGNT
<i>Saurida tumbil</i>	SYN10	NA	Dubai, UAE	This study	NTUM
<i>Saurida tumbil</i>	SYN11	NA	Dubai, UAE	This study	NTUM

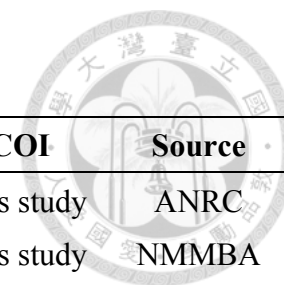


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Saurida tumbil</i>	SYN316	TR2	India	This study	ANRC
<i>Saurida umeyoshii</i>	SYN188	NMMBA23620	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida umeyoshii</i>	PNG3170	NTUM11218	Papua New Guinea (CP4457)	This study	NTUM
<i>Saurida umeyoshii</i>	PNG3209	NTUM11240	Papua New Guinea (CP4458)	This study	NTUM
<i>Saurida umeyoshii</i>	PNG3240	NTUM11254	Papua New Guinea (CP4459)	This study	NTUM
<i>Saurida umeyoshii</i>	PNG3241	NTUM11254	Papua New Guinea (CP4459)	This study	NTUM
<i>Saurida umeyoshii</i>	SYN276	NTUM14369	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Saurida umeyoshii</i>	SYN277	NTUM14369	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Saurida umeyoshii</i>	WJC5757	NA	South China Sea	This study	NTUM
<i>Saurida undosquamis</i>	SYN33	S.18015-002	Hong Kong	This study	MAGNT
<i>Saurida undosquamis</i>	SYN34	S.18015-002	Hong Kong	This study	MAGNT
<i>Saurida undosquamis</i>	SYN35	S.18015-002	Hong Kong	This study	MAGNT
<i>Saurida undosquamis</i>	SYN46	S.18018-001	Hong Kong	This study	MAGNT
<i>Saurida undosquamis</i>	SYN25	S.17500-004	NW Australia	This study	MAGNT
<i>Saurida undosquamis</i>	SYN97	MUFS 33030	Kagoshima, Japan	This study	MUFS
<i>Saurida undosquamis</i>	SYN81	MUFS 24581	Miyazaki, Japan	This study	MUFS
<i>Saurida undosquamis</i>	SYN210	NMMBA23618	Kaohsiung, Taiwan	This study	NMMBA
<i>Saurida undosquamis</i>	SYN216	NMMBA23635	Pingtung, Taiwan	This study	NMMBA

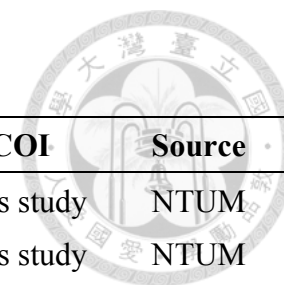


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Saurida undosquamis</i>	SYN286	NTUM14373	Tosa Bay, Iburi fishing port, Japan	This study	NTUM
<i>Saurida undosquamis</i>	SYN278	NTUM14370	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Saurida undosquamis</i>	SYN279	NTUM14370	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Synodus capricornis</i>	SYN124	NMMBA956	NE Taiwan	This study	NMMBA
<i>Synodus dermatogenys</i>	SYN146	Photo only	NE Taiwan	This study	NMMBA
<i>Synodus fuscus</i>	SYN298	FAKU 130316	Kushimoto, Wakayama, Japan	This study	FAKU
<i>Synodus fuscus</i>	SYN299	FAKU 145237	off Maizuru, Sea of Japan, Japan	This study	FAKU
<i>Synodus fuscus</i>	SYN120	NMMBA952	NE Taiwan	This study	NMMBA
<i>Synodus hoshinonis</i>	SYN22	NMMBA23626	Pingtung, Taiwan	This study	NMMBA
<i>Synodus indicus</i>	SYN26	S.17504-001	NW Australia	This study	MAGNT
<i>Synodus jaculum</i>	SYN68	KD83A	New Ireland, PNG	This study	MAGNT
<i>Synodus kaianus</i>	PNG0925	NTUM10957	Papua New Guinea (CP4016)	This study	NTUM
<i>Synodus kaianus</i>	PNG0942	NTUM10958	Papua New Guinea (CP4017)	This study	NTUM
<i>Synodus kaianus</i>	PNG1733	NTUM10993	Papua New Guinea (CP4254)	This study	NTUM
<i>Synodus kaianus</i>	PNG2551	NTUM11070	Papua New Guinea (CP4418)	This study	NTUM
<i>Synodus kaianus</i>	WJC5512	NTUM12441	South China Sea	This study	NTUM
<i>Synodus kaianus</i>	SYN122	NMMBA954	Tosa Bay	This study	NMMBA
<i>Synodus macrops</i>	SYN111	KAUM-I.91859	Pan, Philippine	This study	KAUM

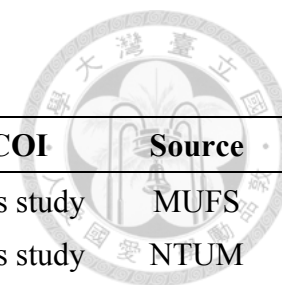


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Synodus macrops</i>	SYN84	MUFS 25676	Miyazaki, Japan	This study	MUFS
<i>Synodus macrops</i>	PNG3472	NTUM11324	Papua New Guinea (CP4491)	This study	NTUM
<i>Synodus macrops</i>	PNG3573	NTUM11361	Papua New Guinea (CP4501)	This study	NTUM
<i>Synodus macrops</i>	SYN280	NTUM14371	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Synodus macrops</i>	SYN281	NTUM14371	Tosa Bay, Mimase fishing port, Japan	This study	NTUM
<i>Synodus macrops</i>	SYN287	NTUM14374	Tosa Bay, Saga fishing port, Japan	This study	NTUM
<i>Synodus macrops</i>	SYN288	NTUM14374	Tosa Bay, Saga fishing port, Japan	This study	NTUM
<i>Synodus macrops</i>	NC620	DW4734	New Caledonia (DW4734)	This study	NTUM
<i>Synodus macrops</i>	SYN110	KAUM-I.62996	Pan, Philippines	This study	KAUM
<i>Synodus nsp.</i>	PNG3113	NTUM11197	Papua New Guinea (CP4455)	This study	NTUM
<i>Synodus nsp.</i>	PNG3114	NTUM11197	Papua New Guinea (CP4455)	This study	NTUM
<i>Synodus nsp.</i>	PNG3116	NTUM11199	Papua New Guinea (CP4455)	This study	NTUM
<i>Synodus oculeus</i>	SYN113	KAUM-I.62995	Philippines	This study	KAUM
<i>Synodus oculeus</i>	SYN109	KAUM-I.63038	Philippines	This study	KAUM
<i>Synodus oculeus</i>	NC507	CP4709	New Caledonia (CP4709)	This study	NTUM
<i>Synodus oculeus</i>	WJC5903	NTUM12444	South China Sea	This study	NTUM
<i>Synodus sp.</i>	SYN139	NMMBA16496	Pingtung, Taiwan	This study	NMMBA
<i>Synodus sp.</i>	PNG3123	NTUM11200	Papua New Guinea (CP4455)	This study	NTUM

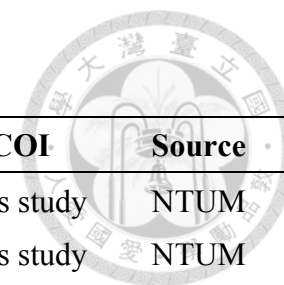


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Synodus</i> sp.	PNG3124	NTUM11200	Papua New Guinea (CP4455)	This study	NTUM
<i>Synodus</i> sp.	PNG3125	NTUM11200	Papua New Guinea (CP4455)	This study	NTUM
<i>Synodus</i> sp.	PNG3169	NTUM11217	Papua New Guinea (CP4457)	This study	NTUM
<i>Synodus</i> sp.	PNG3261	NTUM11263	Papua New Guinea (DW4464)	This study	NTUM
<i>Synodus</i> sp.	PNG3262	NTUM11263	Papua New Guinea (DW4464)	This study	NTUM
<i>Synodus</i> sp.	PNG3394	NTUM11291	Papua New Guinea (DW4488)	This study	NTUM
<i>Synodus</i> sp.	WIO464	DW4836	Western Indo-Pacific	This study	NTUM
<i>Synodus</i> sp.	SYN65	S.18118-001	FAO, Myanmar	This study	MAGNT
<i>Synodus taiwanensis</i>	SYN125	NMMBA957	Pingtung, Taiwan	This study	NMMBA
<i>Synodus ulae</i>	SYN300	FAKU 131205	Iburi, Tosashimizu, Kochi, Japan	This study	FAKU
<i>Synodus variegatus</i>	SYN47	S.18022-002	Myiek Arch. Myanmar	This study	MAGNT
<i>Synodus variegatus</i>	SYN150	photo only	Pingtung, Taiwan	This study	NMMBA
<i>Synodus variegatus</i>	ASIZP00911874	ASIZP0066653	Taiwan	This study	ASIZ Museum
<i>Synodus variegatus</i>	SYN128	NMMBA960	Pingtung, Taiwan	This study	NMMBA
<i>Synodus variegatus</i>	SYN129	NMMBA14219	Pingtung, Taiwan	This study	NMMBA
<i>Synodus variegatus</i>	SYN133	NMMBA14219	Pingtung, Taiwan	This study	NMMBA
<i>Synodus variegatus</i>	PNG0451	NTUM10216	Madang Bay	This study	NTUM
<i>Trachinocephalus gauguini</i>	PNG3127	NTUM 11085	Papua New Guinea (CP4455)	This study	NTUM

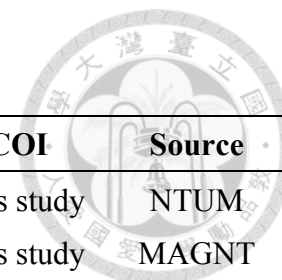


Table 1. (continued)

Species name	Sample ID	Voucher ID	Sample location	COI	Source
<i>Trachinocephalus gauguini</i>	PNG3163	NTUM 11212	Papua New Guinea (CP4456)	This study	NTUM
<i>Trachinocephalus trachinus</i>	SYN27	S.17505-001	NW Australia	This study	MAGNT
<i>Trachinocephalus trachinus</i>	SYN224	NMMBA23606	Kaohsiung, Taiwan	This study	NMMBA
<i>Trachinocephalus trachinus</i>	PNG3126	NTUM11201	Papua New Guinea (CP4455)	This study	NTUM
<i>Trachinocephalus trachinus</i>	SYN304	NTUM XXXX	Ranong, Thailand	This study	NTUM
<i>Trachinocephalus trachinus</i>	WJC1780	NTUM13170	Xincun Harbor, HaiNan	This study	NTUM
Outgroup		NA			
<i>Hime japonica</i>	WJC480	NA		This study	NTUM

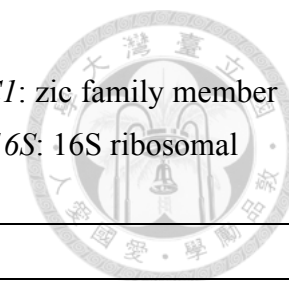


Table 2. Primers used in this study. Abbreviations of genes: *RAG1*, recombination activation gene 1; *RH*: Rhodopsin; *ZIC1*: zic family member 1; *ENC1*: ectodermal-neural cortex 1; *COI*, mitochondrial cytochrome c oxidase subunit 1; *12S*: 12S ribosomal RNA gene; *16S*: 16S ribosomal RNA gene. Reverse primers in italics.

Locus/ Primer		Primer sequences (5'-3')	Source
<i>RAG1</i>	R1 2533F	CTGAGCTGCAGTCAGTACCATAAGATGT	López <i>et al.</i> (2004)
	<i>R1 4078R</i>	<i>TGAGCCTCCATGAACTTCTGAAGRTAYTT</i>	López <i>et al.</i> (2004)
<i>RH</i>	RH 1F	ATGAACGGCACAGARGGAC	Chen <i>et al.</i> (2003)
	RH 193F	CNTATGAATAYCCTCAGTACTACC	Chen <i>et al.</i> (2003)
	<i>RH 1039R</i>	<i>TGCTTGTTTCATGCAGATGTAGA</i>	Chen <i>et al.</i> (2003)
	<i>RH 1073R</i>	<i>CCRCAGCACARCGTGGTGATCATG</i>	Chen <i>et al.</i> (2003)
<i>ENC1</i>	ENC1_F85	GACATGCTGGAGTTTCAGGA	Li <i>et al.</i> (2007)
	<i>ENC1_R982</i>	<i>ACTTGTTTRGCMACTGGGTCAAA</i>	Li <i>et al.</i> (2007)
<i>ZIC1</i>	zic1_F9	GGACGCAGGACCGCARTAYC	Li <i>et al.</i> (2007)
	<i>zic1_R967</i>	<i>CTGTGTGTGTCCTTTTGTGRATYTT</i>	Li <i>et al.</i> (2007)
<i>COI</i>	CoxI_FishF1	TCAACCAACCACAAAGACATTGGCAC	Ward <i>et al.</i> (2005)
	CoxI_FishF2	TCGACTAATCATAAAGATATCGGCAC	Ward <i>et al.</i> (2005)
	<i>CoxI_FishR1</i>	<i>TAGACTTCTGGGTGGCCAAAGAATCA</i>	Ward <i>et al.</i> (2005)
	<i>CoxI_FishR2</i>	<i>ACTTCAGGGTGACCGAAGAATCAGAA</i>	Ward <i>et al.</i> (2005)
<i>12S</i>	L1091	AAACTGGGATTAGATACCCCACTAT	Kocher <i>et al.</i> (1989)
	<i>H1478</i>	<i>TGACTGCAGAGGGTGACGGGCGGTGTGT</i>	Kocher <i>et al.</i> (1989)

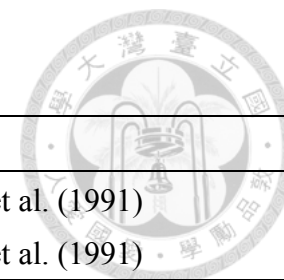


Table 2. (continued)

Locus/ Primer		Primer sequences (5'-3')	Source
16S	16S-ArL	CGCCTGTTTATCAAAAACAT	Palumbi et al. (1991)
	16S-BrH	CCGGTCTGAACTCAGATCACGT	Palumbi et al. (1991)

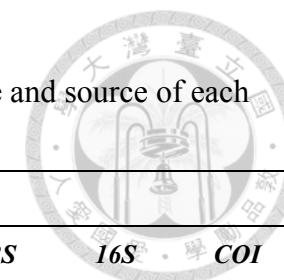


Table 3. Species list of sequences included in the multi-gene dataset, including the species name, Sample ID, family name and source of each sequences. Sample with underline are retrieved from the sequences published in Davis (2010).

Taxon	Sample ID	Family	GenBank accession no.						
			<i>RAG1</i>	<i>RH</i>	<i>ZIC1</i>	<i>ENC1</i>	<i>12S</i>	<i>16S</i>	<i>COI</i>
Synodontidae									
<i>Harpadon "microchir" (= nehereus)</i>	CBM-ZF T99-148	Synodontidae	EU366700	-	EU366745	EU366605	-	-	EU366558
<i>Harpadon microchir</i>	WJC431	Synodontidae	KC442193	KC442220	This study	This study	This study	This study	KC442068
<i>Harpadon nehereus</i>	WJC1085	Synodontidae	-	This study	This study	This study	This study	This study	This study
<i>Harpadon translucens</i>	SYN28	Synodontidae	-	This study	This study	This study	This study	This study	This study
<i>Saurida</i> aff. <i>tumbil</i>	SYN13	Synodontidae	-	-	This study	-	This study	This study	This study
<i>Saurida tumbil</i>	SYN10	Synodontidae	This study	-	This study	-	This study	This study	This study
<i>Saurida umeyoshii</i>	PNG3209	Synodontidae	This study	This study	This study	This study	This study	This study	This study
<i>Saurida eso</i>	WJC6525	Synodontidae	This study	This study	This study	-	This study	This study	This study
<i>Saurida gracilis</i>	WJC2244	Synodontidae	This study	This study	This study	This study	This study	This study	This study
<i>Saurida lessepsianus</i>	SYN7	Synodontidae	This study	-	This study	This study	This study	This study	This study
<i>Saurida longimanus</i>	SYN20	Synodontidae	-	-	-	-	This study	This study	This study
<i>Saurida macroptoralis</i>	WJC453	Synodontidae	KC442192	KC442219	This study	-	This study	This study	FJ238024
<i>Saurida undosquamis</i>	SYN278	Synodontidae	This study	This study	This study	This study	This study	This study	This study
<i>Saurida "undosquamis" (= macrolepis)</i>	CBM-ZF T99-162	Synodontidae	EU366712	-	EU366755	EU366618	-	-	EU366571
<i>Saurida grandisquamis</i>	NC41	Synodontidae	This study	-	This study	This study	This study	This study	This study

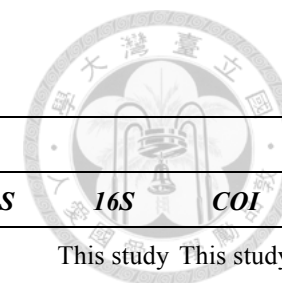


Table 3. (continued)

Taxon	Sample ID	Family	GenBank accession no.						
			<i>RAG1</i>	<i>RH</i>	<i>ZIC1</i>	<i>ENC1</i>	<i>12S</i>	<i>16S</i>	<i>COI</i>
<i>Synodus dermatogenys</i>	SYN146	Synodontidae	This study	This study	This study	This study	-	This study	This study
<i>Synodus foetens</i> (Linnaeus 1766)	WJC278	Synodontidae	JN230900	JN231001	This study	This study	This study	This study	FJ918940
<u><i>Synodus intermedius</i></u>	<u>KU T5219</u>	<u>Synodontidae</u>	<u>EU366721</u>	-	<u>EU366763</u>	<u>EU366627</u>	-	-	<u>EU366580</u>
<u><i>Synodus "kaianus"</i> (= sp. II)</u>	<u>CBM-ZF T99-128</u>	<u>Synodontidae</u>	<u>EU366719</u>	-	<u>EU366761</u>	<u>EU366625</u>	-	-	<u>EU366578</u>
<i>Synodus kaianus</i>	WJC5512	Synodontidae	This study	This study	This study	This study	This study	This study	This study
<i>Synodus macrops</i>	PNG3472	Synodontidae	This study	This study	This study	-	This study	This study	This study
<i>Synodus</i> nsp.	PNG3113	Synodontidae	This study	This study	This study	This study	This study	This study	This study
<i>Synodus oculus</i>	WJC5903	Synodontidae	This study	-	This study	This study	This study	This study	This study
<i>Synodus</i> sp.	PNG3124	Synodontidae	This study	This study	This study	This study	This study	This study	This study
<u><i>Synodus variegatus</i></u>	<u>KU T6901</u>	<u>Synodontidae</u>	<u>EU366720</u>	-	<u>EU366762</u>	<u>EU366626</u>	-	-	<u>EU366579</u>
<i>Synodus variegatus</i>	PNG0451	Synodontidae	This study	This study	This study	This study	-	This study	This study
<i>Trachinocephalus gauguini</i>	PNG3127	Synodontidae	This study	This study	This study	This study	-	This study	This study
<u><i>Trachinocephalus "myops"</i> (= <i>trachinus</i>)</u>	<u>KU T5225</u>	<u>Synodontidae</u>	<u>EU366723</u>	-	<u>EU366765</u>	<u>EU366629</u>	-	-	<u>EU366582</u>
<i>Trachinocephalus trachinus</i>	PNG3126	Synodontidae	This study	This study	This study	This study	-	This study	This study
Aulopiform allies									
<u><i>Aulopus filamentosus</i></u>	<u>USNM T3816</u>	<u>Aulopidae</u>	<u>EU366688</u>	-	<u>EU366733</u>	<u>EU366593</u>	-	-	<u>EU366546</u>
<u><i>Aulopus</i> sp.</u>	<u>SIO T02-68</u>	<u>Aulopidae</u>	<u>EU366701</u>	-	<u>EU366746</u>	<u>EU366606</u>	-	-	<u>EU366559</u>

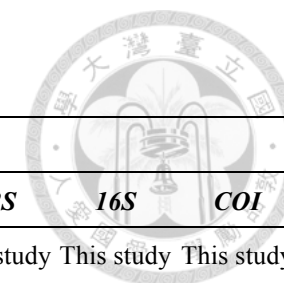


Table 3. (continued)

Taxon	Sample ID	Family	GenBank accession no.						
			<i>RAG1</i>	<i>RH</i>	<i>ZIC1</i>	<i>ENC1</i>	<i>12S</i>	<i>16S</i>	<i>COI</i>
<i>Bathypterois atricolor</i>	WJC6291	Inopidae	This study	This study	This study	This study	This study	This study	This study
<i>Bathysauroides gigas</i>	WJC6034	Bathysauroididae		This study	This study	This study	This study	This study	This study
<i>Bathysauroides gigas</i>	WIO221	Bathysauridae	This study	This study	This study	This study	This study	This study	This study
<i>Bathysaurus ferox</i>	KU T5934	Bathysauridae	EU366689	-	EU366734	EU366594	-	-	EU366547
<i>Benthalbella dentata</i>	KU T3239	Scopelarchidae	EU366693	-	EU366738	EU366598	-	-	EU366552
<i>Chlorophthalmus acutifrons</i>	WJC494	Chlorophthalmidae	KC442195	KC442222	This study	This study	This study	This study	KC442069
<i>Gigantura chuni</i>	KU T6533	Giganturidae	EU366698	-	EU366743	EU366603	-	-	EU366556
<i>Hime japonica</i>	WJC480	Aulopidae	KC442194	KC442221	This study	This study	This study	This study	AB047821
<i>Hime japonica</i>	CBM-ZF T99-124	Aulopidae	EU366687	-	EU366732	EU366592	-	-	EU366545
<i>Hime</i> sp.	NC783	Aulopidae	This study	This study	This study	This study	This study	This study	This study
<i>Ipynops</i> sp.	CBM-ZF T99-144	Ipynopidae	EU366702	-	EU366747	EU366607	-	-	EU366560
<i>Lestrolepis japonica</i>	WJC495	Paralepididae	KC442196	KC442223	This study	This study	This study	This study	-
<i>Magnisudis atlantica</i>	KU T5928	Paralepididae	-	-	EU366748	EU366611	-	-	EU366564
<i>Odontostomops</i> sp.	CBM-ZF T99-129	Evermannellidae	EU366706	-	EU366749	EU366612	-	-	EU366565
<i>Omosudis lowei</i>	KU T5909	Alepisauridae	EU366707	-	EU366750	EU366613	-	-	EU366566
<i>Paraulopus oblongus</i>	CBM-ZF T99-109	Paraulopidae	EU366709	-	EU366752	EU366615	-	-	EU366568
<i>Paraulopus oblongus</i>	PNG2584	Paraulopidae	This study	This study	This study	This study	This study	This study	-

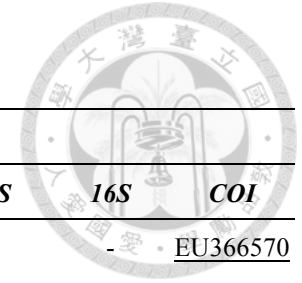


Table 3. (continued)

Taxon	Sample ID	Family	GenBank accession no.						
			<i>RAG1</i>	<i>RH</i>	<i>ZIC1</i>	<i>ENC1</i>	<i>12S</i>	<i>16S</i>	<i>COI</i>
<i>Pseudotrichonotus altivelis</i>	CBM-ZF T99-156	Pseudotrichonotidae	EU366711	-	EU366754	EU366617	-	-	EU366570
<i>Scopelarchus</i> sp.	KU T3783	Scopelarchidae	EU366715	-	EU366758	EU366621	-	-	EU366574
<i>Scopelosaurus harryi</i>	KU T3244	Notosudidae	EU366713	-	EU366756	EU366619	-	-	EU366572
<i>Sudis</i> sp.	KU T3798	Paralepididae	EU366718	-	EU366760	EU366624	-	-	EU366577
Out groups: Ateleopodiformes									
<i>Ateleopus japonicus</i>	WJC532	Ateleopodidae	KC442191	KC442218	This study	This study	This study	This study	AP002916
<i>Ijimaia antillarum</i>	KU T5411	Ateleopodidae	EU366725	-	EU366769	EU366631	-	-	EU366585

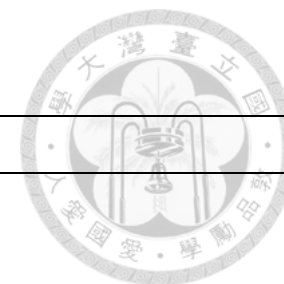


Table 4. Species list of the downloaded *COI* sequences. NA: No data available, (supp): suppressed sequence.

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Harpadon microchir</i>	NA	KC442068	
<i>Harpadon microchir</i>	NA	AP002919	
<i>Harpadon microchir</i>	NA	EU366558	
<i>Harpadon nehereus</i>	India,Gujarat	ANGEN060-15	
<i>Harpadon nehereus</i>	China,Guangdong	EF607398/FSCS326-06	
<i>Harpadon nehereus</i>	China,Guangdong	EF607399/FSCS307-06	
<i>Harpadon nehereus</i>	Vietnam	EF609369/FOAD185-05	
<i>Harpadon nehereus</i>	India	EU148582	
<i>Harpadon nehereus</i>	India	EU148583	
<i>Harpadon nehereus</i>	India	EU148584	
<i>Harpadon nehereus</i>	NA	FOAD186-05	
<i>Harpadon nehereus</i>	Vietnam	FOAD187-05	
<i>Harpadon nehereus</i>	NA	FOAD188-05	
<i>Harpadon nehereus</i>	NA	FOAD189-05	
<i>Harpadon nehereus</i>	Indonesia,Jawa Barat	FOAH871-08	
<i>Harpadon nehereus</i>	Indonesia,Jawa Barat	FOAH872-08	
<i>Harpadon nehereus</i>	Indonesia,Jawa Barat	FOAH873-08	

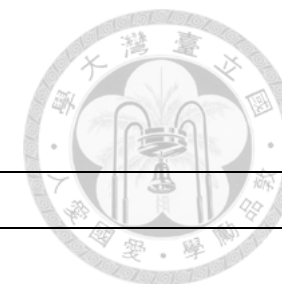


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Harpadon nehereus</i>	China,Hainan	FSCS945-11	
<i>Harpadon nehereus</i>	China,Guangdong	FSCS946-11	
<i>Harpadon nehereus</i>	China,Fujian	FSCS947-11	
<i>Harpadon nehereus</i>	China,Guangdong	FSCS948-11	
<i>Harpadon nehereus</i>	China,Guangdong	FSCS949-11	
<i>Harpadon nehereus</i>	China,Guangxi	FSCS950-11	
<i>Harpadon nehereus</i>	China,Guangxi	FSCS951-11	
<i>Harpadon nehereus</i>	China,Guangdong	FSCS952-11	
<i>Harpadon nehereus</i>	China,Guangdong	FSCS953-11	
<i>Harpadon nehereus</i>	China,Guangxi	FSCS954-11	
<i>Harpadon nehereus</i>	China,Guangxi	FSCS955-11	
<i>Harpadon nehereus</i>	China: South China Sea	JN242630	
<i>Harpadon nehereus</i>	China: South China Sea	JN242631	
<i>Harpadon nehereus</i>	China: South China Sea	JN242632	
<i>Harpadon nehereus</i>	China: South China Sea	JN242633	
<i>Harpadon nehereus</i>	China: South China Sea	JN242634	

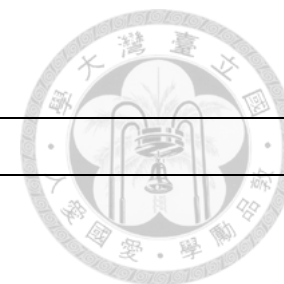


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Harpadon nehereus</i>	China: South China Sea	JN242635	
<i>Harpadon nehereus</i>	China: South China Sea	JN242636	
<i>Harpadon nehereus</i>	China: South China Sea	JN242637	
<i>Harpadon nehereus</i>	China: South China Sea	JN242638	
<i>Harpadon nehereus</i>	China: South China Sea	JN242639	
<i>Harpadon nehereus</i>	China: South China Sea	JN242640	
<i>Harpadon nehereus</i>	NA	JQ738573	
<i>Harpadon nehereus</i>	NA	JQ738574	
<i>Harpadon nehereus</i>	India,Gujarat	KF214300/DBFN384-12	
<i>Harpadon nehereus</i>	China: Hubei	KP112247	
<i>Harpadon nehereus</i>	China	KP260457	
<i>Harpadon nehereus</i>	India,Maharashtra	WLIND610-07	
<i>Harpadon nehereus</i>	India,Maharashtra	WLIND611-07	
<i>Harpadon nehereus</i>	India,Maharashtra	WLIND612-07	
<i>Harpadon nehereus</i>	NA	JX534239	
<i>Harpadon nudus</i>	India	JN120759	Revised as <i>H. squamosus</i>
<i>Harpadon squamosus</i>	India: Bay Of Bengal	KF453198	

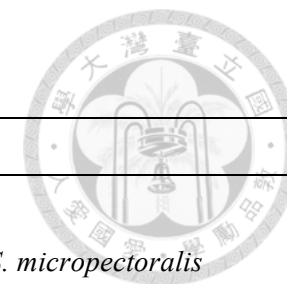


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Harpadon squamosus</i>	India: Bay Of Bengal	KF453199	
<i>Saurida argentea</i>	Australia, Queensland	HQ956200 (supp) / FOAL459-10	Revised as <i>S. micropectoralis</i>
<i>Saurida argentea</i>	Philippines: Samar, Region 8	KF809417	Revised as <i>S. micropectoralis</i>
<i>Saurida argentea</i>	Philippines: Batangas, Calabarzon	KJ202199	Revised as <i>S. micropectoralis</i>
<i>Saurida badimottah</i>	Kerala, India	KR105884	Revised as <i>S. tumbil</i>
<i>Saurida badimottah</i>	Kerala, India	KR105887	Revised as <i>S. tumbil</i>
<i>Saurida badimottah</i>	Kerala, India	KR105888	Revised as <i>S. tumbil</i>
<i>Saurida badimottah</i>	Kerala, India	KR105889	Revised as <i>S. tumbil</i>
<i>Saurida badimottah</i>	India	KR105885	Revised as <i>S. tumbil</i>
<i>Saurida badimottah</i>	India	KR105886	Revised as <i>S. tumbil</i>
<i>Saurida brasiliensis</i>	Panama, Colon	BVCOR010-08	
<i>Saurida brasiliensis</i>	Panama, Colon	BVCOR011-08	
<i>Saurida brasiliensis</i>	Panama, Colon	BVCOR020-08	
<i>Saurida brasiliensis</i>	Belize	JQ840359/BZLWA402-06	
<i>Saurida brasiliensis</i>	Belize	JQ841833/BZLWE329-08	
<i>Saurida brasiliensis</i>	USA: Gulf of Mexico	JX519394	
<i>Saurida caribbaea</i>	Panama: Caribbean Sea	JX519372	

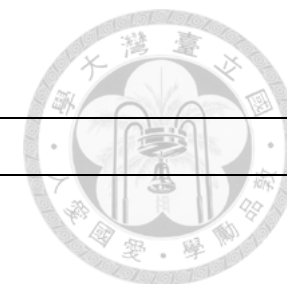


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida caribbaea</i>	Nicaragua: Caribbean Sea	JX519373	
<i>Saurida cf. micropectoralis</i>	Australia, Western Australia	FOAG747-08	
<i>Saurida cf. micropectoralis</i>	Australia, Western Australia	FOAG748-08	
<i>Saurida cf. micropectoralis</i>	NA	FOAMP094-06	
<i>Saurida cf. micropectoralis</i>	Australia, Western Australia	GU673086 (supp) / FOAG749-08	
<i>Saurida cf. micropectoralis</i>	Australia, Western Australia	GU673087 (supp) / FOAG750-08	
<i>Saurida cf. nebulosa</i>	Indonesia, Jawa Timur	HM422417 (supp) / FOAJ278-09	
<i>Saurida cf. undosquamis</i>	Australia, Queensland	FOAL502-10	Revised as <i>S. grandisquamis</i>
<i>Saurida cf. undosquamis</i>	NA	HQ579407	
<i>Saurida cf. undosquamis</i>	Australia, Western Australia	HQ956094 (supp) / FOAL317-10	
<i>Saurida cf. undosquamis</i>	Mozambique	SAIAC500-09	
<i>Saurida elongata</i>	China, Guangdong	EF607514/FSCS100-06	Revised as <i>S. eso</i>
<i>Saurida elongata</i>	China	EU595267/FSCS358-07	Revised as <i>S. eso</i>
<i>Saurida elongata</i>	China	EU595268/FSCS357-07	Revised as <i>S. eso</i>
<i>Saurida elongata</i>	China	EU595269/FSCS356-07	Revised as <i>S. eso</i>
<i>Saurida elongata</i>	China	EU595270/FSCS355-07	Revised as <i>S. eso</i>
<i>Saurida elongata</i>	China	FJ238024/FSCS766-08	

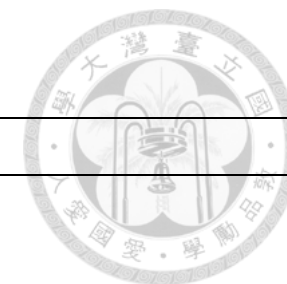


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida elongata</i>	Japan	JF952845/ABFJ234-07	
<i>Saurida elongata</i>	Japan	JF952846/ABFJ235-07	
<i>Saurida elongata</i>	Japan	JF952847/ABFJ236-07	
<i>Saurida elongata</i>	NA	JQ681486	Revised as <i>S. macrolepis</i>
<i>Saurida elongata</i>	NA	JQ681517	Revised as <i>S. macrolepis</i>
<i>Saurida elongata</i>	China	KP260467	
<i>Saurida filamentosa</i>	NA	FOAH341-08	
<i>Saurida filamentosa</i>	Australia,Queensland	FOAL492-10	
<i>Saurida filamentosa</i>	Australia,Queensland	FOAN1052-11	
<i>Saurida filamentosa</i>	Australia,Queensland	FOAN1053-11	
<i>Saurida filamentosa</i>	Australia,Queensland	FOAN1054-11	
<i>Saurida filamentosa</i>	Australia,Queensland	GU673187 (supp) / FOAH342-08	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956222 (supp) / FOAL484-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956223 (supp) / FOAL485-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956224 (supp) / FOAL486-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956225 (supp) / FOAL487-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956226 (supp) / FOAL488-10	

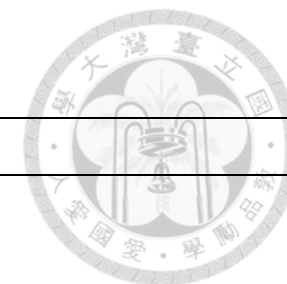


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956227 (supp) / FOAL489-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956228 (supp) / FOAL490-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956229 (supp) / FOAL491-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956230 (supp) / FOAL493-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956231 (supp) / FOAL494-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956232 (supp) / FOAL495-10	
<i>Saurida filamentosa</i>	Australia,Queensland	HQ956233 (supp) / FOAL496-10	
<i>Saurida gracilis</i>	Mozambique	HQ561491/DSFSG152-10	
<i>Saurida gracilis</i>	Mozambique	JF494426/DSFSE700-08	
<i>Saurida gracilis</i>	French Polynesia	JQ432093/MBFA418-07	
<i>Saurida gracilis</i>	French Polynesia	JQ432094/MBFA419-07	
<i>Saurida gracilis</i>	South Africa	KF489742/DSFSG765-11	
<i>Saurida gracilis</i>	French Polynesia: Society Islands	KJ968252	
<i>Saurida gracilis</i>	French Polynesia,Society Islands	KJ968259/FPFLB073-12	
<i>Saurida gracilis</i>	Madagascar,Toliara	SAIAD345-11	
<i>Saurida grandisquamis</i>	Australia,Western Australia	FOAL465-10	
<i>Saurida grandisquamis</i>	Australia,Queensland	FOAL467-10	

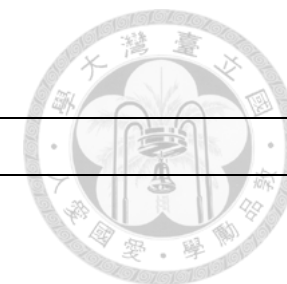


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida grandisquamis</i>	NA	FOAL497-10	
<i>Saurida grandisquamis</i>	Australia, Queensland	HQ956100 (supp) / FOAL324-10	
<i>Saurida grandisquamis</i>	Australia, Western Australia	HQ956192 (supp) / FOAL451-10	
<i>Saurida grandisquamis</i>	Australia, Queensland	HQ956218 (supp) / FOAL480-10	
<i>Saurida grandisquamis</i>	NA	FOAMP095-06	
<i>Saurida isarankurai</i>	Australia, Queensland	HQ956197 (supp) / FOAL456-10	
<i>Saurida isarankurai</i>	Australia, Queensland	HQ956198 (supp) / FOAL457-10	
<i>Saurida longimanus</i>	NA	FOAK810-10	
<i>Saurida longimanus</i>	Indonesia, Jawa Timur	HM422407 (supp) / FOAJ076-09	
<i>Saurida longimanus</i>	Australia, Western Australia	HQ956193 (supp) / FOAL452-10	
<i>Saurida longimanus</i>	Kerala, India	KR105860	
<i>Saurida longimanus</i>	India	KR105857	
<i>Saurida longimanus</i>	Kerala, India	KR105853	
<i>Saurida longimanus</i>	India	KR105854	
<i>Saurida longimanus</i>	Kerala, India	KR105861	
<i>Saurida longimanus</i>	Kerala, India	KR105862	
<i>Saurida longimanus</i>	India	KR105855	

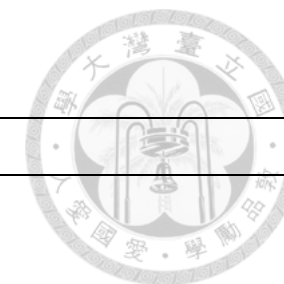


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida longimanus</i>	Kerala, India	KR105859	
<i>Saurida longimanus</i>	India	KR105856	
<i>Saurida longimanus</i>	India	KR105858	
<i>Saurida macrolepis</i>	Israel	BIM176-13	Revised as <i>S. lessepsianus</i>
<i>Saurida macrolepis</i>	Israel	BIM177-13	Revised as <i>S. lessepsianus</i>
<i>Saurida macrolepis</i>	Israel	BIM178-13	Revised as <i>S. lessepsianus</i>
<i>Saurida macrolepis</i>	Israel	BIM313-13	Revised as <i>S. lessepsianus</i>
<i>Saurida macrolepis</i>	Israel	BIM367-13	Revised as <i>S. lessepsianus</i>
<i>Saurida macrolepis</i>	Indonesia,Nusa Tenggara Barat	FOAI026-08	Revised as <i>S. macrolepis</i>
<i>Saurida macrolepis</i>	Israel	KF564314	Revised as <i>S. lessepsianus</i>
<i>Saurida macrolepis</i>	China	KP260474	
<i>Saurida microlepis</i>	Russia: Sea of Japan, Ussuri Bay	KM036504	Revised as <i>S. eso</i>
<i>Saurida microlepis</i>	NA	KJ194275	Revised as <i>S. eso</i>
<i>Saurida micropectoralis</i>	NA	FJ265846	
<i>Saurida micropectoralis</i>	NA	FOAL075-10	
<i>Saurida micropectoralis</i>	Indonesia,Jawa Barat	FOAM446-10	
<i>Saurida micropectoralis</i>	Indonesia,Jawa Barat	FOAM447-10	

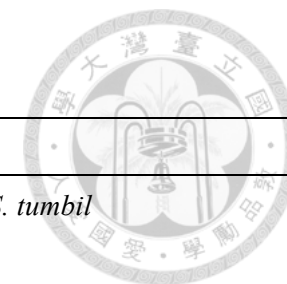


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida micropectoralis</i>	Indonesia,Nusa Tenggara Barat	HQ564337 (supp) / FOAK863-10	Revised as <i>S. tumbil</i>
<i>Saurida micropectoralis</i>	Indonesia,Bali	HQ564428 (supp) / FOAL076-10	
<i>Saurida micropectoralis</i>	Indonesia,Jawa Tengah	HQ564515 (supp) / FOAL191-10	
<i>Saurida nebulosa</i>	Australia,Queensland	FOAH591-08	
<i>Saurida nebulosa</i>	Indonesia,Nusa Tenggara Barat	GU674410 (supp) / FOAJ433-09	
<i>Saurida nebulosa</i>	Indonesia,Nusa Tenggara Barat	GU674411 (supp) / FOAJ434-09	
<i>Saurida nebulosa</i>	Reunion: Ouest, St Gilles, Planche Alizee	JQ350326	
<i>Saurida nebulosa</i>	NA	KF876020	
<i>Saurida nebulosa</i>	Madagascar,Toliara	SAIAD217-11	
<i>Saurida normani</i>	Nicaragua: Caribbean Sea	JX519365	
<i>Saurida normani</i>	Nicaragua: Caribbean Sea	JX519374	
<i>Saurida normani</i>	USA: Gulf of Mexico	JX519393	
<i>Saurida nsp.</i>	Australia,Western Australia	FOAG745-08	Revised as <i>S. umeyoshii</i>
<i>Saurida nsp.</i>	Australia,Western Australia	FOAG746-08	Revised as <i>S. umeyoshii</i>
<i>Saurida nsp.</i>	Australia,Queensland	FOAL474-10	
<i>Saurida nsp.</i>	Australia,Queensland	HQ956201 (supp) / FOAL460-10	
<i>Saurida nsp.</i>	Australia,Queensland	HQ956202 (supp) / FOAL461-10	

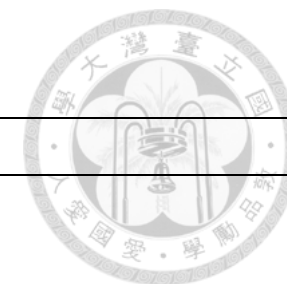


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida nsp.</i>	Australia,Queensland	HQ956209 (supp) / FOAL470-10	
<i>Saurida nsp.</i>	Australia,Queensland	HQ956210 (supp) / FOAL471-10	
<i>Saurida nsp.</i>	Australia,Queensland	HQ956211 (supp) / FOAL472-10	
<i>Saurida nsp.</i>	Australia,Queensland	HQ956212 (supp) / FOAL473-10	
<i>Saurida nsp.</i>	Australia,Northern Territory	HQ956213 (supp) / FOAL475-10	Revised as <i>S. tumbil</i>
<i>Saurida nsp.</i>	Australia,Northern Territory	HQ956214 (supp) / FOAL476-10	Revised as <i>S. tumbil</i>
<i>Saurida nsp.</i>	Australia,Northern Territory	HQ956215 (supp) / FOAL477-10	Revised as <i>S. tumbil</i>
<i>Saurida nsp.</i>	Australia,Northern Territory	HQ956216 (supp) / FOAL478-10	Revised as <i>S. tumbil</i>
<i>Saurida pseudotumbil</i>	NA	KF876337	
<i>Saurida pseudotumbil</i>	NA	KM459005	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR017-08	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR448-08	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR501-09	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR502-09	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR530-09	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR531-09	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR532-09	

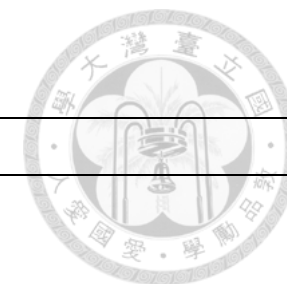


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR533-09	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR534-09	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	DSLAR535-09	
<i>Saurida sp.</i>	China,Guangdong	EF607515/FSCS277-06	Revised as <i>S. tumbil</i>
<i>Saurida sp.</i>	NA	FOAH303-08	
<i>Saurida sp.</i>	NA	FOAH304-08	
<i>Saurida sp.</i>	Australia,Queensland	GU673295 (supp) / FOAI546-09	
<i>Saurida sp.</i>	Australia,Queensland	GU673296 (supp) / FOAI547-09	
<i>Saurida sp.</i>	Australia,Queensland	GU673297 (supp) / FOAI544-09	Revised as <i>S. grandisquamis</i>
<i>Saurida sp.</i>	Australia,Queensland	GU673298 (supp) / FOAI543-09	Revised as <i>S. grandisquamis</i>
<i>Saurida sp.</i>	Australia,Queensland	HM422394 (supp) / FOAI542-09	Revised as <i>S. tumbil</i>
<i>Saurida sp.</i>	China,Hong Kong	HQ564552 (supp) / FOAL234-10	Revised as <i>S. macrolepis</i>
<i>Saurida sp.</i>	China,Hong Kong	HQ564553 (supp) / FOAL235-10	Revised as <i>S. macrolepis</i>
<i>Saurida sp.</i>	Australia,Queensland	HQ955944 (supp) / FOAI545-09	Revised as <i>S. grandisquamis</i>
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	JF494427/TZMSB039-04	
<i>Saurida sp.</i>	South Africa	JF494428/DSFSE475-08	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	JF494429/TZMSB040-04	

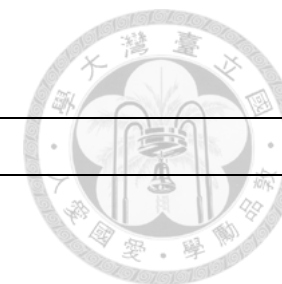


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida sp.</i>	South Africa	JF494430/DSFSE289-07	
<i>Saurida sp.</i>	South Africa	JF494431/DSFSE290-07	
<i>Saurida sp.</i>	South Africa	JF494432/DSFSE288-07	
<i>Saurida sp.</i>	Belize	JQ841786/BZLWE397-08	Revised as <i>S. braziliensis</i>
<i>Saurida sp.</i>	Barbados	LIDM1383-08	Revised as <i>S. suspicio</i>
<i>Saurida sp.</i>	Panama	LIDM1392-08	Revised as <i>S. braziliensis</i>
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	TZSAL095-04	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	TZSAL096-04	
<i>Saurida sp.</i>	South Africa,KwaZulu-Natal	TZSAN155-06	
<i>Saurida sp.</i>	NA	HM382761	
<i>Saurida sp. I</i>	Australia,Western Australia	HQ956219 (supp) / FOAL481-10	Revised as <i>S. elongata</i>
<i>Saurida sp. I</i>	Australia,Western Australia	HQ956220 (supp) / FOAL482-10	Revised as <i>S. elongata</i>
<i>Saurida sp. I</i>	Australia,Western Australia	HQ956221 (supp) / FOAL483-10	Revised as <i>S. elongata</i>
<i>Saurida sp. B</i>	Mangalore, India	KR105900	Revised as <i>S. isarankurai</i>
<i>Saurida sp.B</i>	Kochi, India	KR105901	Revised as <i>S. isarankurai</i>
<i>Saurida sp.B</i>	Kochi, India	KR105902	Revised as <i>S. isarankurai</i>
<i>Saurida sp.B</i>	Kochi, India	KR105903	Revised as <i>S. isarankurai</i>



Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida sp.B</i>	Kochi, India	KR105899	Revised as <i>S. isarankurai</i>
<i>Saurida suspicio</i>	Barbados	BVCOR023-08	
<i>Saurida suspicio</i>	Belize	GU225024/MFLII228-07	
<i>Saurida suspicio</i>	Belize	JQ841832/BZLWE398-08	
<i>Saurida suspicio</i>	Belize	JQ841834/BZLWE393-08	
<i>Saurida suspicio</i>	Barbados	LIDM1220-08	
<i>Saurida suspicio</i>	Barbados	LIDM1382-08	
<i>Saurida tumbil</i>	India,Gujarat	ANGEN149-15	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	India,Maharashtra	EF609599/WLIND618-07	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	India,Maharashtra	EF609600/WLIND617-07	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	India,Maharashtra	EF609601/WLIND616-07	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	India,Maharashtra	EF609602/WLIND615-07	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	Iran,Bushehr	HQ149924/NNPF140-10	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	Iran,Bushehr	HQ149925/NNPF075-10	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	Iran,Bushehr	HQ149926/NNPF057-10	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	Iran,Bushehr	HQ149927/NNPF033-10	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	NA	JQ681396	

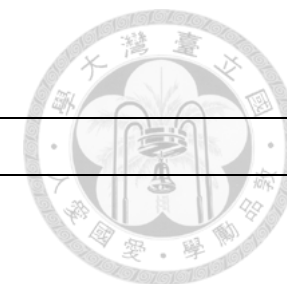


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida tumbil</i>	NA	JQ681397	
<i>Saurida tumbil</i>	NA	JQ681398	
<i>Saurida tumbil</i>	India	KJ713184	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	NA	KM459006	Revised as <i>Saurida</i> n. sp. (aff. <i>tumbil</i>)
<i>Saurida tumbil</i>	Chennai, India	KR105892	Revised as <i>S. aff. tumbil</i>
<i>Saurida tumbil</i>	Chennai, India	KR105897	Revised as <i>S. aff. tumbil</i>
<i>Saurida tumbil</i>	Chennai, India	KR105894	Revised as <i>S. aff. tumbil</i>
<i>Saurida tumbil</i>	Chennai, India	KR105896	Revised as <i>S. aff. tumbil</i>
<i>Saurida tumbil</i>	Mumbai, India	KR105893	Revised as <i>S. aff. tumbil</i>
<i>Saurida tumbil</i>	Ratnagiri, India	KR105895	Revised as <i>S. aff. tumbil</i>
<i>Saurida tumbil</i>	Ratnagiri, India	KR105898	Revised as <i>S. aff. tumbil</i>
<i>Saurida umeyoshii</i>	NA	KM189365	
<i>Saurida undosquamis</i>	India	FJ347930	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	India	FJ347931	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	India	FJ347932	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Western Australia	FOAG742-08	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Western Australia	FOAG743-08	Revised as <i>S. grandisquamis</i>

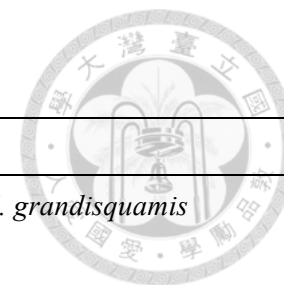


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida undosquamis</i>	Western Australia	FOAG744-08	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Western Australia	FOAG752-08	
<i>Saurida undosquamis</i>	Western Australia	FOAG753-08	
<i>Saurida undosquamis</i>	Western Australia	FOAG754-08	
<i>Saurida undosquamis</i>	Western Australia	FOAG755-08	
<i>Saurida undosquamis</i>	Western Australia	FOAG756-08	
<i>Saurida undosquamis</i>	Western Australia	FOAG757-08	
<i>Saurida undosquamis</i>	Australia, Queensland	FOAL323-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	NA	FOAMP096-06	
<i>Saurida undosquamis</i>	NA	FOAMP097-06	
<i>Saurida undosquamis</i>	NA	FOAMP098-06	
<i>Saurida undosquamis</i>	NA	FOAMP105-06	
<i>Saurida undosquamis</i>	NA	FOAMP106-06	
<i>Saurida undosquamis</i>	NA	FOAMP108-06	
<i>Saurida undosquamis</i>	NA	FOAMP109-06	
<i>Saurida undosquamis</i>	Western Australia	FOAN132-11	
<i>Saurida undosquamis</i>	Western Australia	FOAN133-11	

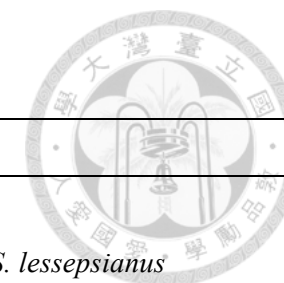


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida undosquamis</i>	Western Australia	GU673088 (supp) / FOAG751-08	
<i>Saurida undosquamis</i>	NA	HM382781	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956093 (supp) / FOAL315-10	
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956095 (supp) / FOAL318-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956096 (supp) / FOAL319-10	
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956097 (supp) / FOAL320-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956098 (supp) / FOAL321-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956099 (supp) / FOAL322-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Western Australia	HQ956194 (supp) / FOAL453-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956195 (supp) / FOAL454-10	
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956196 (supp) / FOAL455-10	
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956199 (supp) / FOAL458-10	
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956203 (supp) / FOAL462-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956204 (supp) / FOAL463-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956205 (supp) / FOAL464-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Western Australia	HQ956206 (supp) / FOAL466-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia,Queensland	HQ956207 (supp) / FOAL468-10	Revised as <i>S. grandisquamis</i>

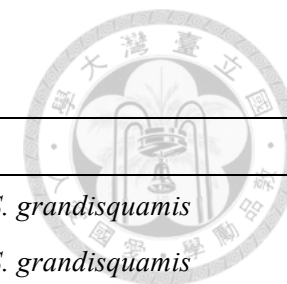


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida undosquamis</i>	Australia, Queensland	HQ956208 (supp) / FOAL469-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia, Queensland	HQ956217 (supp) / FOAL479-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia, Queensland	HQ956234 (supp) / FOAL498-10	
<i>Saurida undosquamis</i>	Western Australia	HQ956235 (supp) / FOAL499-10	
<i>Saurida undosquamis</i>	Australia, Northern Territory	HQ956236 (supp) / FOAL500-10	
<i>Saurida undosquamis</i>	Australia, Queensland	HQ956237 (supp) / FOAL501-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia, Queensland	HQ956238 (supp) / FOAL503-10	Revised as <i>S. grandisquamis</i>
<i>Saurida undosquamis</i>	Australia, Queensland	HQ956239 (supp) / FOAL504-10	
<i>Saurida undosquamis</i>	Turkey	JQ623982/DNATR079-12	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501273/DNATR1306-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501274/DNATR1312-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501275/DNATR1313-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501276/DNATR1314-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501277/DNATR1315-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501278/DNATR1316-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501279/DNATR1309-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501280/DNATR1317-13	Revised as <i>S. macrolepis</i>

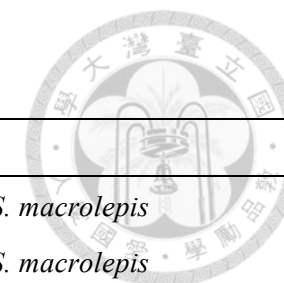


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida undosquamis</i>	Turkey	KC501281/DNATR1318-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501282/DNATR1319-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501283/DNATR1310-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501284/DNATR1301-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501285/DNATR1300-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501286/DNATR1302-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501287/DNATR1303-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501288/DNATR1304-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501289/DNATR1311-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501290/DNATR1305-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501291/DNATR1307-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Turkey	KC501292/DNATR1308-13	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	NA	KF876019	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	NA	KJ511779	Revised as <i>S. macrolepis</i>
<i>Saurida undosquamis</i>	Israel	KM538517/JFS275-14	
<i>Saurida undosquamis</i>	Israel	KM538518/JFS382-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538519/JFS381-14	Revised as <i>S. lessepsianus</i>



Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Saurida undosquamis</i>	Israel	KM538520/JFS273-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538521/JFS274-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538522/JFS383-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538523/JFS384-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538524/JFS379-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538525/JFS278-14	
<i>Saurida undosquamis</i>	Israel	KM538526/JFS071-09	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538527/JFS072-09	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538528/JFS380-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538529/JFS277-14	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Israel	KM538530/JFS276-14	
<i>Saurida undosquamis</i>	South Africa,Eastern Cape	SAIAB252-06	
<i>Saurida undosquamis</i>	Tanzania,Tanga	SAIAB806-08	Revised as <i>S. lessepsianus</i>
<i>Saurida undosquamis</i>	Tanzania,Tanga	SAIAB889-08	Revised as <i>S. tumbil</i>
<i>Saurida undosquamis</i>	NA	AP002920/GBGC0360-06	
<i>Saurida undosquamis</i>	NA	EU366571	Revised as <i>S. macrolepis</i>
<i>Saurida wanieso</i>	Taiwan	KP027408	Revised as <i>S. elongata</i>

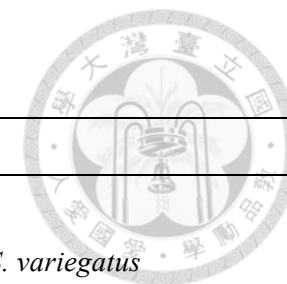


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus binotatus</i>	Madagascar,Antananarivo	JQ350383/SBF058-11	
<i>Synodus binotatus</i>	Madagascar,Antananarivo	JQ350384/SBF411-11	Revised as <i>S. variegatus</i>
<i>Synodus binotatus</i>	Madagascar,Antananarivo	JQ350385/SBF182-11	Revised as <i>S. variegatus</i>
<i>Synodus binotatus</i>	Madagascar,Antananarivo	JQ350386/SBF280-11	Revised as <i>S. variegatus</i>
<i>Synodus binotatus</i>	Madagascar,Antananarivo	JQ350387/SBF279-11	Revised as <i>S. variegatus</i>
<i>Synodus binotatus</i>	Madagascar,Antananarivo	JQ350388/SBF281-11	Revised as <i>S. variegatus</i>
<i>Synodus binotatus</i>	Madagascar,Antananarivo	JQ350389/SBF410-11	
<i>Synodus binotatus</i>	Seychelles,Mahe	SAIAB044-06	
<i>Synodus binotatus</i>	Seychelles,Mahe	SAIAB308-06	
<i>Synodus bondi</i>	Panama,Colon	BVCOR009-08	
<i>Synodus bondi</i>	Belize	JX519392	
<i>Synodus cf. fuscus</i>	Australia,Queensland	GU673288 (supp) / FOAI557-09	
<i>Synodus cf. fuscus</i>	NA	HQ579393	
<i>Synodus cf. tectus</i>	China,Hong Kong	HQ564541 (supp) / FOAL222-10	Revised as <i>S. hoshinonis</i>
<i>Synodus dermatogenys</i>	Indonesia,Nusa Tenggara Barat	FOAM160-10	
<i>Synodus dermatogenys</i>	Indonesia,Nusa Tenggara Barat	FOAM664-10	
<i>Synodus dermatogenys</i>	Australia,Queensland	HM422386 (supp) / FOAH553-08	

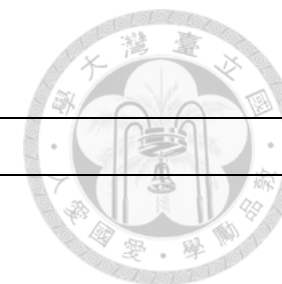


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus dermatogenys</i>	NA	HQ972582	
<i>Synodus dermatogenys</i>	Reunion: Ouest, St Gilles, Planche Alizee	JQ350390	
<i>Synodus dermatogenys</i>	French Polynesia	JQ432182/MBFA528-07	
<i>Synodus dermatogenys</i>	French Polynesia	JQ432183/MBFA329-07	
<i>Synodus dermatogenys</i>	Seychelles, Mahe	KF930486/UKFBJ989-08	
<i>Synodus dermatogenys</i>	Australia, Queensland	KP194826/LIFSA170-08	
<i>Synodus dermatogenys</i>	Seychelles, Mahe	SAIAB043-06	
<i>Synodus dermatogenys</i>	Seychelles, Mahe	SAIAB377-06	
<i>Synodus doaki</i>	NA	FOAH335-08	
<i>Synodus doaki</i>	Australia, Queensland	FOAH737-08	
<i>Synodus doaki</i>	Seychelles, Mahe	KF930487/UKFBJ990-08	
<i>Synodus evermanni</i>	East Pacific Ocean	MF957076/MOP208-12	
<i>Synodus evermanni</i>	East Pacific Ocean	MF957074/MOP209-12	
<i>Synodus evermanni</i>	East Pacific Ocean	MF957075/MOP210-12	
<i>Synodus evermanni</i>	East Pacific Ocean	MF957073/MOP788-12	
<i>Synodus evermanni</i>	East Pacific Ocean	MF957077/MOP790-12	
<i>Synodus foetens</i>	USA	JX519368	

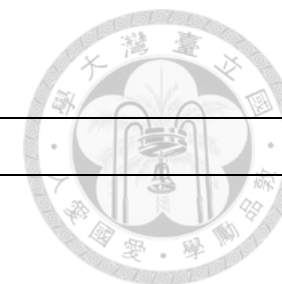


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus foetens</i>	USA	JX519369	
<i>Synodus foetens</i>	USA	JX519370	
<i>Synodus foetens</i>	USA	JX519371	
<i>Synodus foetens</i>	USA	JX519375	
<i>Synodus foetens</i>	USA: Gulf of Mexico	JX519400	
<i>Synodus foetens</i>	USA: Gulf of Mexico	JX519401	
<i>Synodus foetens</i>	USA: Gulf of Mexico	JX519409	
<i>Synodus foetens</i>	Atlantic Ocean	JX519410	
<i>Synodus foetens</i>	USA: Gulf of Mexico	JX519411	
<i>Synodus foetens</i>	United States,Alabama	KF461243/CFSAN186-11	
<i>Synodus foetens</i>	Belize	KF930488/UKFBI774-08	
<i>Synodus foetens</i>	NA	KUBV001-09	
<i>Synodus foetens</i>	NA	KUBV004-09	
<i>Synodus foetens</i>	United States	KUBV006-09	
<i>Synodus foetens</i>	NA	KUBV007-09	
<i>Synodus foetens</i>	NA	KUBV008-09	
<i>Synodus foetens</i>	NA	FJ918940	

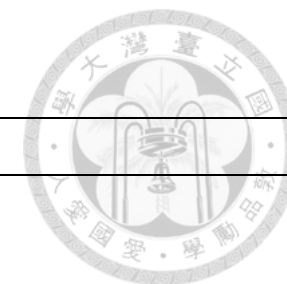


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus hoshinonis</i>	Australia, Western Australia	GU673089 (supp) / FOAG758-08	
<i>Synodus houlti</i>	Australia, Queensland	GU673287 (supp) / FOAI556-09	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR395-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR396-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR397-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR398-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR399-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR400-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR402-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR403-08	
<i>Synodus indicus</i>	South Africa, KwaZulu-Natal	DSLAR404-08	
<i>Synodus indicus</i>	South Africa	HQ945836/DSFSG057-10	
<i>Synodus indicus</i>	South Africa	HQ945935/DSFSG354-10	
<i>Synodus indicus</i>	South Africa	HQ945942/DSFSG362-10	
<i>Synodus indicus</i>	South Africa	JF494654/DSFSE564-08	
<i>Synodus intermedius</i>	NA	EU366580	Revised as <i>S. macrostigmus</i>
<i>Synodus intermedius</i>	Mexico, Quintana Roo, Xcalak	GU225062/MFLII491-07	

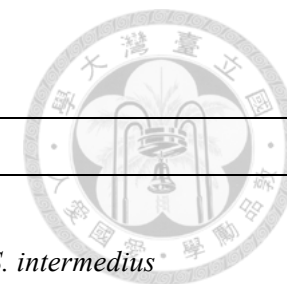


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus intermedius</i>	Mexico, Quintana Roo	GU225495/MEFM480-06	
<i>Synodus intermedius</i>	Mexico, Quintana Roo	GU225496/MEFM451-06	Revised as <i>S. intermedius</i>
<i>Synodus intermedius</i>	Bahamas	JX519366	
<i>Synodus intermedius</i>	Belize	JX519367	
<i>Synodus intermedius</i>	Bahamas	JX519386	
<i>Synodus intermedius</i>	Bahamas	JX519387	
<i>Synodus intermedius</i>	Bahamas	JX519402	
<i>Synodus intermedius</i>	USA: South Sargasso Sea	KF930489/UKFBJ1169-08	
<i>Synodus jaculum</i>	Indonesia, Nusa Tenggara Barat	FOAM696-10	
<i>Synodus jaculum</i>	Mozambique	JF494655/DSFSF048-09	
<i>Synodus jaculum</i>	Mozambique	JF494656/DSFSF029-09	
<i>Synodus jaculum</i>	Mozambique	JF494658/DSFSE683-08	
<i>Synodus jaculum</i>	Madagascar, Antananarivo	JQ350391/SBF412-11	
<i>Synodus jaculum</i>	Madagascar, Antananarivo	JQ350392/SBF413-11	
<i>Synodus jaculum</i>	French Polynesia	JQ432184/MBFA655-07	
<i>Synodus jaculum</i>	French Polynesia	JQ432185/MBFA656-07	
<i>Synodus jaculum</i>	Seychelles: Ile du Nord, Ile du Nord	KF930490/UKFBJ1028-08	

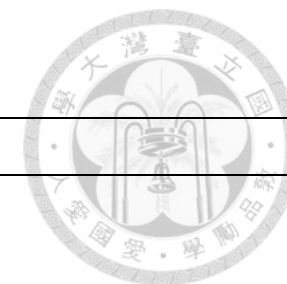


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus jaculum</i>	French Polynesia: Society Islands	KJ968293	
<i>Synodus kaianus</i>	NA	AP004202/GBGCA9935-15	
<i>Synodus kaianus</i>	NA	EU366578	
<i>Synodus lacertinus</i>	North Pacific Ocean	GU440545/MFC207-08	
<i>Synodus lucioiceps</i>	United States, California	GU440546/MFC208-08	
<i>Synodus lucioiceps</i>	United States, California	JQ354511/FMV499-11	
<i>Synodus lucioiceps</i>	USA: California, Monterey	KF930491	
<i>Synodus lucioiceps</i>	United States, California	Pending (#4870)/FMV861-16	
<i>Synodus lucioiceps</i>	United States, California	Pending (#4870)/FMV866-16	
<i>Synodus lucioiceps</i>	United States, California	Pending (#4870)/FMV867-16	
<i>Synodus lucioiceps</i>	United States, California	Pending (#4870)/FMV892-16	
<i>Synodus macrocephalus</i>	NA	FOAH492-08	
<i>Synodus macrocephalus</i>	NA	FOAH493-08	
<i>Synodus macrocephalus</i>	Indonesia, Nusa Tenggara Barat	FOAI011-08	Revised as <i>S. macrops</i>
<i>Synodus macrocephalus</i>	Indonesia, Nusa Tenggara Barat	FOAI025-08	Revised as <i>S. macrops</i>
<i>Synodus macrocephalus</i>	Indonesia, Nusa Tenggara Barat	FOAM607-10	Revised as <i>S. macrops</i>
<i>Synodus macrops</i>	NA	FOAH428-08	

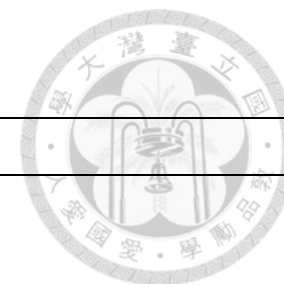


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus macrops</i>	Australia,Queensland	FOAN1055-11	
<i>Synodus macrostigmus</i>	USA: Gulf of Mexico	JX519377	
<i>Synodus macrostigmus</i>	USA: Gulf of Mexico	JX519380	
<i>Synodus oculus</i>	Indonesia,Nusa Tenggara Barat	FOAM157-10	
<i>Synodus poeyi</i>	USA: Gulf of Mexico	JX519378	
<i>Synodus poeyi</i>	USA: Gulf of Mexico	JX519379	
<i>Synodus poeyi</i>	USA: Gulf of Mexico	JX519381	
<i>Synodus poeyi</i>	Panama: Caribbean Sea	JX519397	
<i>Synodus poeyi</i>	Nicaragua: Caribbean Sea	JX519398	
<i>Synodus poeyi</i>	Panama: Caribbean Sea	JX519399	
<i>Synodus poeyi</i>	USA: Slope water, mid Atlantic bight	KF930492/UKFBJ182-08	
<i>Synodus poeyi</i>	NA	KUBV002-09	
<i>Synodus poeyi</i>	NA	KUBV003-09	
<i>Synodus randalli</i>	South Africa	HQ945938/DSFSG358-10	
<i>Synodus randalli</i>	South Africa	KF489775/DSFSG550-11	
<i>Synodus randalli</i>	Tanzania,Tanga	SAIAB826-08	
<i>Synodus randalli</i>	Tanzania,Tanga	SAIAB827-08	

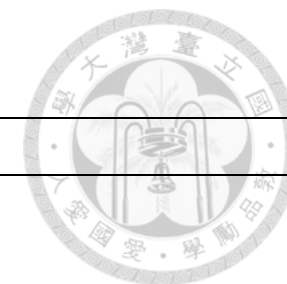


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus sageneus</i>	Australia, Queensland	GU673174 (supp) / FOAH259-08	
<i>Synodus sageneus</i>	Australia, Queensland	GU673293 (supp) / FOAI550-09	
<i>Synodus sageneus</i>	Australia, Queensland	GU673294 (supp) / FOAI551-09	
<i>Synodus saurus</i>	Israel	BIM271-13	
<i>Synodus saurus</i>	Israel	BIM350-13	
<i>Synodus saurus</i>	Bahamas	JX519385	
<i>Synodus saurus</i>	Israel	KM538601/JFS460-14	
<i>Synodus scituliceps</i>	Ecuador, Galapagos	BVCOR015-08	
<i>Synodus scituliceps</i>	Ecuador, Galapagos	BVCOR016-08	
<i>Synodus scituliceps</i>	Ecuador, Galapagos	BVCOR017-08	
<i>Synodus scituliceps</i>	Ecuador, Galapagos	LIDMA834-11	
<i>Synodus scituliceps</i>	Ecuador, Galapagos	LIDMA835-11	
<i>Synodus sp.</i>	Australia, New South Wales	AMSF138-09	Revised as <i>S. doaki</i>
<i>Synodus sp.</i>	Australia, New South Wales	AMSF139-09	Revised as <i>S. doaki</i>
<i>Synodus sp.</i>	Australia, New South Wales	AMSF141-09	Revised as <i>S. doaki</i>
<i>Synodus sp.</i>	United States Virgin Islands	BVCOR026-08	
<i>Synodus sp.</i>	United States Virgin Islands	BVCOR027-08	

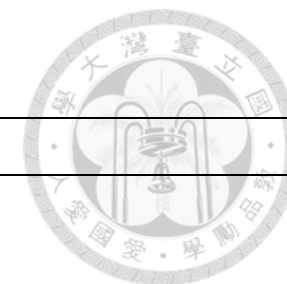


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus sp.</i>	Peru	FISHP082-15	
<i>Synodus sp.</i>	Peru	FISHP101-15	
<i>Synodus sp.</i>	Peru	FISHP102-15	
<i>Synodus sp.</i>	NA	FOAH324-08	Revised as <i>S. hoshinonis</i>
<i>Synodus sp.</i>	Bahamas	JQ839915/BAHA059-08	
<i>Synodus sp.</i>	Bahamas	JQ839916/BAHA058-08	
<i>Synodus sp.</i>	Belize	JQ840360/BZLWA027-06	
<i>Synodus sp.</i>	Belize	JQ840361/BZLWA026-06	
<i>Synodus sp.</i>	Belize	JQ840362/BZLWA503-06	
<i>Synodus sp.</i>	Belize	JQ840363/BZLWA206-06	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Belize	JQ840364/BZLWA328-06	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Belize	JQ840725/BZLWB455-06	
<i>Synodus sp.</i>	Belize	JQ841024/BZLWC429-06	Revised as <i>S. foetens</i>
<i>Synodus sp.</i>	Belize	JQ841411/BZLWD225-07	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Belize	JQ841412/BZLWD151-07	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Belize	JQ841835/BZLWE163-08	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Belize	JQ841836/BZLWE006-08	Revised as <i>S. intermedius</i>



Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus sp.</i>	United States,Florida	JQ841978/FCCA070-09	Revised as <i>S. foetens</i>
<i>Synodus sp.</i>	Curacao	JQ842339/CURA386-09	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	United States,Florida	JQ842743/SMSA502-09	Revised as <i>S. foetens</i>
<i>Synodus sp.</i>	Trinidad and Tobago	JQ843082/TOBA090-09	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Trinidad and Tobago	JQ843083/TOBA161-09	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	USA: Gulf of Mexico	JX519376	Revised as <i>S. macrostigmus</i>
<i>Synodus sp.</i>	Panama	LIDM1388-08	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Panama	LIDM1389-08	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Panama	LIDM1393-08	Revised as <i>S. intermedius</i>
<i>Synodus sp.</i>	Panama	LIDM1399-08	
<i>Synodus sp.</i>	Panama	LIDM1402-08	Revised as <i>S. intermedius</i>
<i>Synodus sp. 1</i>	NA	FOAH472-08	Revised as <i>S. oculus</i>
<i>Synodus sp. 1</i>	Australia,Queensland	GU673201 (supp) / FOAH351-08	Revised as <i>S. oculus</i>
<i>Synodus sp. 4</i>	Australia,Queensland	FOAH677-08	Revised as <i>S. oculus</i>
<i>Synodus sp. 4</i>	Australia,Queensland	GU673159 (supp) / FOAH676-08	Revised as <i>S. oculus</i>
<i>Synodus sp. 4</i>	Australia,Queensland	GU673160 (supp) / FOAH678-08	Revised as <i>S. oculus</i>
<i>Synodus sp. A</i>	Western Australia	FOAG762-08	

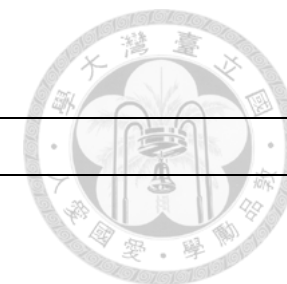


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus sp. A</i>	Western Australia	GU673090 (supp) / FOAG760-08	
<i>Synodus sp. A</i>	Western Australia	GU673091 (supp) / FOAG761-08	
<i>Synodus sp. A</i>	Western Australia	GU673092 (supp) / FOAG763-08	
<i>Synodus sp. A</i>	Western Australia	GU673093 (supp) / FOAG764-08	
<i>Synodus sp. B</i>	Western Australia	FOAG765-08	Revised as <i>S. oculus</i>
<i>Synodus sp. B</i>	NA	FOAH473-08	
<i>Synodus sp. C</i>	Western Australia	FOAG766-08	
<i>Synodus sp. C</i>	Western Australia	GU673094 (supp) / FOAG767-08	
<i>Synodus sp. C</i>	Western Australia	GU673095 (supp) / FOAG768-08	
<i>Synodus sp. D</i>	Western Australia	FOAG769-08	
<i>Synodus sp. D</i>	Western Australia	GU673096 (supp) / FOAG770-08	Revised as <i>S. oculus</i>
<i>Synodus sp. D</i>	Western Australia	GU673097 (supp) / FOAG771-08	
<i>Synodus sp. D</i>	Western Australia	GU673098 (supp) / FOAG772-08	Revised as <i>S. oculus</i>
<i>Synodus sp. D</i>	Western Australia	GU673099 (supp) / FOAG773-08	Revised as <i>S. oculus</i>
<i>Synodus sp. E</i>	Western Australia	GU673071 (supp) / FOAG774-08	
<i>Synodus synodus</i>	Panama,Colon	BVCOR012-08	
<i>Synodus synodus</i>	Panama,Colon	BVCOR018-08	

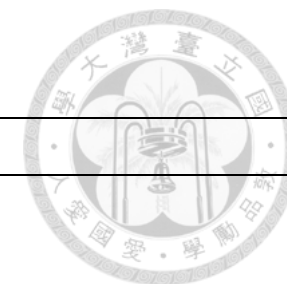


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus synodus</i>	Panama,Colon	BVCOR019-08	
<i>Synodus synodus</i>	Panama,Colon	BVCOR022-08	
<i>Synodus synodus</i>	Mexico: Quintana Roo, Northeast of Cozumel	GU225063/MFLII431-07	
<i>Synodus synodus</i>	Belize	HQ987867 (supp) / LIDMA346-10	
<i>Synodus synodus</i>	Belize	JQ840727/BZLWB133-06	
<i>Synodus synodus</i>	Belize	JQ840728/BZLWB240-06	
<i>Synodus synodus</i>	Belize	JQ840729/BZLWB159-06	
<i>Synodus synodus</i>	Belize	JQ840730/BZLWB214-06	
<i>Synodus synodus</i>	Belize	JQ841025/BZLWC297-06	
<i>Synodus synodus</i>	Bahamas	JX519382	
<i>Synodus synodus</i>	Bahamas	JX519383	
<i>Synodus synodus</i>	Bahamas	JX519384	
<i>Synodus synodus</i>	Bahamas	JX519388	
<i>Synodus synodus</i>	Turks and Caicos Islands	JX519389	
<i>Synodus synodus</i>	Turks and Caicos Islands	JX519390	
<i>Synodus synodus</i>	Turks and Caicos Islands	JX519391	
<i>Synodus synodus</i>	Bahamas	JX519403	

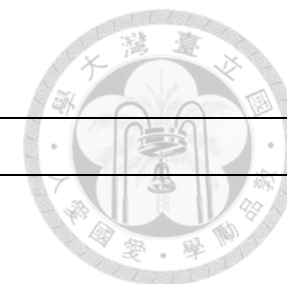


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus synodus</i>	Turks and Caicos Islands	JX519404	
<i>Synodus synodus</i>	Turks and Caicos Islands	JX519405	
<i>Synodus synodus</i>	Turks and Caicos Islands	JX519407	
<i>Synodus synodus</i>	Turks and Caicos Islands	JX519408	
<i>Synodus synodus</i>	Barbados	LIDM1398-08	
<i>Synodus tectus</i>	Australia, Queensland	GU673289 (supp) / FOAI554-09	Revised as <i>S. hoshinonis</i>
<i>Synodus tectus</i>	Australia, Queensland	GU673290 (supp) / FOAI555-09	Revised as <i>S. hoshinonis</i>
<i>Synodus tectus</i>	Australia, Queensland	GU673291 (supp) / FOAI552-09	Revised as <i>S. hoshinonis</i>
<i>Synodus tectus</i>	Australia, Queensland	GU673292 (supp) / FOAI553-09	Revised as <i>S. hoshinonis</i>
<i>Synodus tectus</i>	NA	FOAH281-08	Revised as <i>S. hoshinonis</i>
<i>Synodus usitatus</i>	Northwestern Hawaiian Islands	DQ521022/GBGC1443-06	
<i>Synodus variegatus</i>	Indonesia, Nusa Tenggara Barat	FOAM158-10	
<i>Synodus variegatus</i>	Indonesia, Nusa Tenggara Barat	GU673719 (supp) / FOAJ873-09	
<i>Synodus variegatus</i>	Indonesia, Bali	GU673920 (supp) / FOAJ644-09	
<i>Synodus variegatus</i>	Australia, Western Australia	HM376352 (supp) / FOAG775-08	
<i>Synodus variegatus</i>	South Africa	HQ561450/DSFSG096-10	
<i>Synodus variegatus</i>	South Africa	HQ945851/DSFSG080-10	

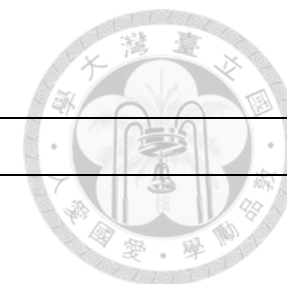


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Synodus variegatus</i>	South Africa,KwaZulu-Natal	JF494659/DSFSE342-08	
<i>Synodus variegatus</i>	French Polynesia	JQ432186/MBFA427-07	
<i>Synodus variegatus</i>	French Polynesia	JQ432187/MBFA426-07	
<i>Synodus variegatus</i>	French Polynesia	JQ432188/MBFA032-07	
<i>Synodus variegatus</i>	French Polynesia	JQ432189/MBFA031-07	
<i>Synodus variegatus</i>	South Africa	KF489776/DSFSG717-11	
<i>Synodus variegatus</i>	Seychelles,Mahe	KF930493/UKFBJ943-08	
<i>Synodus variegatus</i>	Australia,Queensland	KP194289/LIFS201-08	
<i>Synodus variegatus</i>	Australia,Queensland	KP194423/LIFS202-08	
<i>Synodus variegatus</i>	Australia,Queensland	KP194472/LIFS311-08	
<i>Synodus variegatus</i>	Australia,Queensland	KP194799/LIFS247-08	
<i>Synodus variegatus</i>	Australia: Queensland, Lizard Island	KP194877/LIFS592-08	
<i>Synodus variegatus</i>	Seychelles,Mahe	SAIAB173-06	
<i>Synodus variegatus</i>	Seychelles,Mahe	SAIAB423-06	
<i>Synodus variegatus</i>	NA	AY524977	Revised as <i>S. dermatogenys</i>
<i>Synodus variegatus</i>	NA	EU366579	
<i>Trachinocephalus gauguini</i>	France: Marquesas Islands	KP099622	



Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Trachinocephalus myops</i>	NA	AP004203/GBGCA9936-15	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Northwestern Hawaiian Islands	DQ521015/GBGC1436-06	
<i>Trachinocephalus myops</i>	India,Kerala	EF609630/WLIND607-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	India,Kerala	EF609631/WLIND606-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	India,Kerala	EF609632/WLIND605-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	India,Kerala	EF609633/WLIND604-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	EU366582	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	China	EU595323/FSCS496-07	
<i>Trachinocephalus myops</i>	China	EU595324/FSCS495-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	FOAG777-08	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	FOAN669-11	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	FOAN670-11	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Australia,Queensland	GU673286 (supp) / FOAI560-09	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Brazil: Sao Paulo	GU702530	
<i>Trachinocephalus myops</i>	Brazil: Sao Paulo	GU702531	
<i>Trachinocephalus myops</i>	Brazil: Sao Paulo	GU702532	
<i>Trachinocephalus myops</i>	Brazil: Sao Paulo	GU702533	



Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Trachinocephalus myops</i>	Brazil: Sao Paulo	GU702533	
<i>Trachinocephalus myops</i>	China,Hong Kong	HQ564550 (supp) / FOAL232-10	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	China,Hong Kong	HQ564551 (supp) / FOAL233-10	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	South Africa: Park Rynie	JF494712	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	South Africa: KwaZulu-Natal	JF494713	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	South Africa: KwaZulu-Natal	JF494714	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	JQ681513	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Belize: Stann Creek District	JQ841030	
<i>Trachinocephalus myops</i>	Belize: CB07-07	JQ841415	
<i>Trachinocephalus myops</i>	Trinidad and Tobago	JQ843093/TOBA157-09	
<i>Trachinocephalus myops</i>	USA: Gulf of Mexico	JX519395	
<i>Trachinocephalus myops</i>	USA: Gulf of Mexico	JX519396	
<i>Trachinocephalus myops</i>	South Africa: KwaZulu-Natal	KF489785	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	South Africa: Richards Bay	KF489786	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Philippines: Pangasinan	KF715033	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	USA: Texas, Off Freeport	KF930506	
<i>Trachinocephalus myops</i>	NA	KP266842	Revised as <i>T. trachinus</i>

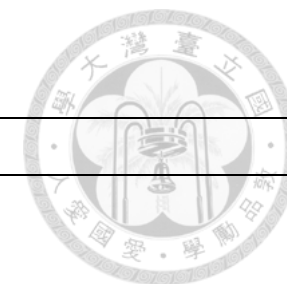


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Trachinocephalus myops</i>	USA	KT075301	
<i>Trachinocephalus myops</i>	USA	KT075319	
<i>Trachinocephalus myops</i>	Taiwan	KT718201	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KT718213	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KT718275	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KT718317	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KT718365	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KT718379	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KT718396	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KT718452	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KU943072	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KU943074	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KU943075	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KU943076	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KU943077	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KU943079	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Taiwan	KU943085	

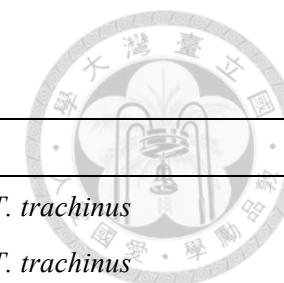


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Trachinocephalus myops</i>	Australia, New South Wales	MF040900/FOAF185-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	South Africa, KwaZulu-Natal	MF040901/TZSAL011-04	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Indonesia, Nusa Tenggara Barat	MF040902/FOAN428-11	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Western Australia	MF040903/FOAG215-08	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Australia, New South Wales	MF040904/FOAF182-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Mozambique	MF040905/DSLAR528-09	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Australia, New South Wales	MF040906/FMVIC376-08	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	South Africa, KwaZulu-Natal	MF040909/DSLAL121-10	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Mozambique	MF040912/DSLAR527-09	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Western Australia	MF040913/FOAG214-08	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Australia, New South Wales	MF040914/FOAF181-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Indonesia, Nusa Tenggara Barat	MF040915/FOAN427-11	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Western Australia	MF040916/FOAG216-08	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Western Australia	MF040918/FOAG217-08	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Australia, New South Wales	MF040919/FOAF183-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Australia, New South Wales	MF040920/FOAF184-07	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	Tanzania, Tanga	MF120959/SAIAB807-08	

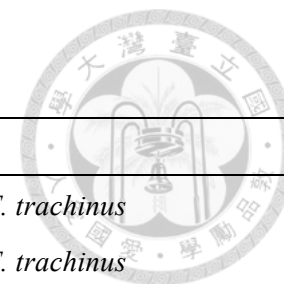


Table 4. (continued)

Taxa	Sample location	GenBank/Bold Number	Remark
<i>Trachinocephalus myops</i>	NA	PHILA1119-13	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	PHILA1776-16	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	PHILA796-13	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	KJ679905	Revised as <i>T. trachinus</i>
<i>Trachinocephalus myops</i>	NA	KT284892	Revised as <i>T. trachinus</i>
<i>Trachinocephalus sp.</i>	NA	PHILA202-13	Revised as <i>T. trachinus</i>



Table 5. List of *COI* sequences retrieved from private resources. NA: No data available.

Taxa	Locality	Sample ID	Source
<i>Harpadon nehereus</i>	NA	R19-7922-13-5168	ANRC
<i>Harpadon nehereus</i>	NA	R19-7922-14-5168	ANRC
<i>Harpadon nehereus</i>	NA	R23-7922-19-5168	ANRC
<i>Harpadon nehereus</i>	NA	R76-7922-45-5169	ANRC
<i>Harpadon nehereus</i>	NA	R76-7922-46-5169	ANRC
<i>Harpadon nehereus</i>	NA	WB18-3733-2-P9	ANRC
<i>Saurida cf. lessepsianus</i>	Ranong, Thailand	MAGNT-A05040	MAGNT
<i>Saurida cf. lessepsianus</i>	Ranong, Thailand	MAGNT-A05039	MAGNT
<i>Saurida cf. trmbil</i>	Pondicherry market, India	PON1	ANRC
<i>Saurida cf. tumbil</i>	Ranong, Thailand	MAGNT-A05037	MAGNT
<i>Saurida cf. tumbil</i>	Ranong, Thailand	MAGNT-A05038	MAGNT
<i>Saurida cf. tumbil</i>	Visakhapatnam fishing port , India	VZ12	ANRC
<i>Saurida elongata</i>	Japan	MUFS-27245	MUFS
<i>Saurida elongata</i>	NA	BR7	NTM
<i>Saurida filamentosa</i>	NE Australia	GT5490Qld	CSIRO
<i>Saurida flamma</i>	French Polynesia	GAM-686	CRIOBE
<i>Saurida flamma</i>	French Polynesia	SCIL-0606	CRIOBE



Table 5. (continued)

Taxa	Locality	Sample ID	Source
<i>Saurida gracilis</i>	Taiwan	ASIZP0066106	ASIZ Museum
<i>Saurida gracilis</i>	Red Sea	KAU13-390	KAU
<i>Saurida gracilis</i>	French Polynesia	FLMOO-374	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	FLMOO-451	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	FLMOO-480	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	FLMOO-326	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	FLMOO-346	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	FLMOO-452	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	FLMOO-504	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	FLMOO-524	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	Mbio7096	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	SCIL-0596	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	GAM-299	CRIOBE
<i>Saurida gracilis</i>	French Polynesia	Mbio7086	CRIOBE
<i>Saurida grandisquamis</i>	NW Australia	CSIROH8215-09	CSIRO
<i>Saurida grandisquamis</i> 1	NE Australia	GT4390Qld	CSIRO
<i>Saurida lessepsianus</i>	Chennai, India	PC18A-1981-30	ANRC



Table 5. (continued)

Taxa	Locality	Sample ID	Source
<i>Saurida lessepsianus</i>	India	CC13-T355	ANRC
<i>Saurida lessepsianus</i>	Kerala, India	D174-1981-28	ANRC
<i>Saurida lessepsianus</i>	Kerala, India	D175-1981-29	ANRC
<i>Saurida lessepsianus</i>	Red Sea	KAU14-0332	KAU
<i>Saurida lessepsianus</i>	Red Sea	KAU14-0434	KAU
<i>Saurida lessepsianus</i>	Chennai, India	PC18-1981-32	ANRC
<i>Saurida lessepsianus</i>	India	CC10-T355	ANRC
<i>Saurida lessepsianus</i>	Kerala, India	E133-3733-9	ANRC
<i>Saurida lessepsianus</i>	Red Sea	KAU14-0284	KAU
<i>Saurida lessepsianus</i>	Red Sea	KAU14-0285	KAU
<i>Saurida lessepsianus</i>	Red Sea	KAU14-0386	KAU
<i>Saurida lessepsianus</i>	Red Sea	KAU14-0576	KAU
<i>Saurida lessepsianus</i>	India	CC12-T355	ANRC
<i>Saurida lessepsianus</i>	India	CC11-T355	ANRC
<i>Saurida lessepsianus</i>	Chennai, India	PC17-T355	ANRC
<i>Saurida lessepsianus</i>	India	CC9-T355	ANRC
<i>Saurida lessepsianus</i>	India	CC14	ANRC



Table 5. (continued)

Taxa	Locality	Sample ID	Source
<i>Saurida lessepsianus</i>	Mangalore, India	K75	ANRC
<i>Saurida lessepsianus</i>	Visakhapatnam fishing port , India	VZ11	ANRC
<i>Saurida longimanus</i>	Red Sea	KAU14-0185	KAU
<i>Saurida longimanus</i>	Red Sea	KAU14-0279	KAU
<i>Saurida longimanus</i>	Red Sea	KAU14-0487	KAU
<i>Saurida macrolepis</i>	Taiwan	ASIZP0076109	ASIZ Museum
<i>Saurida macrolepis</i>	Taiwan	ASIZP0076110	ASIZ Museum
<i>Saurida macrolepis</i>	Taiwan	ASIZP0076111	ASIZ Museum
<i>Saurida macrolepis 1</i>	NE Australia	GT5485Qld	CSIRO
<i>Saurida micropectoralis</i>	NW Australia	CSIROH8223-03	CSIRO
<i>Saurida nebulosa</i>	French Polynesia	GAM-239	CRIOBE
<i>Saurida nebulosa</i>	French Polynesia	GAM-240	CRIOBE
<i>Saurida nebulosa</i>	French Polynesia	GAM-241	CRIOBE
<i>Saurida nebulosa 1</i>	Taiwan	BCR09-08	NTM
<i>Saurida nsp. moustache</i>	India	CC17-1981-56	ANRC
<i>Saurida nsp. moustache</i>	India	CC19-1981-7	ANRC
<i>Saurida nsp. moustache</i>	Kerala, India	E129-3733-13	ANRC



Table 5. (continued)

Taxa	Locality	Sample ID	Source
<i>Saurida nsp. moustache</i>	India	CC16-T355	ANRC
<i>Saurida nsp. moustache</i>	India	CC18-T355	ANRC
<i>Saurida nsp. moustache</i>	India	CC15-T355	ANRC
<i>Saurida sp.</i>	Red Sea	KAU14-0331	KAU
<i>Saurida sp.</i>	Red Sea	KAU14-0437	KAU
<i>Saurida sp.</i>	NA	NI1165	AMS
<i>Saurida sp.</i>	NA	NI1166	AMS
<i>Saurida sp.</i>	Pondicherry market, India	PON2	ANRC
<i>Saurida sp. 2</i>	Japan	MUFS-25074	MUFS
<i>Saurida sp. B</i>	Taiwan	BCR09-09	NTM
<i>Saurida sp. C</i>	Taiwan	BCR09-02	NTM
<i>Saurida tumbil</i>	Red Sea	KAU14-0312	KAU
<i>Saurida tumbil</i>	Red Sea	KAU14-0409	KAU
<i>Saurida tumbil</i>	Red Sea	KAU14-0410	KAU
<i>Saurida tumbil</i>	Red Sea	KAU14-0288	KAU
<i>Saurida tumbil</i>	Red Sea	KAU14-0289	KAU
<i>Saurida tumbil</i>	Red Sea	KAU14-0496	KAU



Table 5. (continued)

Taxa	Locality	Sample ID	Source
<i>Saurida tumbil</i>	NA	BR1	NTM
<i>Saurida tumbil</i>	Tranquebar fish landing port	TR1	ANRC
<i>Saurida undosquamis</i>	Taiwan	ASIZP0076118	ASIZ Museum
<i>Saurida undosquamis</i>	Taiwan	ASIZP0076119	ASIZ Museum
<i>Saurida undosquamis</i>	Mangalore, India	K66	ANRC
<i>Saurida undosquamis</i>	Kochi, India	VN7	ANRC
<i>Saurida undosquamis</i> 1	Taiwan	BCR09-05	NTM
<i>Saurida wanieso</i>	Taiwan	BCR09-09	NTM
<i>Saurida wanieso</i>	Taiwan	ASIZP0065965	ASIZ Museum
<i>Saurida wanieso</i>	Taiwan	ASIZP0065948	ASIZ Museum
<i>Synodus binotatus</i>	French Polynesia	AUST-373	CRIOBE
<i>Synodus binotatus</i>	French Polynesia	AUST-476	CRIOBE
<i>Synodus binotatus</i>	French Polynesia	mbio542	CRIOBE
<i>Synodus binotatus</i>	French Polynesia	mbio71	CRIOBE
<i>Synodus binotatus</i>	French Polynesia	mbio72	CRIOBE
<i>Synodus capricornis</i>	French Polynesia	AUST-581	CRIOBE
<i>Synodus dermatogenys</i>	Red Sea	KAU13-388	KAU

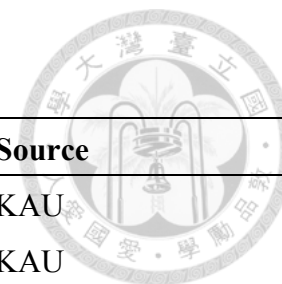


Table 5. (continued)

Taxa	Locality	Sample ID	Source
<i>Synodus dermatogenys</i>	Red Sea	KAU13-385	KAU
<i>Synodus dermatogenys</i>	Red Sea	KAU13-386	KAU
<i>Synodus dermatogenys</i>	French Polynesia	AUST-016	CRIOBE
<i>Synodus dermatogenys</i>	French Polynesia	GAM-849	CRIOBE
<i>Synodus jaculum</i>	French Polynesia	FLMOO-357	CRIOBE
<i>Synodus jaculum</i>	French Polynesia	mbio1117	CRIOBE
<i>Synodus jaculum</i>	French Polynesia	MOH-070	CRIOBE
<i>Synodus sp.</i>	French Polynesia	MARQ-321	CRIOBE
<i>Synodus variegatus</i>	Red Sea	KAU13-621	KAU
<i>Synodus variegatus</i>	Red Sea	KAU13-687	KAU
<i>Synodus variegatus</i>	French Polynesia	AUST-146	CRIOBE
<i>Synodus variegatus</i>	French Polynesia	AUST-036	CRIOBE
<i>Synodus variegatus</i>	French Polynesia	MARQ-126	CRIOBE
<i>Synodus variegatus</i>	French Polynesia	mbio721	CRIOBE
<i>Synodus variegatus</i>	French Polynesia	SCIL-061	CRIOBE
<i>Synodus variegatus</i>	French Polynesia	GAM-348	CRIOBE
<i>Synodus variegatus</i>	French Polynesia	GAM-400	CRIOBE

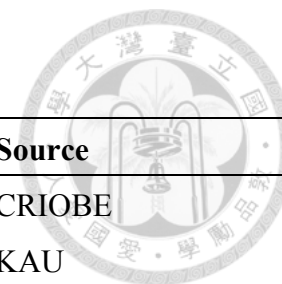


Table 5. (continued)

Taxa	Locality	Sample ID	Source
<i>Synodus variegatus</i>	French Polynesia	GAM-440	CRIOBE
<i>Trachinocephalus myops</i>	Red Sea	KAU12-0623	KAU
<i>Trachinocephalus myops</i>	Red Sea	KAU12-0622	KAU

Abbreviations of the sources: AMS, Australia Marine Services, Australia; ANRC, Andaman & Nicobar Regional Centre, India; ASIZ, Academia Sinica Institute of Zoology, Taiwan; CRIOBE, Centre de Recherches Insulaires et Observatoire de l'Environnement, French Polynesia; KAU, Kagoshima University, Japan; MAGNT, Museum and Art Gallery of the Northern Territory, Australia; MUFS, Division of Fisheries Science, Miyazaki University, Japan.

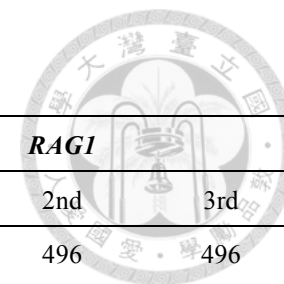


Table 6. Gene characteristics of the multi-gene dataset

	<i>12S</i>			<i>16S</i>			<i>COI</i>			<i>RAG1</i>		
Codon position	1st			2nd			3rd			1st		
Analyzed length (bp)	378			512			212			211		
No. parsimony informative sites	121			168			43			2		
No. variable sites (in %)	156 (41.27%)			206 (40.23%)			51 (24.06%)			3 (1.42%)		
Base frequencies homogeneity*	1			1			0			1		

**p* value from Chi-square test of homogeneity of base frequencies across taxa.

	<i>Rh</i>			<i>zic1</i>			<i>ENC1</i>			Total
Codon position	1st	2nd	3rd	1st	2nd	3rd	1st	2nd	3rd	
Analyzed length (bp)	275	275	275	298	298	297	287	287	287	3012
No. parsimony informative sites	53	25	161	27	2	191	25	3	210	1107
No. variable sites (in %)	68 (24.73%)	33 (12.00%)	187 (68.00%)	42 (14.09%)	13 (4.36%)	229 (77.10%)	40 (13.94%)	11 (3.83%)	241 (83.97%)	2211 (39.55%)
Base frequencies homogeneity*	1	1	0.99	1	1	0	1	1	0	N/A

**p* value from Chi-square test of homogeneity of base frequencies across taxa.

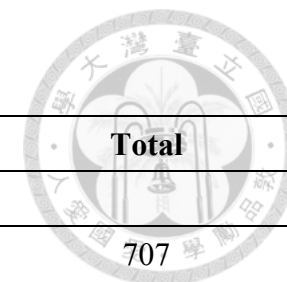


Table 7. Gene characteristics of the two *COI* datasets

	<i>COI</i> (<i>Synodus</i> + <i>Trachinocephalus</i>)			Total
Codon position	1st	2nd	3rd	
Analyzed length (bp)	236	236	235	707
No. parsimony informative sites	49	5	217	271
No. variable sites (in %)	62 (26.27%)	21 (8.90%)	218 (93.19%)	301 (42.57%)
Base frequencies homogeneity*	1	1	0	NA

**p* value from Chi-square test of homogeneity of base frequencies across taxa.

	<i>COI</i> (<i>Saurida</i> + <i>Harpadon</i>)			Total
Codon position	1st	2nd	3rd	
Analyzed length (bp)	228	228	228	684
No. parsimony informative sites	33	6	216	255
No. variable sites (in %)	50 (21.93%)	19 (8.33%)	222 (97.37%)	291 (42.54%)
Base frequencies homogeneity*	1	1	0.00167148	NA

**p* value from Chi-square test of homogeneity of base frequencies across taxa.

Gosline et al. (1966) Order Iniomi Myctophoidea Aulopidae Bathysauridae Synodontidae Harpadontidae Bathypteroidae Ipnopidae Chlorophthalmidae Notosudidae (=Scopelosauridae) Myctophidae Neoscopelidae Alepisauroidae Paralepididae Omosudidae Alepisauridae Anotopteridae Evermannellidae Scopelarchidae	Rosen (1973) Order Aulopiformes, new name Suborder Aulopoidei, new name Aulopidae Bathysauridae Ipnopidae Chlorophthalmidae Notosudidae (=Scopelosauridae) Suborder Alepisauroidae Superfamily Synodontoidea, new usage Synodontidae Harpadontidae Giganturidae Superfamily Alepisauroidae Paralepididae Omosudidae Alepisauridae Anotopteridae Evermannellidae Scopelarchidae
Sulak (1977) Benthic Myctophiformes: Aulopidae (<i>Aulopus</i>, <i>Hime Latropiscus</i>) Synodontidae Subfamily Harpadontinae (<i>Harpadon</i>, <i>Saurida</i>) Subfamily Bathysaurinae (<i>Bathysaurus</i>) Subfamily Synodontinae (<i>Synodus</i>, <i>Trachinocephalus</i>) Chlorophthalmidae Subfamily Chlorophthalminae (<i>Chlorophthalmus</i>, <i>Parasudis</i>, <i>Bathysauropsis</i>) Subfamily Ipnopinae Tribe Ipnopini (<i>Ipnops</i>) Tribe Bathypteroini (<i>Bathypterois</i>) Tribe Bathymicropini (<i>Bathymicrops</i>, <i>Bathytrophops</i>)	R. K. Johnson (1982) Myctophiformes: Aulopoids Aulopidae Myctophoids + Chlorophthalmoids Myctophoids Myctophidae Neoscopelidae Chlorophthalmoids Notosudidae Scopelarchidae Chlorophthalmidae Ipnopidae Synodontoids + Alepisauroids Synodontoids Synodontidae Harpadontidae Bathysauridae Alepisauroids Paralepididae Anotopteridae Evermannellidae Omosudidae Alepisauridae

Figure 1. Previously proposed classifications relative to the traditional family Synodontidae (Partial). Author's name and proposed years were shown in **Bold**.



Baldwin & Johnson (1996)

Order Aulopiformes

Suborder Synodontoidei

- Family Aulopidae (*Aulopus*)
- Family Pseudotrichonotidae (*Pseudotrichonotus*)
- Family Synodontidae (*Harpadon*, *Saurida*, *Synodus*, *Trachinocephalus*)

Suborder Chlorophthalmoidei

- Family Chlorophthalmidae (*Chlorophthalmus*, *Parasudis*)
- Bathysauropsis (*B. gracilis*, *B. malayanus*)
- Family Notosudidae (*Ahliesaurus*, *Luciosudis*, *Scopelosaurus*)
- Family Ipnopidae (*Bathymicrops*, *Bathypterois*, *Bathytyphlops*, *Ipnops*)

Suborder Alepisauroidae

- Family Alepisauridae (*Alepisaurus*, *Omosudis*)
- Family Paralepididae
- Family Evermannellidae (*Coccorella*, *Evermannella*, *Odontostomops*)
- Family Scopelarchidae

Suborder Giganturoidei

- Bathysauroides gigas*
- Family Bathysauridae (*Bathysaurus*)
- Family Giganturidae (*Gigantura*)

Sato & Nakabo (2002)

Order Aulopiformes

Suborder Synodontoidei

- Family Paraulopidae (*Paraulopus*)
- Family Aulopidae (*Aulopus*)
- Family Pseudotrichonotidae (*Pseudotrichonotus*)
- Family Synodontidae (*Harpadon*, *Saurida*, *Synodus*, *Trachinocephalus*)

Suborder Chlorophthalmoidei

- Family Bathysauroididae (*Bathysauroides*)
- Family Chlorophthalmidae (*Chlorophthalmus*, *Parasudis*)
- Family Bathysauropsidae (*Bathysauropsis*)
- Family Notosudidae (*Ahliesaurus*, *Luciosudis*, *Scopelosaurus*)
- Family Ipnopidae (*Bathymicrops*, *Bathypterois*, *Bathytyphlops*, *Ipnops*)

Suborder Alepisauroidae

- Family Alepisauridae (*Alepisaurus*, *Omosudis*)
- Family Paralepididae
- Family Evermannellidae (*Coccorella*, *Evermannella*, *Odontostomops*)
- Family Scopelarchidae

Suborder Giganturoidei

- Family Bathysauridae (*Bathysaurus*)
- Family Giganturidae (*Gigantura*)

Davis (2010)

Order Aulopiformes

Suborder Aulopoidei

- Family Synodontidae (*Synodus*, *Trachinocephalus*, *Harpadon*, *Saurida*)
- Family Aulopidae (*Aulopus*)
- Family Pseudotrichonotidae (*Pseudotrichonotus*)

Suborder Paraulopoidei

- Family Paraulopidae (*Paraulopus*)

Suborder Alepisauroidae

Superfamily Ipnopoidea

Epifamily Giganturoidea

- Family Giganturidae (*Gigantura*)
- Family Bathysauridae (*Bathysaurus*)
- Family Bathysauroididae (*Bathysauroides*)

Epifamily Ipnopidae

- Family Bathysauropsidae (*Bathysauropsis*)
- Family Ipnopidae (*Bathypterois*, *Ipnops*, *Bathymicrops*, *Bathytyphlops*)

Superfamily Chlorophthalmoidea

- Family Chlorophthalmidae (*Chlorophthalmus*, *Parasudis*)

Superfamily Notosudoidea

- Family Notosudidae (*Scopelosaurus*, *Ahliesaurus*, *Luciosudis*)

Superfamily Alepisauroidae sensu nov.

- Family Scopelarchidae (*Benthalbella*, *Rosenblattichthys*, *Scopelarchus*, *Scopelarchoides*)
- Family Evermannellidae (*Odontostomops*, *Coccorella*, *Evermannella*)
- Family Sudidae (*Sudis*)
- Family Alepisauridae sensu nov. (*Anotopterus*, *Magnisudis*, *Omosudis*, *Alepisaurus*)
- Family Paralepididae sensu nov. (*Macroparalepis*, *Paralepis*, *Arctozenus*, *Stemonosudis*, *Lestidiops*, *Uncisudis*, *Lestrodium*, *Dolichosudis*)

Figure 1. (continued)

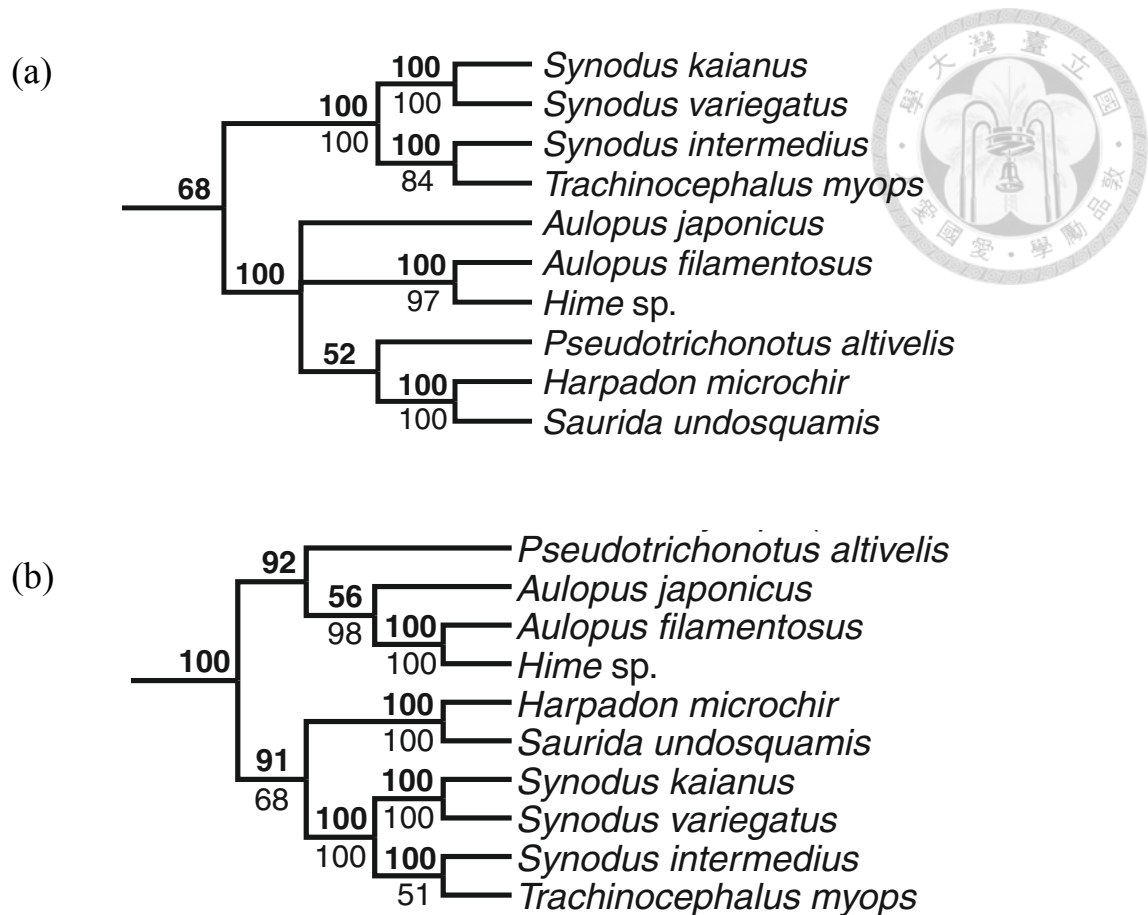


Figure 2. Partial result of relationships of the Aulopiformes proposed by Davis (2010) modified from Fig.6 and 7 of the original paper. Bayesian posterior probabilities denoted by bold numbers above node, with significant support ≥ 95 . Parsimony bootstrap support values denoted by numbers below node, with significant support ≥ 70 . Values below 50 not shown. (a) based on Bayesian and Maximum likelihood analysis of five genes (*RAG1*, *zic1*, *ENC1*, *plagl2*, and *COI*) (b) based on Bayesian and Maximum likelihood analyses of five genes and 138 morphological characters.

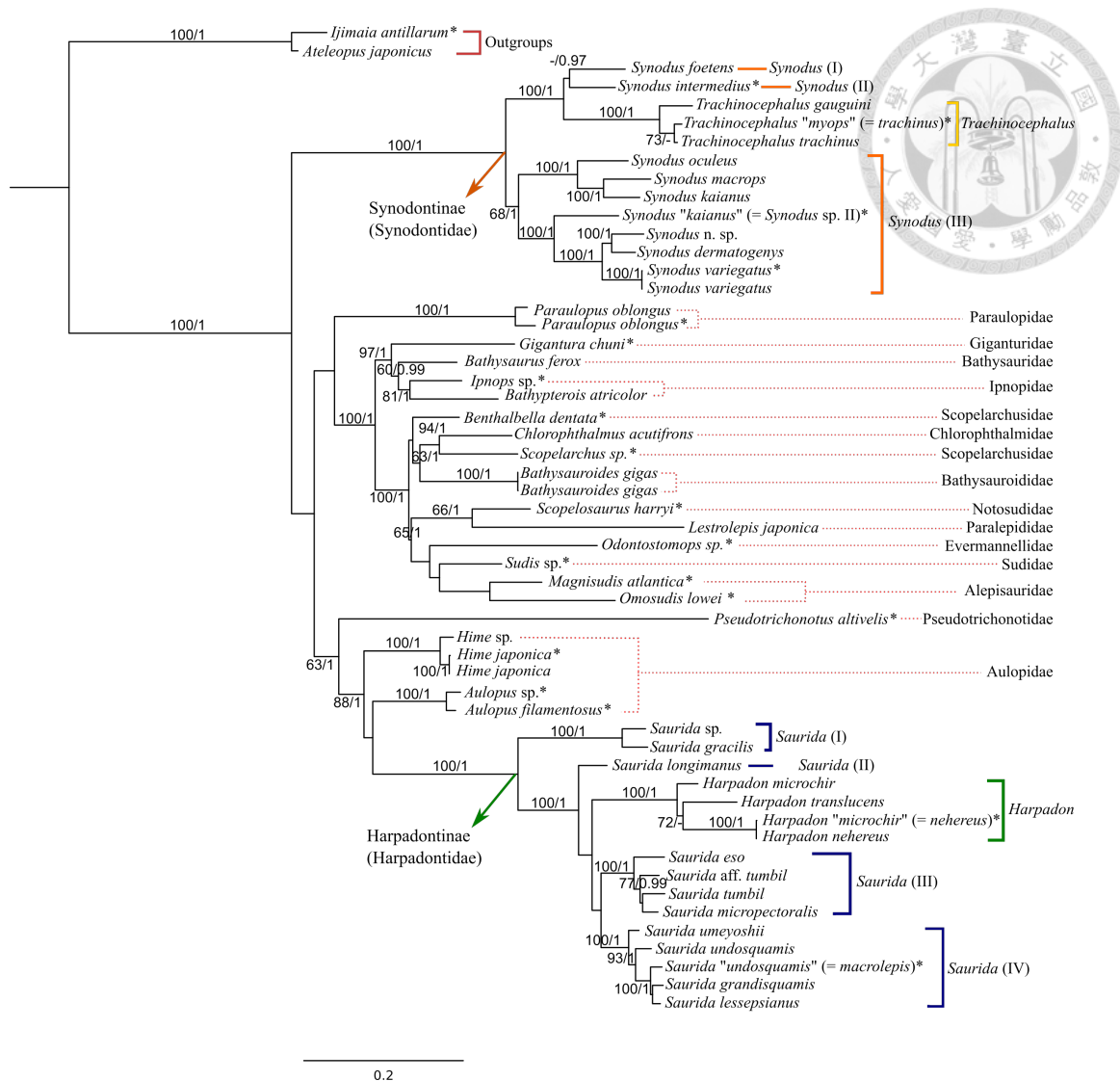


Figure 3. Phylogenetic tree of the synodontids and their aulopiform allies constructed using the maximum-likelihood (ML) and Bayesian approaches. Numbers at nodes are represented as bootstrap values (BP)/bayesian posterior probabilities (PP). Values below 60/0.95 are not shown. Sequences retrieved from previous study (Davis *et al.*, 2010) were labeled with an asterisk behind the species name.

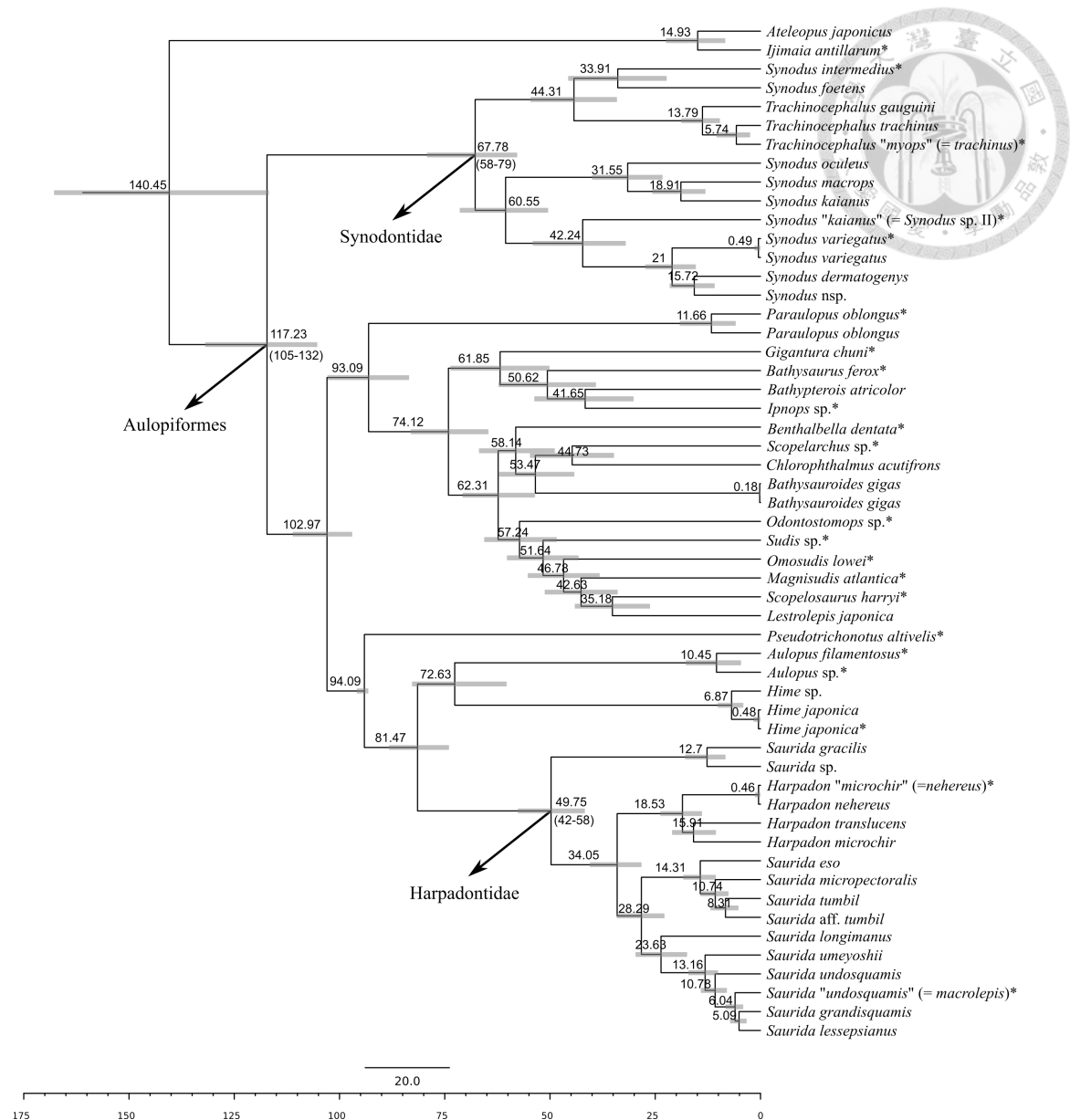


Figure 4. Fossil calibrated time tree of the synodontids and their aulopiform allies. Scale was in millions of years. Numbers at nodes showed the mean clade age, and the bars denote 95%HPD. Sequences retrieved from previous study (Davis *et al.* 2010) were labeled with an asterisk behind.

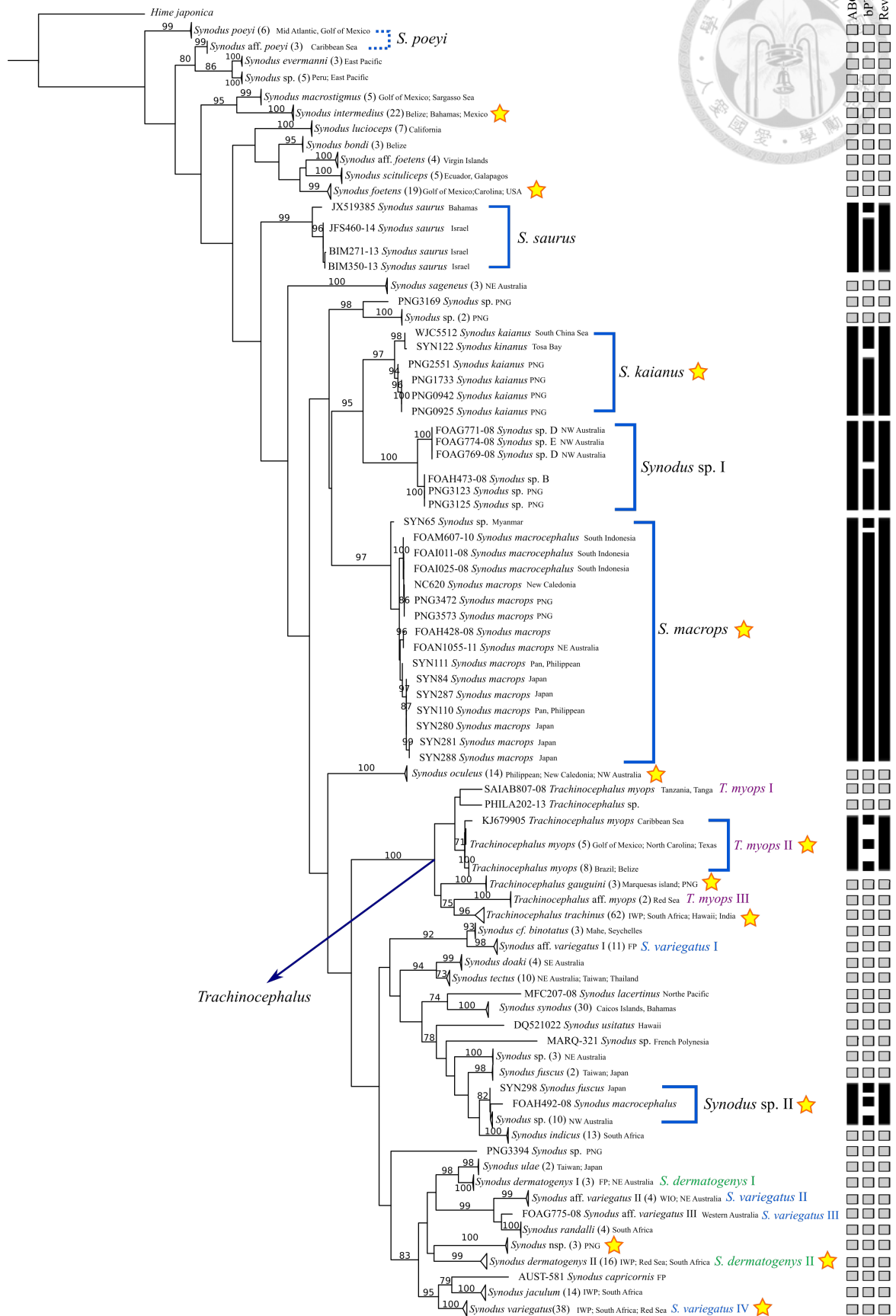


Figure 5. *COI* gene tree of Synodontinae under ML criterion, combined with the results of species delimitation analyses (ABGD, bPTP, and final revision). Numbers at nodes are bootstrap values (BP), with an exclusion of values below 70. Gray bars indicate consistent results with both results while black bars represent the discordant results. The clades containing the taxa used in high-level phylogeny analysis were indicated by asterisk.

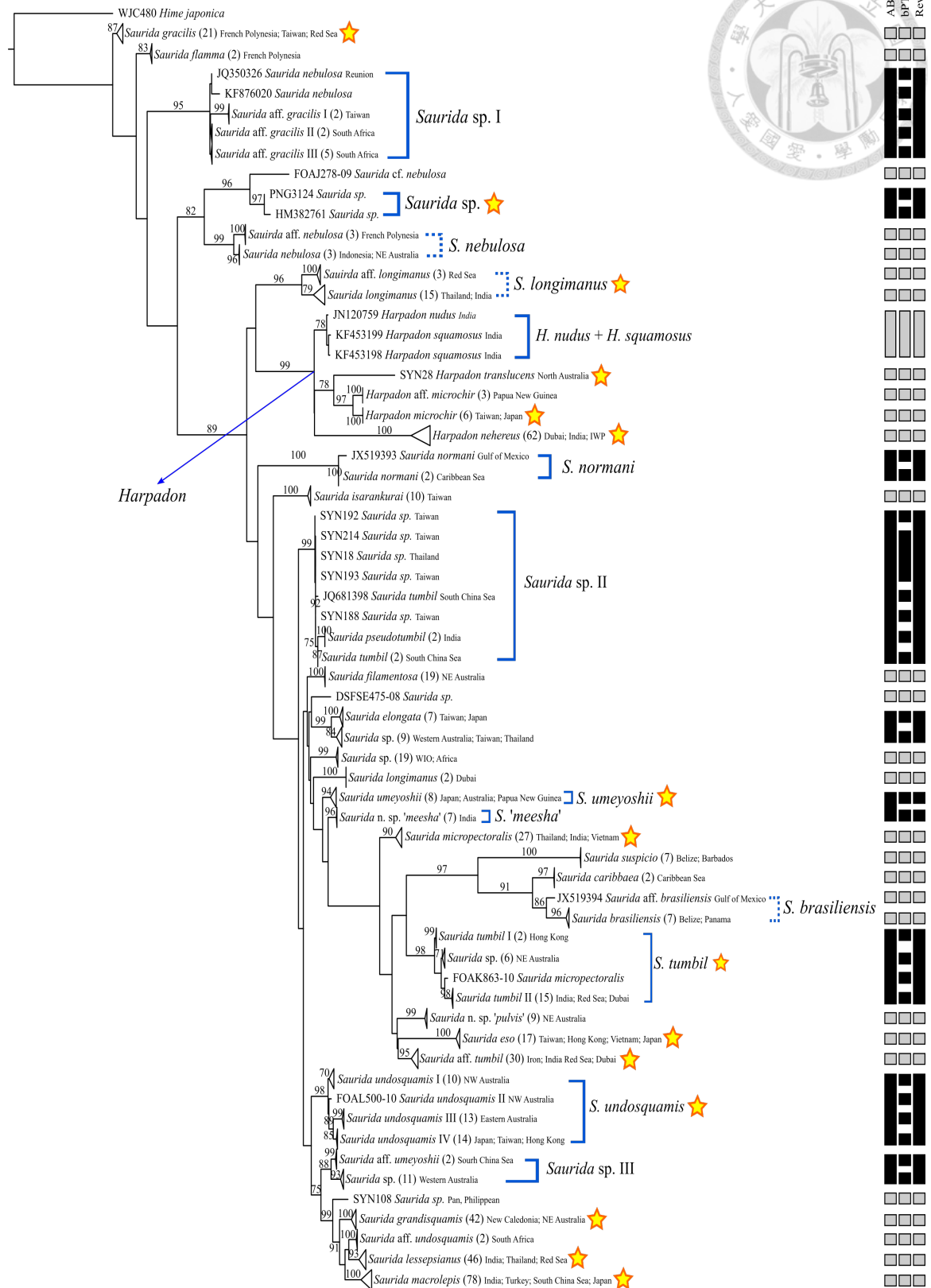
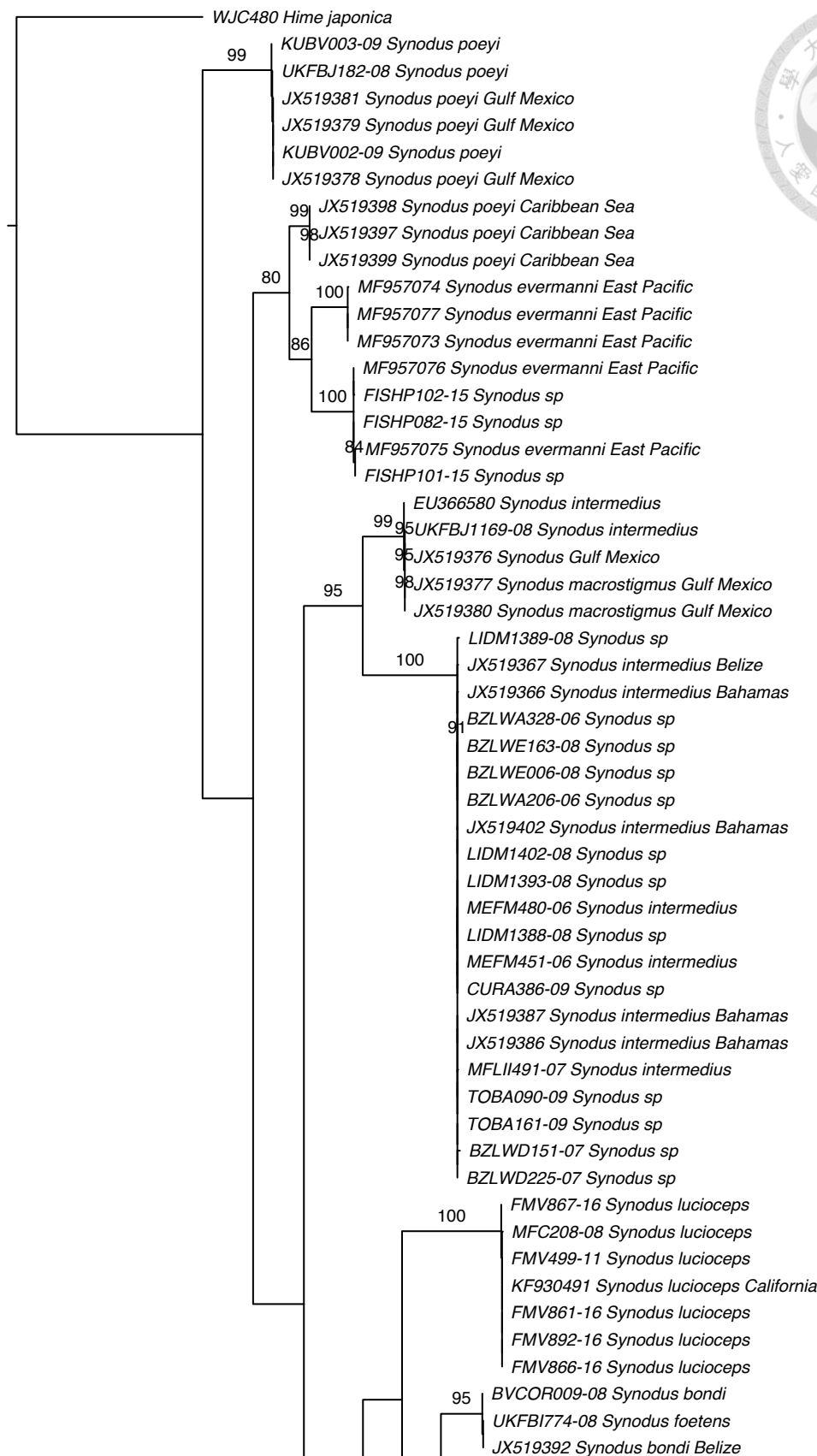
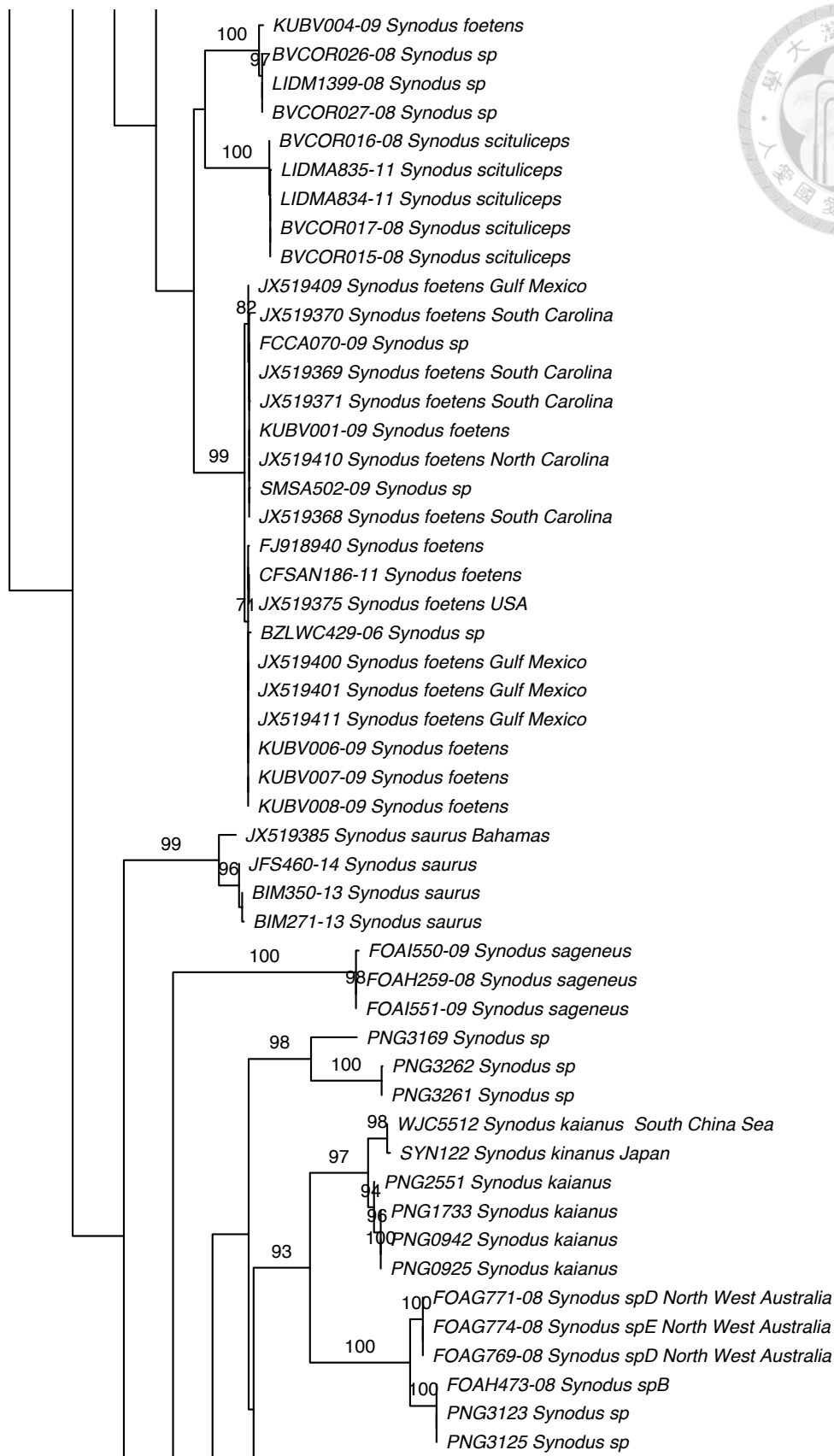


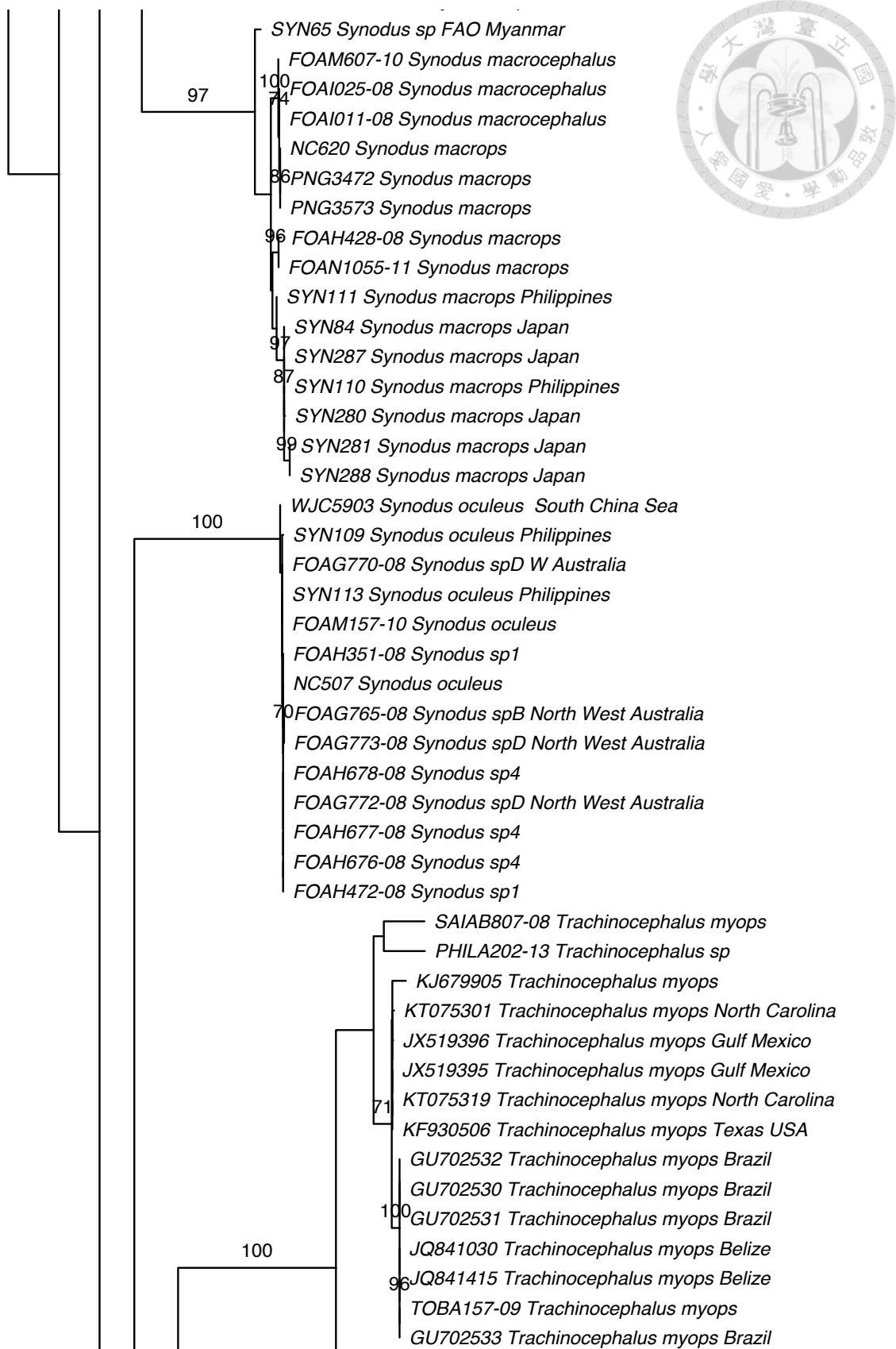
Figure 6. *COI* gene tree of Harpadontinae under ML criterion, combined with the results of species delimitation analyses (ABGD, bPTP, and final revision). Numbers at nodes are bootstrap values (BP), with an exclusion of values below 70. Gray bars indicate consistent results with both results while black bars represent the discordant results. The clade contained the taxa used in high-level phylogeny analysis were indicated by the asterisk.



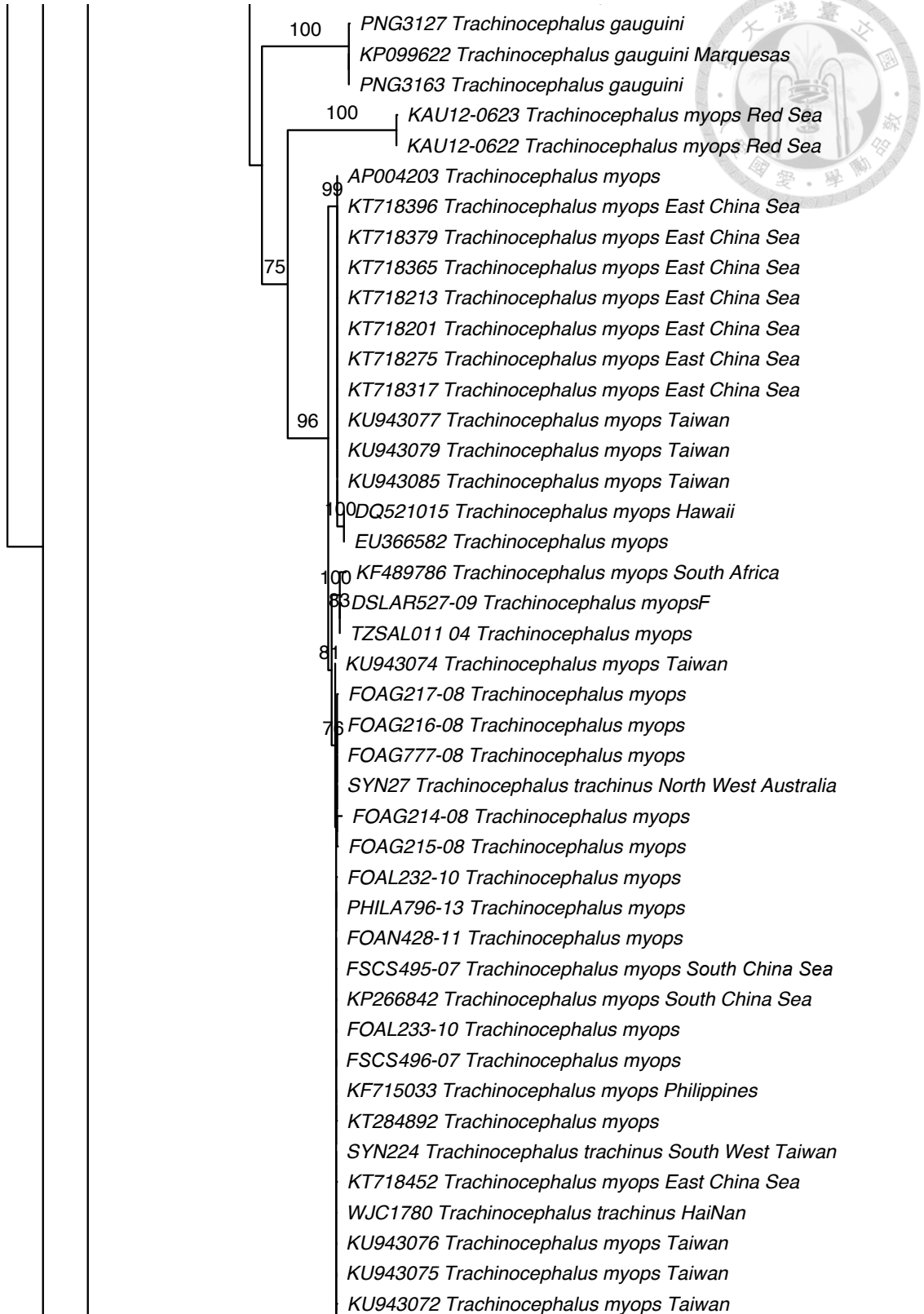
Appendix I. The partial results of *COI* tree of Synodontinae (*Synodus* + *Trachinocephalus*) under the ML criterion. Numbers at nodes are bootstrap values (BP), with an exclusion of values below 70.



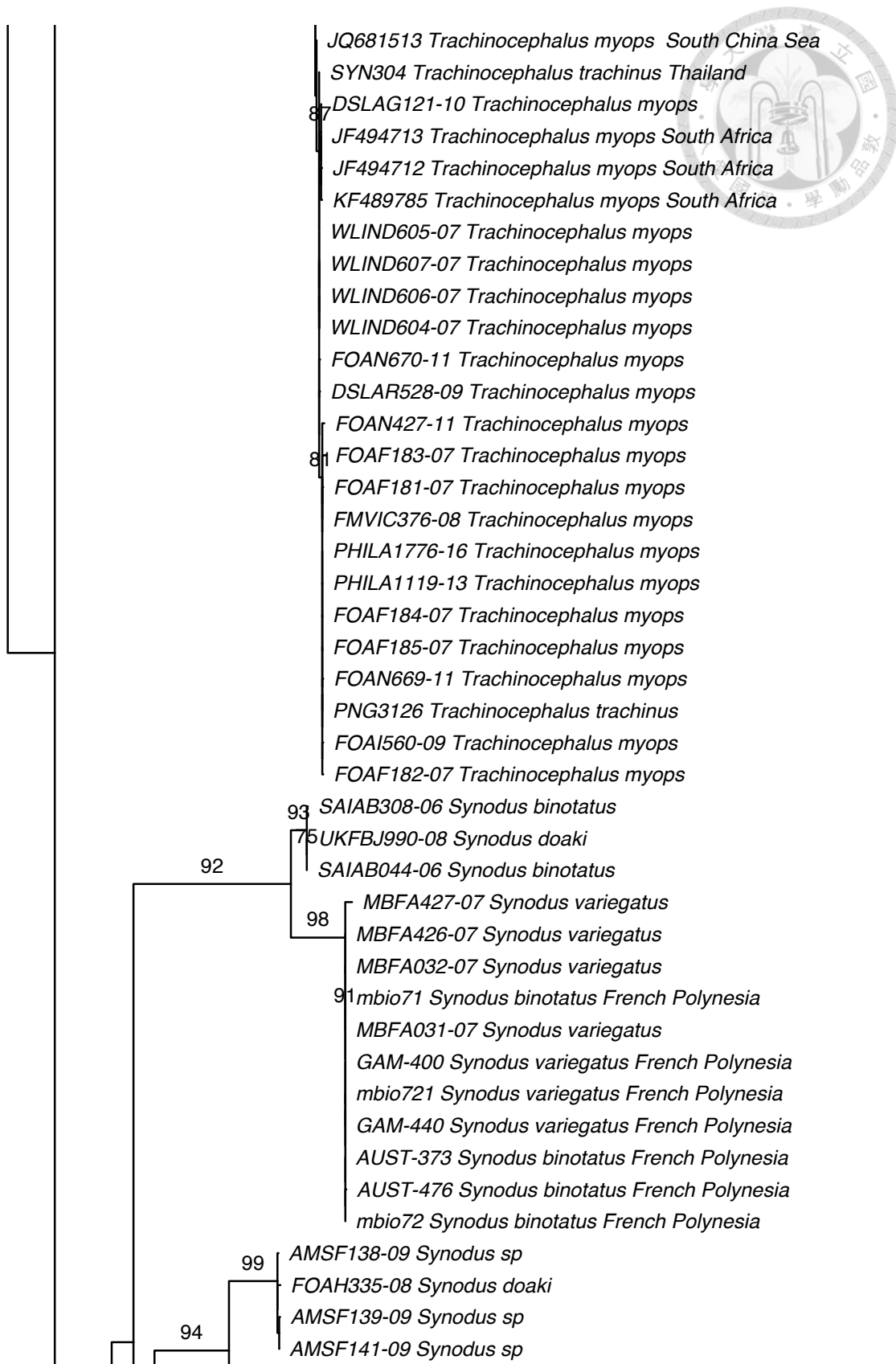
Appendix I. (continued)



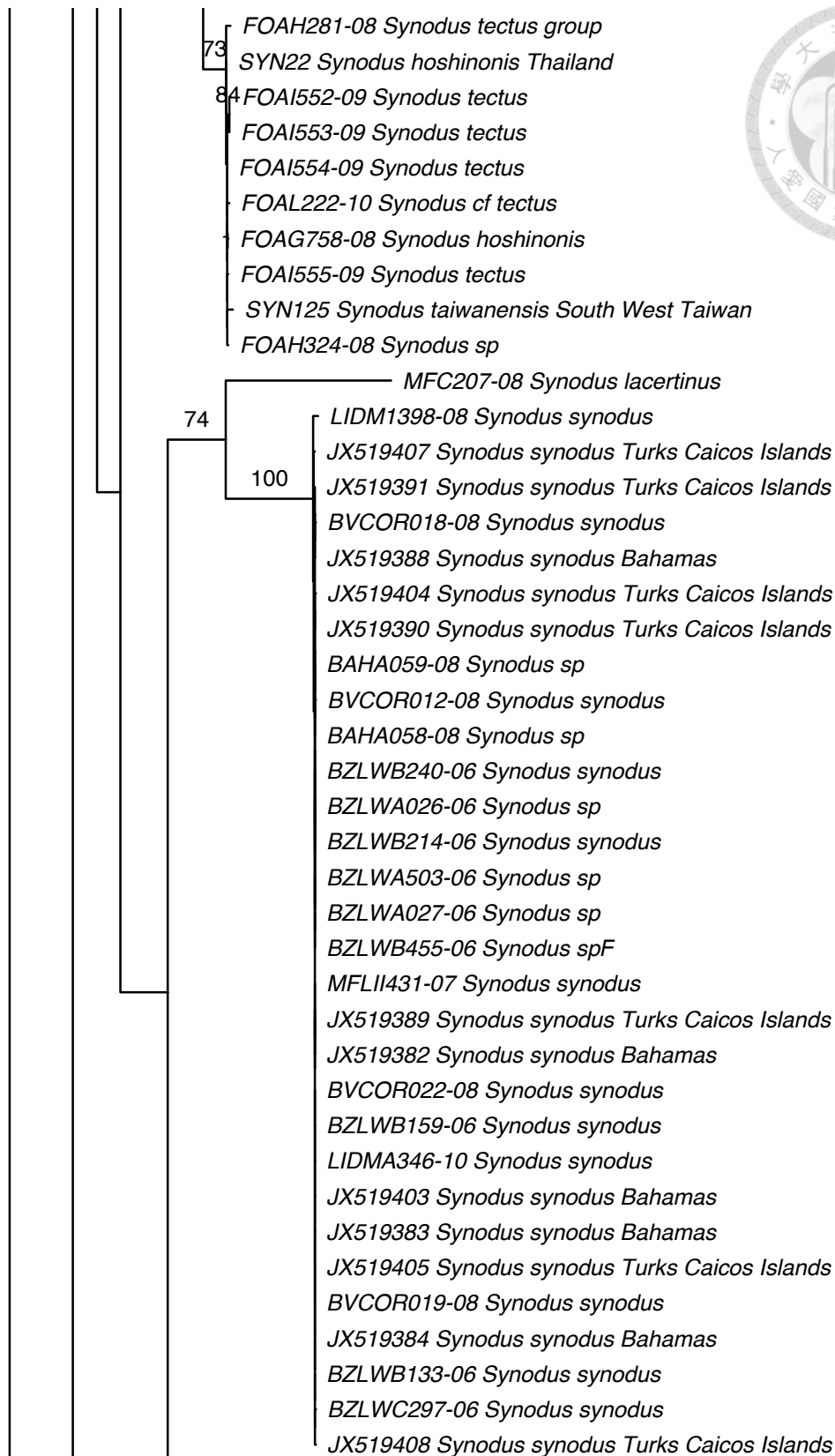
Appendix I. (continued)



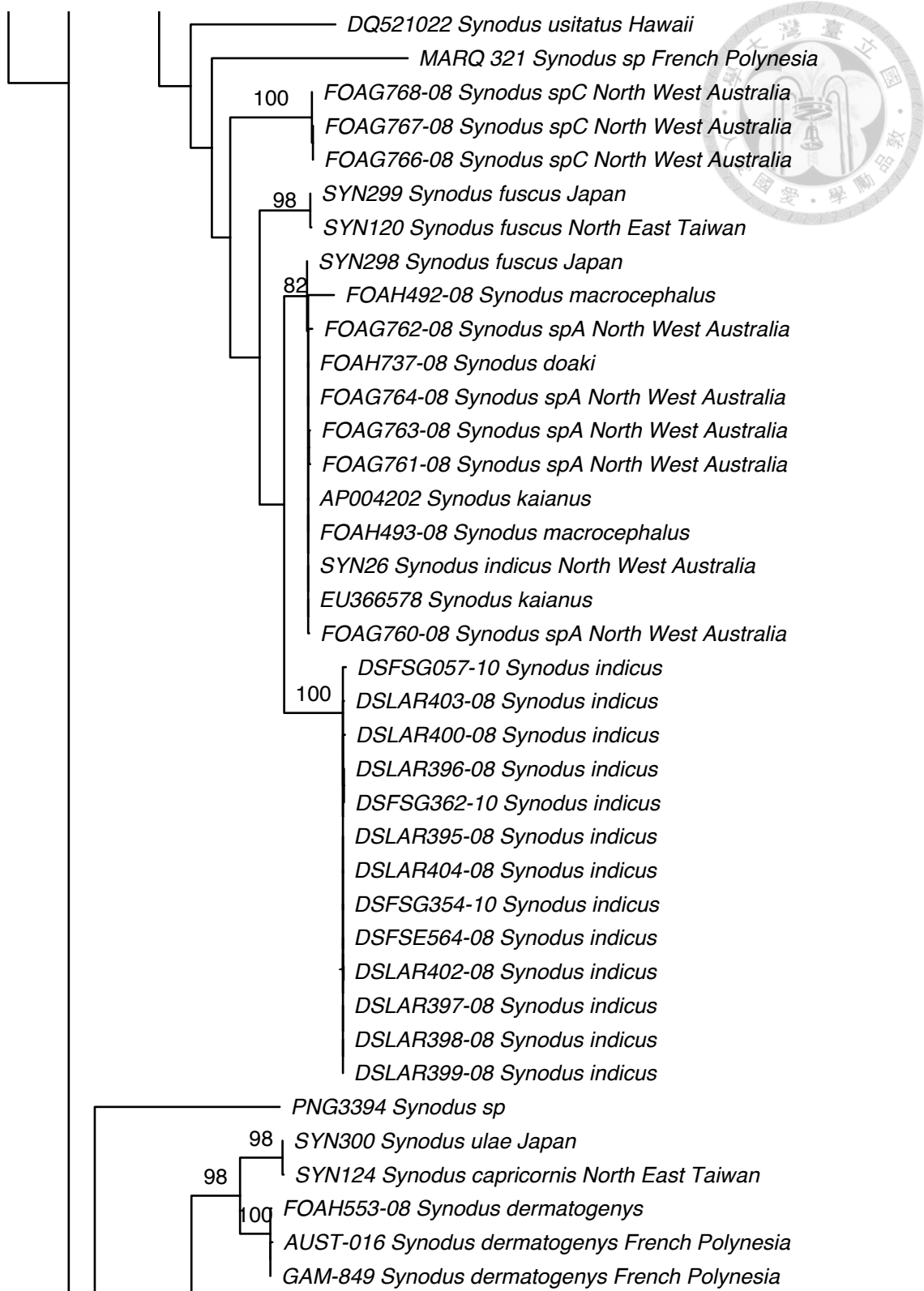
Appendix I. (continued)



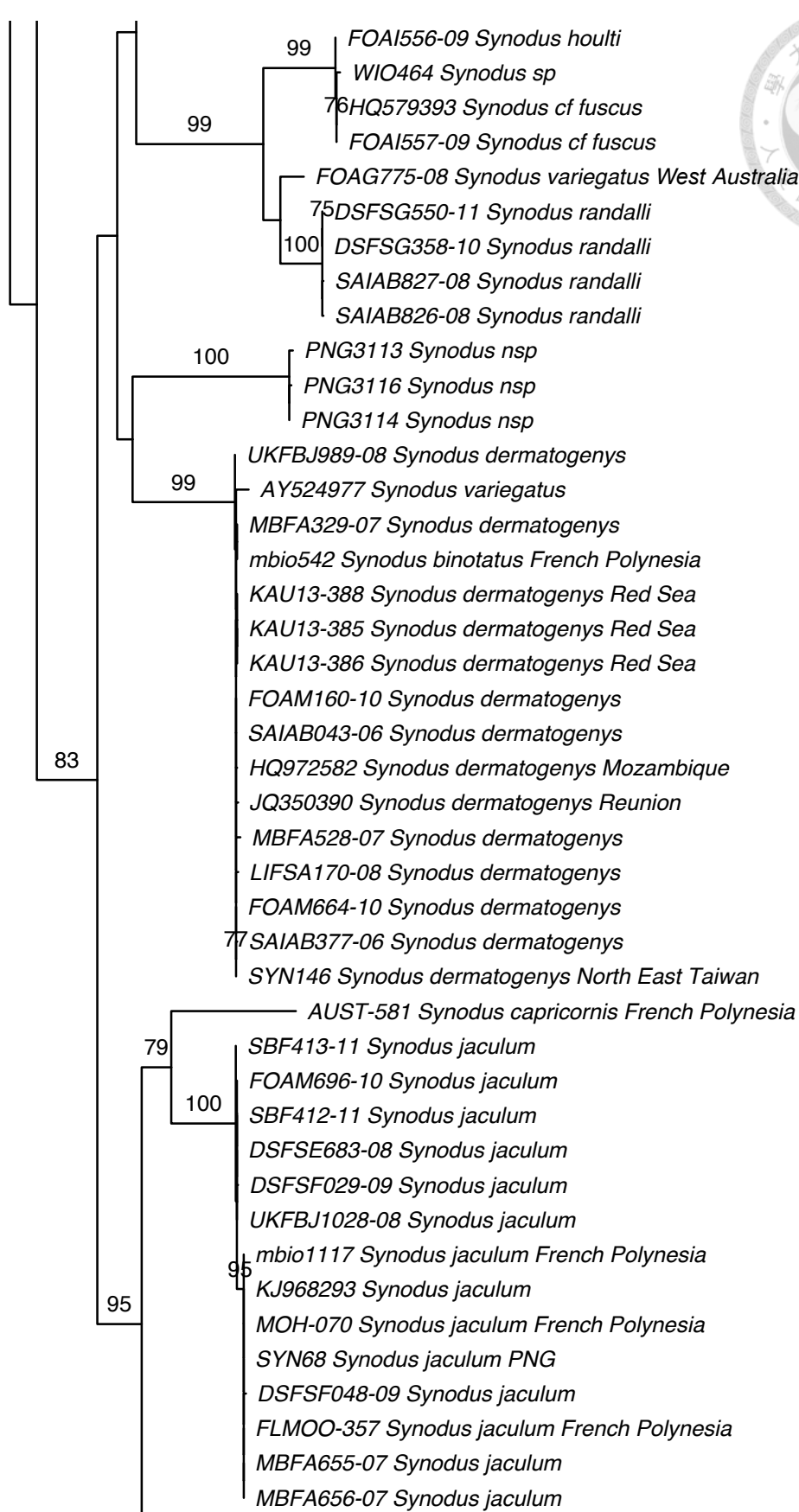
Appendix I. (continued)



Appendix I. (continued)



Appendix I. (continued)



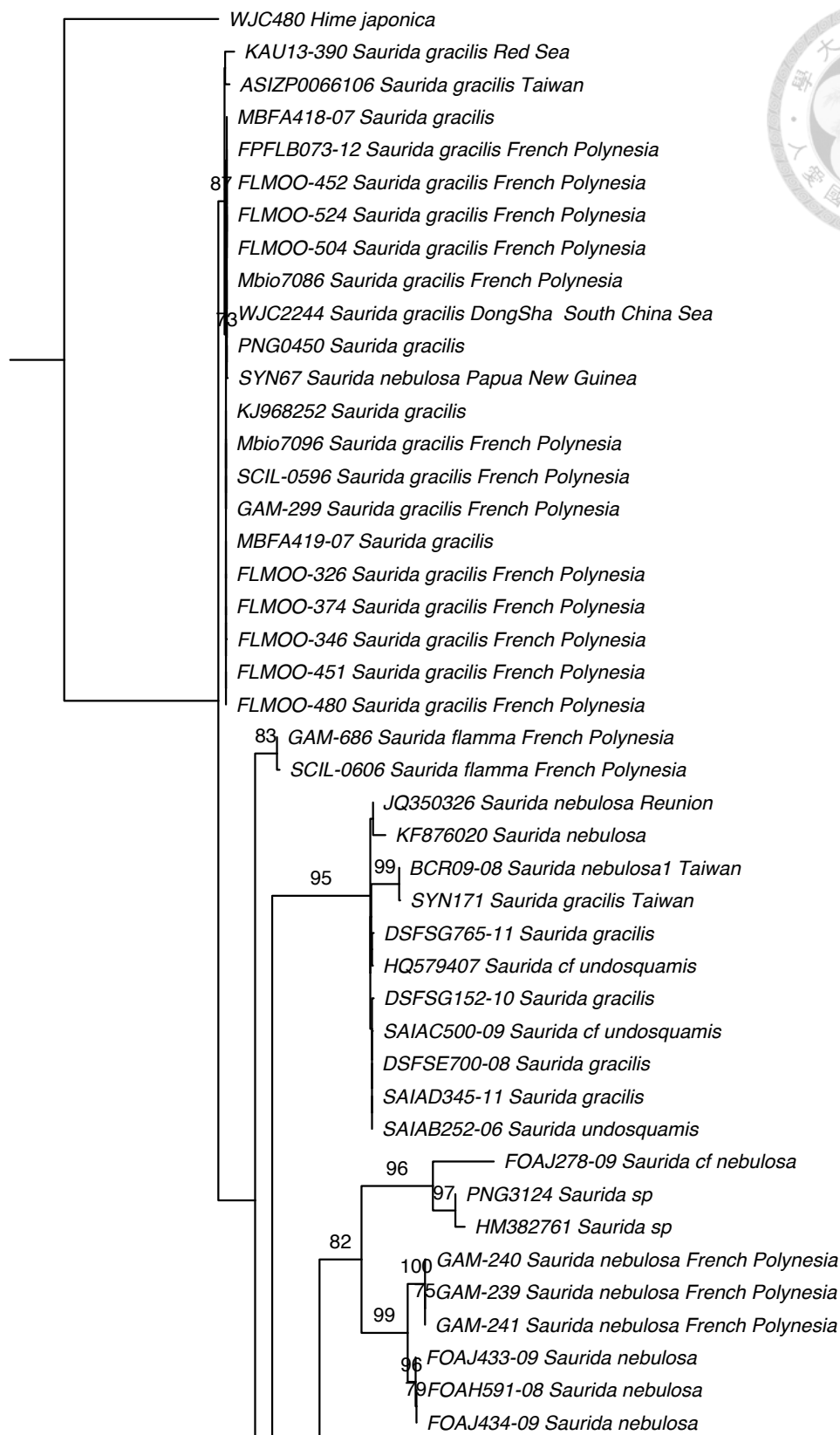
Appendix I. (continued)



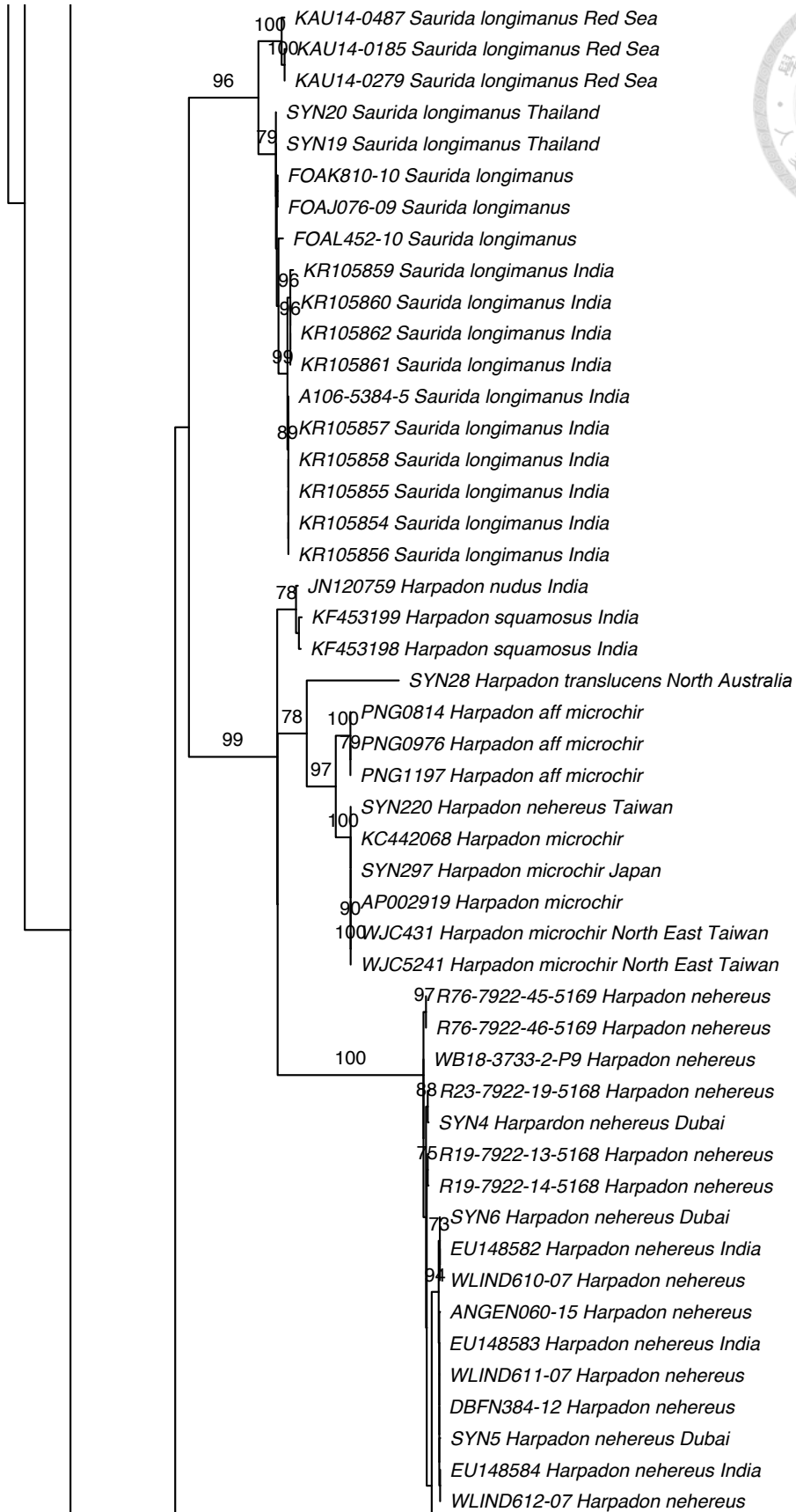
100

SYN129 *Synodus variegatus* Taiwan
 LIFS592-08 *Synodus variegatus*
 91 KAU13-687 *Synodus variegatus* Red Sea
 KAU13-621 *Synodus variegatus* Red Sea
 DSFSE342-08 *Synodus variegatus*
 ASIZP911874 *Synodus variegatus* Taiwan
 SYN133 *Synodus variegatus* Taiwan
 SYN150 *Synodus variagatus* South West Taiwan
 SYN139 *Synodus* sp Taiwan
 SYN128 *Synodus variegatus* South West Taiwan
 UKFBJ943-08 *Synodus variegatus*
 FOAM158-10 *Synodus variegatus*
 LIFS201-08 *Synodus variegatus*
 LIFS202-08 *Synodus variegatus*
 SAIAB173-06 *Synodus variegatus*
 DSFSG096-10 *Synodus variegatus*
 DSFSG080-10 *Synodus variegatus*
 FOAJ644-09 *Synodus variegatus*
 DSFSG717-11 *Synodus variegatus*
 SAIAB423-06 *Synodus variegatus*
 LIFS247-08 *Synodus variegatus*
 LIFS311-08 *Synodus variegatus*
 FOAJ873-09 *Synodus variegatus*
 SBF058-11 *Synodus binotatus*
 SBF410-11 *Synodus binotatus*
 SBF280-11 *Synodus binotatus*
 SBF279-11 *Synodus binotatus*
 SBF411-11 *Synodus binotatus*
 SBF281-11 *Synodus binotatus*
 SBF182-11 *Synodus binotatus*
 AUST-036 *Synodus variegatus* French Polynesia
 GAM-348 *Synodus variegatus* French Polynesia
 PNG0451 *Synodus variegatus*
 EU366579 *Synodus variegatus*
 SYN47 *Synodus variagatus* Myanmar
 82 SCIL-061 *Synodus variegatus* French Polynesia
 MARQ-126 *Synodus variegatus* French Polynesia
 AUST-146 *Synodus variegatus* French Polynesia

Appendix I. (continued)



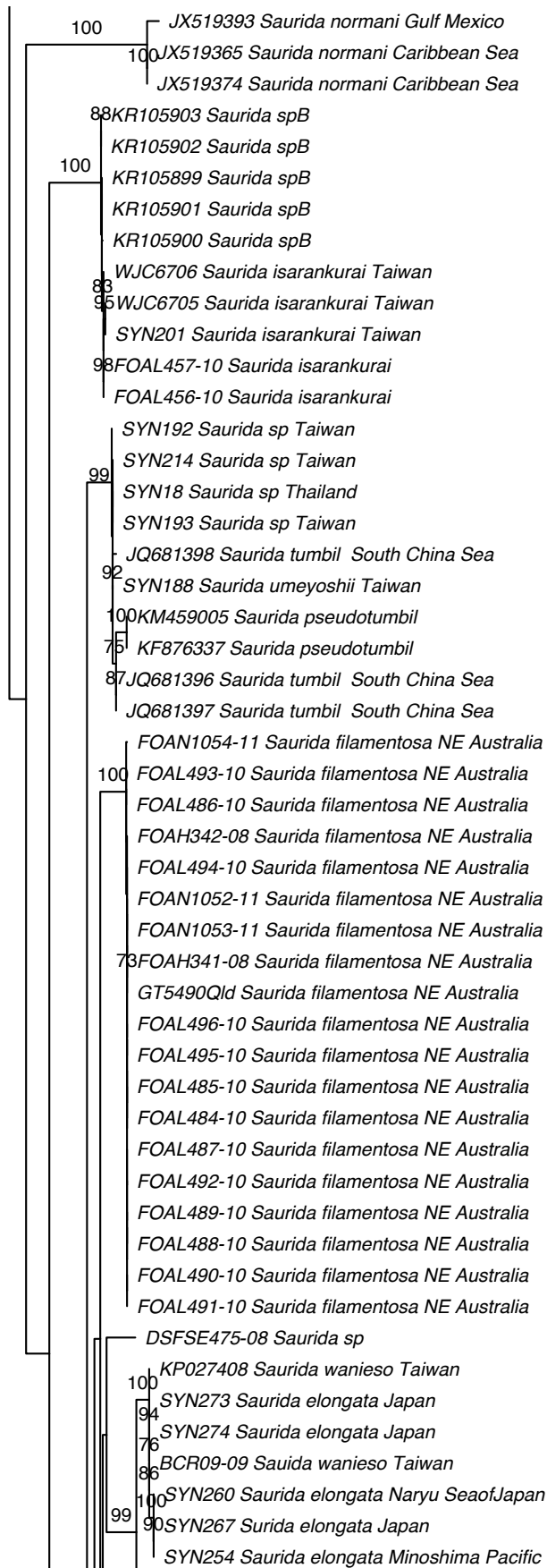
Appendix II. The partial results of *COI* tree of Harpadontinae (*Saurida* + *Harpadon*) under the ML criterion. Numbers at nodes are bootstrap values (BP), with an exclusion of values below 70.



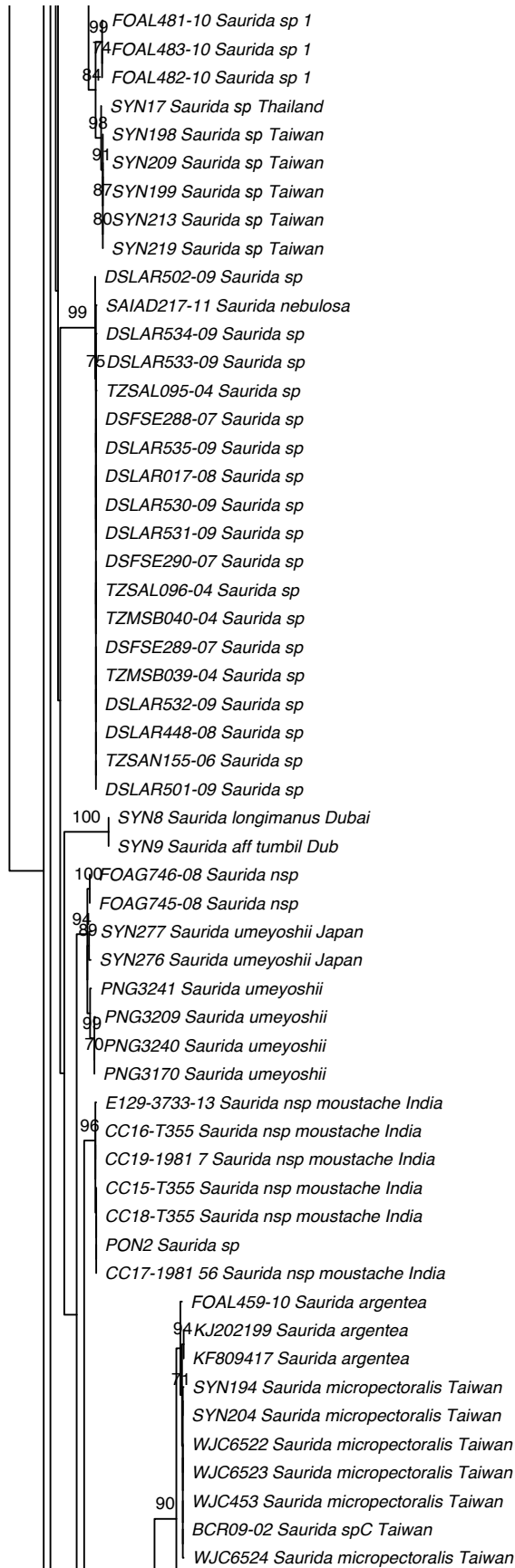
Appendix II. (continued)

FOAH871-08 *Harpadon nehereus*
 84 FOAH872-08 *Harpadon nehereus*
 96 FOAH873-08 *Harpadon nehereus*
 92 SYN3 *Harpadon nehereus* Singapore
 76 SYN1 *Harpadon nehereus* Singapore
 SYN2 *Harpadon nehereus* Singapore
 SYN176 *Harpadon nehereus* West Taiwan
 EU366558 *Harpadon microchir*
 WJC1084 *Harpadon nehereus* Kin Men Island
 WJC1085 *Harpadon nehereus* Kin Men Island
 JQ738574 *Harpadon nehereus* Yellow Sea
 JQ738573 *Harpadon nehereus* Yellow Sea
 FOAD185-05 *Harpadon nehereus*
 FOAD189-05 *Harpadon nehereus*
 FOAD186-05 *Harpadon nehereus*
 JN242637 *Harpadon nehereus* South China Sea
 FSCS949-11 *Harpadon nehereus*
 JN242638 *Harpadon nehereus* South China Sea
 JN242633 *Harpadon nehereus* South China Sea
 JN242640 *Harpadon nehereus* South China Sea
 FSCS946-11 *Harpadon nehereus*
 JN242631 *Harpadon nehereus* South China Sea
 FSCS952-11 *Harpadon nehereus*
 FSCS948-11 *Harpadon nehereus*
 JN242634 *Harpadon nehereus* South China Sea
 FSCS945-11 *Harpadon nehereus*
 FSCS955-11 *Harpadon nehereus*
 FSCS953-11 *Harpadon nehereus*
 JN242635 *Harpadon nehereus* South China Sea
 JN242630 *Harpadon nehereus* South China Sea
 JN242636 *Harpadon nehereus* South China Sea
 FSCS950-11 *Harpadon nehereus*
 JN242632 *Harpadon nehereus* South China Sea
 JN242639 *Harpadon nehereus* South China Sea
 FSCS947-11 *Harpadon nehereus*
 FSCS951-11 *Harpadon nehereus*
 FSCS954-11 *Harpadon nehereus*
 FSCS307-06 *Harpadon nehereus*
 EF607398 *Harpadon nehereus* China
 KP260457 *Harpadon nehereus*
 JX534239 *Harpadon nehereus*
 FOAD188-05 *Harpadon nehereus*
 FOAD187-05 *Harpadon nehereus*
 KP112247 *Harpadon nehereus*
 SYN248 *Harpadon nehereus* Vietnam

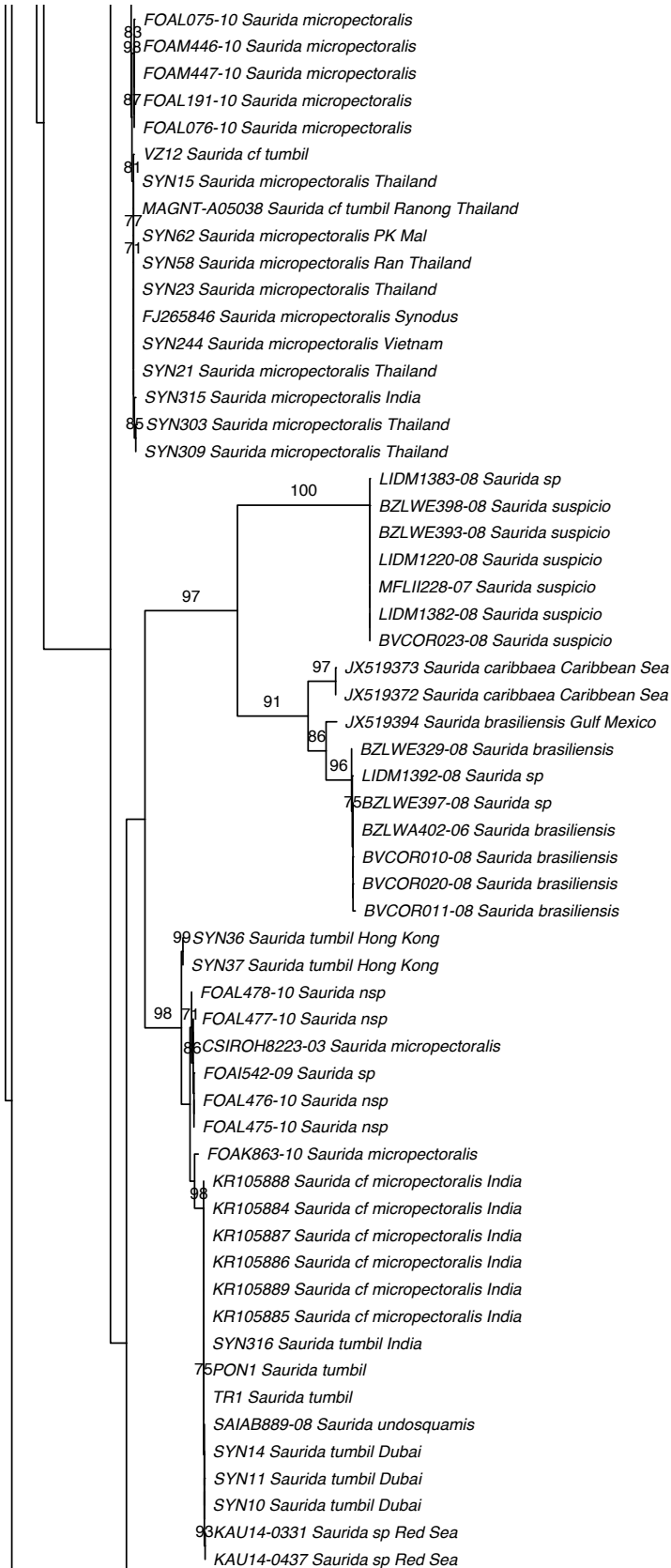




Appendix II. (continued)



Appendix II. (continued)



Appendix II. (continued)



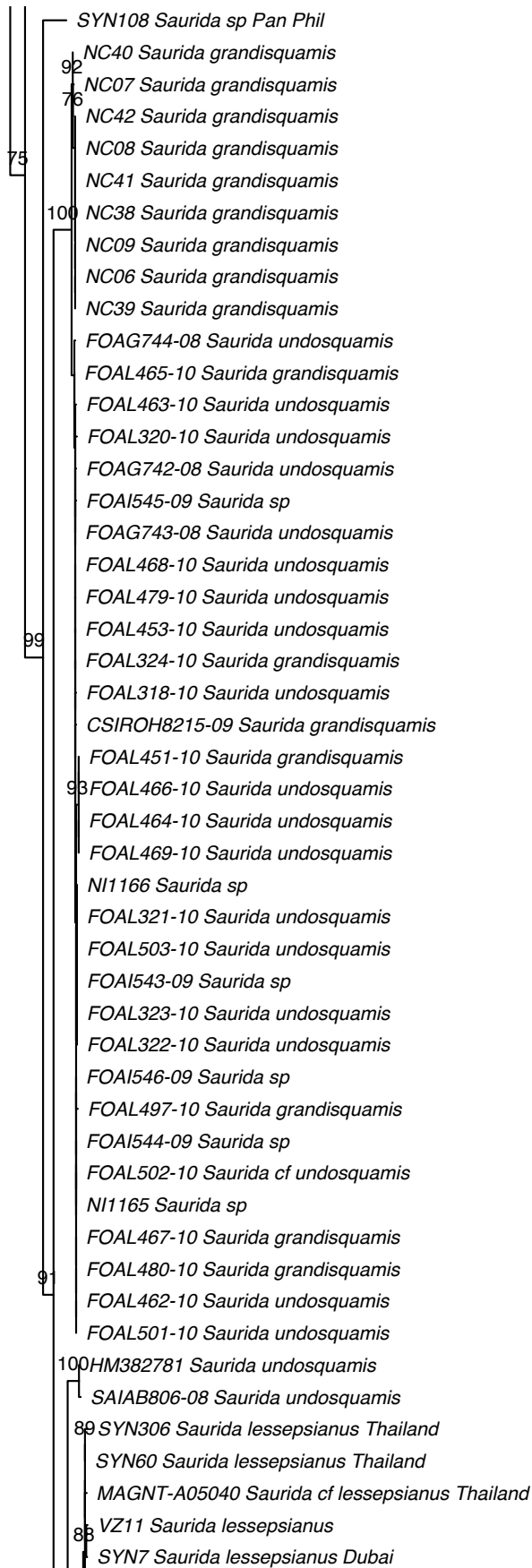
99	FOAL461-10 <i>Saurida nsp</i>
	FOAL474-10 <i>Saurida nsp</i>
	BR <i>Saurida micropectoralis</i>
	FOAH304-08 <i>Saurida sp</i>
	FOAL473-10 <i>Saurida nsp</i>
94	FOAL470-10 <i>Saurida nsp</i>
	FOAL460-10 <i>Saurida nsp</i>
	FOAL472-10 <i>Saurida nsp</i>
	FOAL471-10 <i>Saurida nsp</i> Australia
	KJ194275 <i>Saurida microlepis</i>
100	FSCS356-07 <i>Saurida elongata</i>
84	FSCS100-06 <i>Saurida elongata</i>
	FSCS357-07 <i>Saurida elongata</i>
79	KP260467 <i>Saurida elongata</i>
	FSCS358-07 <i>Saurida elongata</i>
	WJC1693 <i>Saurida eso</i> Vietnam
	EU595270 <i>Saurida elongata</i>
	FSCS766 08 <i>Saurida elongata</i>
	WJC6525 <i>Saurida eso</i> Taiwan
	SYN243 <i>Saurida eso</i> Vietnam
	SYN227 <i>Saurida eso</i> MT Taiwan
	SYN45 <i>Saurida eso</i> Hong Kong
	SYN259 <i>Saurida eso</i> Minoshima Pacific
	SYN86 <i>Saurida eso</i> Miyazaki Japan
	KM036504 <i>Saurida microlepis</i>
	SYN258 <i>Saurida eso</i> Hilizaki Pacific
	KR105892 <i>Saurida tumbil</i> India
	EF609603 <i>Saurida tumbil</i>
95	EF609599 <i>Saurida tumbil</i> India
	SYN12 <i>Saurida aff tumbil</i> Dubai
74	KJ713184 <i>Saurida tumbil</i>
	KAU14-0288 <i>Saurida tumbil</i> Red Sea
	KM459006 <i>Saurida tumbil</i>
	WLIND617-07 <i>Saurida tumbil</i>
	WLIND615-07 <i>Saurida tumbil</i>
	WLIND616-07 <i>Saurida tumbil</i>
	NNPF033-10 <i>Saurida tumbil</i>
	NNPF057-10 <i>Saurida tumbil</i>
	NNPF140-10 <i>Saurida tumbil</i>
	NNPF075-10 <i>Saurida tumbil</i>
	ANGEN149-15 <i>Saurida tumbil</i>
	KAU14-0410 <i>Saurida tumbil</i> Red Sea
	SYN13 <i>Saurida aff tumbil</i> Dubai
	KR105896 <i>Saurida tumbil</i> India
	KR105897 <i>Saurida tumbil</i> India
	KR105894 <i>Saurida tumbil</i> India
	KAU14-0312 <i>Saurida tumbil</i> Red Sea
	KAU14-0289 <i>Saurida tumbil</i> Red Sea
	KAU14-0409 <i>Saurida tumbil</i> Red Sea
	KAU14-0496 <i>Saurida tumbil</i> Red Sea
	KV25 <i>Saurida tumbil</i>
	KV22 <i>Saurida tumbil</i>
	KV16 <i>Saurida tumbil</i>

Appendix II. (continued)



	FOAG752-08 <i>Saurida undosquamis</i> North West Australia
70	FOAG757-08 <i>Saurida undosquamis</i> North West Australia
	FOAL499-10 <i>Saurida undosquamis</i> North West Australia
	FOAG754-08 <i>Saurida undosquamis</i> North West Australia
	FOAL317-10 <i>Saurida cf undosquamis</i> North West Australia
	SYN25 <i>Saurida undosquamis</i> North West Australia
	FOAG755-08 <i>Saurida undosquamis</i> North West Australia
	FOAG756-08 <i>Saurida undosquamis</i> North West Australia
98	FOAG751-08 <i>Saurida undosquamis</i> North West Australia
	FOAG753-08 <i>Saurida undosquamis</i> North West Australia
	FOAL500-10 <i>Saurida undosquamis</i> North West Australia
	FOAI547-09 <i>Saurida</i> sp
99	FOAMP106-06 <i>Saurida undosquamis</i> East Australia
	FOAMP109-06 <i>Saurida undosquamis</i> East Australia
	FOAMP105-06 <i>Saurida undosquamis</i> East Australia
	FOAMP108-06 <i>Saurida undosquamis</i> East Australia
	FOAH303-08 <i>Saurida</i> East Australia
	FOAL455-10 <i>Saurida undosquamis</i> East Australia
	FOAL504-10 <i>Saurida undosquamis</i> East Australia
89	FOAL498-10 <i>Saurida undosquamis</i> East Australia
	FOAL454-10 <i>Saurida undosquamis</i> East Australia
	FOAL315-10 <i>Saurida undosquamis</i> East Australia
	FOAL458-10 <i>Saurida undosquamis</i> East Australia
	FOAL319-10 <i>Saurida undosquamis</i> East Australia
	SYN279 <i>Saurida undosquamis</i> Japan
	ASIZP0076118 <i>Saurida undosquamis</i> Taiwan
85	ASIZP0076119 <i>Saurida undosquamis</i> Taiwan
	BCR09-05 <i>Saurida undosquamis</i> Taiwan
	SYN97 <i>Saurida undosquamis</i> Kago Japan
95	SYN278 <i>Saurida undosquamis</i> Japan
	SYN286 <i>Saurida undosquamis</i> Japan
	SYN81 <i>Saurida undosquamis</i> Miya Japan
92	SYN210 <i>Saurida undosquamis</i> Taiwan
	SYN216 <i>Saurida undosquamis</i> Taiwan
92	SYN35 <i>Saurida undosquamis</i> Hong Kong
	SYN33 <i>Saurida undosquamis</i> Hong Kong
	SYN34 <i>Saurida undosquamis</i> Hong Kong
	SYN46 <i>Saurida undosquamis</i> Hong Kong
99	WJC5757 <i>Saurida umeyoshii</i> South China Sea
	KM189365 <i>Saurida umeyoshii</i>
88	FOAG748-08 <i>Saurida cf micropectoralis</i>
	FOAG750-08 <i>Saurida cf micropectoralis</i>
	FOAG749-08 <i>Saurida cf micropectoralis</i>
93	FOAMP096-06 <i>Saurida undosquamis</i>
82	FOAMP097-06 <i>Saurida undosquamis</i>
72	FOAMP098-06 <i>Saurida undosquamis</i>
	FOAMP094-06 <i>Saurida cf micropectoralis</i>
	FOAMP095-06 <i>Saurida grandisquamis</i> type B
	FOAG747-08 <i>Saurida cf micropectoralis</i>
	FOAN132-11 <i>Saurida undosquamis</i>
	FOAN133-11 <i>Saurida undosquamis</i>

Appendix II. (continued)



Appendix II. (continued)



CC11 T355 *Saurida lessepsianus* India
CC9 T355 *Saurida lessepsianus* India
CC10 T355 *Saurida lessepsianus* India
CC14 *Saurida lessepsianus* India
- E133-3733-9 *Saurida lessepsianus* India
PC17-T355 *Saurida lessepsianus* India
CC12-T355 *Saurida lessepsianus* India
CC13-T355 *Saurida lessepsianus* India
93 D175-198129 *Saurida lessepsianus* India
K75 *Saurida lessepsianus* India
PC18A-1981-30 *Saurida lessepsianus* India
PC18-1981-32 *Saurida lessepsianus* India
D174-1981-28 *Saurida lessepsianus* India
73 K66 *Saurida undosquamis*
VN7 *Saurida undosquamis*
KAU14-0285 *Saurida lessepsianus* Red Sea
76 KAU14-0386 *Saurida lessepsianus* Red Sea
KAU14-0576 *Saurida lessepsianus* Red Sea
KAU14-0284 *Saurida lessepsianus* Red Sea
JFS273-14 *Saurida undosquamis*
BIM177-13 *Saurida macrolepis*
JFS274-14 *Saurida undosquamis*
JFS383-14 *Saurida undosquamis*
BIM178-13 *Saurida macrolepis*
BIM176-13 *Saurida macrolepis*
BIM367-13 *Saurida macrolepis*
KF564314 *Saurida macrolepis*
BIM313-13 *Saurida macrolepis*
80 KAU14-0434 *Saurida lessepsianus* Red Sea
KAU14-0332 *Saurida lessepsianus* Red Sea
JFS381-14 *Saurida undosquamis*
JFS380-14 *Saurida undosquamis*
JFS384-14 *Saurida undosquamis*
JFS277-14 *Saurida undosquamis*
JFS071-09 *Saurida undosquamis*
JFS382-14 *Saurida undosquamis*
JFS379-14 *Saurida undosquamis*
JFS275-14 *Saurida undosquamis*
JFS072-09 *Saurida undosquamis*
JFS278-14 *Saurida undosquamis*
JFS276-14 *Saurida undosquamis*

Appendix II. (continued)



88	FJ347931 <i>Saurida undosquamis</i> India
	KF876019 <i>Saurida undosquamis</i>
89	FJ347930 <i>Saurida undosquamis</i> India
	FJ347932 <i>Saurida undosquamis</i> India
	DNATR1319-13 <i>Saurida undosquamis</i>
100	DNATR1318-13 <i>Saurida undosquamis</i>
	DNATR1317-13 <i>Saurida undosquamis</i>
	DNATR079-12 <i>Saurida undosquamis</i>
	DNATR1301-13 <i>Saurida undosquamis</i>
	DNATR1303-13 <i>Saurida undosquamis</i>
	DNATR1309-13 <i>Saurida undosquamis</i>
82	DNATR1305-13 <i>Saurida undosquamis</i>
	DNATR1307-13 <i>Saurida undosquamis</i>
	DNATR1308-13 <i>Saurida undosquamis</i>
	DNATR1302-13 <i>Saurida undosquamis</i>
	DNATR1306-13 <i>Saurida undosquamis</i>
	DNATR1300-13 <i>Saurida undosquamis</i>
	DNATR1304-13 <i>Saurida undosquamis</i>
	DNATR1310-13 <i>Saurida undosquamis</i>
92	DNATR1311-13 <i>Saurida undosquamis</i>
	DNATR1312-13 <i>Saurida undosquamis</i>
	DNATR1315-13 <i>Saurida undosquamis</i>
	DNATR1316-13 <i>Saurida undosquamis</i>
	DNATR1314-13 <i>Saurida undosquamis</i>
	DNATR1313-13 <i>Saurida undosquamis</i>
	AP002920 <i>Saurida undosquamis</i>
	SYN92 <i>Saurida macrolepis</i> Miya Japan
	ABFJ234-07 <i>Saurida elongata</i>
	KJ511779 <i>Saurida undosquamis</i>
	ABFJ236-07 <i>Saurida elongata</i>
	ABFJ235-07 <i>Saurida elongata</i>
	ASIZP0076110 <i>Saurida macrolepis</i> Taiwan
	EU366571 <i>Saurida undosquamis</i>
	WJC1692 <i>Saurida macrolepis</i> Vietnam
	KP260474 <i>Saurida macrolepis</i>
	FOAL234-10 <i>Saurida</i> sp
	FOAI026-08 <i>Saurida macrolepis</i>
	FOAL235-10 <i>Saurida</i> sp

Appendix II. (continued)



FOAL235-10 *Saurida* sp
ASIZP0065948 *Saurida wanieso* Taiwan
JQ681486 *Saurida elongata* South China Sea
WJC4399 *Saurida macrolepis* North East Taiwan
JQ681517 *Saurida elongata* South China Sea
70 ASIZP0076109 *Saurida macrolepis* Taiwan
ASIZP0076111 *Saurida macrolepis* Taiwan
WJC1781 *Saurida macrolepis* Hain Nan
WJC1691 *Saurida macrolepis* Vietnam
SYN105 *Saurida macrolepis* Kago Japan
SYN106 *Saurida macrolepis* Mut Oma
SYN16 *Saurida macrolepis* Thailand
SYN87 *Saurida macrolepis* Miyazaki Japan
SYN38 *Saurida macrolepis* Hong Kong
SYN90 *Saurida macrolepis* Miyazaki Japan
ASIZP900251 *Saurida cf macrolepis* Taiwan
SYN103 *Saurida macrolepis* Kago Japan
SYN98 *Saurida macrolepis* Kago Japan
SYN95 *Saurida macrolepis* Kago Japan
SYN269 *Saurida macrolepis* Japan
SYN301 *Saurida macrolepis* Thailand
71 ASIZP0065965 *Saurida wanieso* Taiwan
BCR09-09 *Saurida* spB Taiwan
MUFS32564 *Saurida* sp2 Japan
SYN293 *Saurida macrolepis* Japan
MUFS25074 *Saurida* sp2 Japan
SYN93 *Saurida macrolepis* Japan
SYN294 *Saurida macrolepis* Japan
SYN100 *Saurida macrolepis* Japan
SYN39 *Saurida macrolepis* Hong Kong
SYN83 *Saurida macrolepis* Miyazaki Japan
SYN101 *Saurida macrolepis* Japan
SYN99 *Saurida macrolepis* Japan
SYN104 *Saurida macrolepis* Japan
SYN102 *Saurida macrolepis* Japan
SYN24 *Saurida macrolepis* Thailand
SYN96 *Saurida macrolepis* Japan
SYN94 *Saurida macrolepis* Japan
SYN245 *Saurida macrolepis* Vietnam
SYN296 *Saurida macrolepis* Japan
SYN290 *Saurida macrolepis* Japan
SYN289 *Saurida macrolepis* Japan
SYN284 *Saurida macrolepis* Japan
SYN271 *Saurida macrolepis* Japan
SYN283 *Saurida macrolepis* Japan

Appendix II. (continued)

Appendix III. Publication



First record of Gauguin's blunt-nose lizardfish, *Trachinocephalus gauguini* Polanco, Acero & Betancur 2016 (Teleostei: Synodontidae) outside the Marquesas Archipelago

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Abstract

Trachinocephalus gauguini Polanco, Acero & Betancur, 2016 was described based on eighteen specimens collected from the Marquesas Islands, the only location where this species has been recorded until now. Through morphological and molecular examination of *Trachinocephalus* specimens collected from an exploratory cruise conducted in June 2014 under the *Tropical Deep-Sea Benthos* program along the northern coast of the New Ireland Province, Papua New Guinea, we demonstrate the presence of this species in Papua New Guinea waters. This new record suggests a wide distribution for this rarely collected species in the western Pacific Ocean.

Key words: New record, Tropical Deep-Sea Benthos, Papua New Guinea, Synodontidae, Molecular Taxonomy

Introduction

Trachinocephalus Gill 1861 is a genus of lizardfishes belonging to the aulopiform family Synodontidae, a group of small predatory fishes that inhabit inshore and offshore bottom areas at depths down to about 365 meters, but more commonly found in mid-shelf areas at depths between 25 and 90 meters (Russell 2002).

The main characteristics of the genus differentiating *Trachinocephalus* from other lizardfish genera are its blunt head, with relatively short snout, and high number of anal-fin rays (Anderson *et al.* 1966; Russell *et al.* 2002). The genus was previously regarded as monotypic, containing only a single species, *Trachinocephalus myops* (Forster 1801), with nearly circum-tropical and subtropical distribution (Briggs 1960). However, a recent taxonomic revision (Polanco *et al.* 2016) based on morphological and molecular evidence, challenged this traditional classification and recognized three valid species, including a newly described species, *T. gauguini* Polanco, Acero & Betancur 2016, found exclusively in French Polynesian waters around the Marquesas Islands in the western Pacific. The other two congeneric species, *T. myops* and *T. trachinus* (Temminck & Schlegel 1846), recognized by Polanco *et al.* (2016) have much wider distribution ranges in the Atlantic and the Indo-West Pacific Oceans (except the Marquesas), respectively. The three species are currently known to be allopatrically distributed (Polanco *et al.* 2016).

Recently, we examined lizardfish specimens (55 in total) collected during three exploratory cruises (campaigns: PAPUA NIUGINI, MADEEP, and KAVIENG 2014) conducted between 2012 and 2014 under the *Tropical Deep-Sea Benthos* (TDSB) program by the R/V ALIS deployed by the French Oceanographic Fleet in the waters off northern and northeastern Papua New Guinea. Three *Trachinocephalus* specimens were collected from the KAVIENG 2014 cruise. Among them, two are identified as *T. gauguini* and the other as *T. trachinus*.

The purpose of the present work is to record both species from New Ireland Province, Papua New Guinea. Molecular data for the mitochondrial *COI* gene from the three collected specimens were obtained and compared to the available *COI* sequence of the paratype specimen of *T. gauguini* (voucher: USNM 409222) deposited in NCBI GenBank (accession no.: KP099622).

Material and methods

Morphological measurements, meristic features and compared specimens. Methods for obtaining morphological data from the three *Trachinocephalus* specimens followed Anderson et al. (1966). Abbreviations used throughout the text included HL (head length) and SL (standard length); for others see Table 1. All measurements were taken in a straight line, made with a dial caliper and recorded to the nearest 0.1 mm. For each specimen, 21 measurements and five counts were recorded, following Polanco *et al.* (2016). The examined specimens were deposited at the ichthyological collection of the National Taiwan University Museums, Taipei (NTUM) under registration nos: NTUM 11201 (tissue voucher PNG 3126), NTUM 11085 (tissue voucher PNG 3127), and NTUM 11212 (tissue voucher PNG 3163).

Molecular data. Whole genomic DNA was extracted from the tissue samples of the three *Trachinocephalus* specimens using an automatic extractor: LabTurbo 48 Compact System and LGD 480–500 kits (Taigene Biosciences Corp.) following the manufacturer's protocol. A fragment of the mitochondrial protein-coding gene cytochrome oxidase subunit I (*COI*) was amplified and sequenced for this study. Protocols for collecting molecular data followed those outlined in Ward *et al.* (2005) and in a previous study in Lo *et al.* (2015). The *COI* amplicons were sequenced by Sanger sequencing technique at the Genomics BioSci &Tech (Taipei) and at the Center of Biotechnology (National Taiwan University). The chromatograms were edited and assembled using CodonCode Aligner (version 7.1.2). The sequences were further aligned to each other and with the homologous sequence from *T. gauguini* published by Polanco *et al.* (2016) (accession no. KP099622). The software PAUP? (Swofford 2002) was used to compute pairwise *p*-distances to assess the genetic similarity among the samples from the same species and the inter-specific genetic diversity of the *COI* sequences of the included species. The *COI* sequences obtained in this study were deposited in GenBank (accession nos. MG751097–MG751099).

Results and discussion

Morphometric and meristic data of the specimens are summarized in Table 1 and Table 2. The result of the genetic comparison of *COI* sequences between the examined specimens and the homologous sequence retrieved from GenBank are shown in the Table 3.

Trachinocephalus gauguini Polanco, Acero & Betancur, 2016, new record

Figure 1A–B; Table 1–2

Material examined. NTUM 11085 (tissue voucher: PNG 3127) and NTUM 11212 (tissue voucher: PNG 3163). Both specimens were collected from mid-shelf areas around 20 km west of Kavieng, New Ireland Province, Papua New Guinea (Fig. 2) on September 2, 2014 by R/V ALIS from station CP4455, 2° 23.4' S, 150° 37' E, 60–72m, and station CP4456, 2°35' S, 150°40' E, 134–144m, respectively (campaign: KAVIENG 2014).

Diagnosis. Morphometric data and meristic data for the two Papua New Guinea specimens are as in Table 1 and 2 respectively. The morphological characteristics fit within the range of the identification key, description of body color pattern, and photographs provided in Polanco *et al.* (2016): L_{sn} 6.7–10.0% of HL, L_{sn} 12.6–18.9% of D_B , L_{sn} 31.6–51.7% of D_E , W_I 4.0–6.7% of HL; pectoral fin rays 11, anal fin rays 14–16; pectoral, caudal and anal fin yellow; dorsal fin dark yellow; four obvious yellow stripes along the body longitudinally, with several inconspicuous vertical bars across; an oval black spot above the dorsal border of the operculum, and a rather wide dark blotch below the eye (indistinct in NTUM 11212) (Fig. 1A, B). A blunter snout and broader dark blotch beneath the eye distinguish *Trachinocephalus gauguini* from other species of *Trachinocephalus*.

Trachinocephalus trachinus (Temminck & Schlegel 1846)

Figure 1C; Table 1–2

Material examined. NTUM 11201 (tissue voucher: PNG 3126), specimen collected from the same site as *T. gauguini*, NTUM 11085 (see above).

TABLE 1. Morphometric data of *Trachinocephalus* specimens examined in this study. Data from Polanco *et al.* (2016) is included for comparison. Standard lengths (SL) and head lengths (HL) are given in mm. The other measurements are given as ratios (actual lengths or lengths in holotype are shown in the parentheses). Head measurements are expressed as percentage of HL; body measurements are expressed in percentage of SL. Asterisk indicates the number did not fit in the range of the ratio provided by Polanco *et al.* (2016).

	<i>T. trachinus</i>		<i>T. gauquini</i>		
	NTUM 11201	Polanco <i>et al.</i> (2016) n=66	NTUM 11085	NTUM 11212	Polanco <i>et al.</i> (2016) n=17 (Holotype)
Standard length (SL)	40.6	65.3–228	51.3	76.2	40.4–135 (124.5)
Body depth (D _B)	17.48 (7.1)	10.4–20.7	18.09 (9.1)	18.77 (14.3)	16.9–22.9 (25.7)
Body width (W _B)	12.06 (4.9)	9.9–16.9	14.51 (7.3)	13.52 (10.3)	12.4–17.6 (21.9)
Head length (HL)	30.3 (12.3)	25.2–31.8	29.04 (14.9)	31.23 (23.8)	29.4–32.5 (40.4)
Snout length (L _{Sn})	11.38 (1.4)	8.9–14.7	8.05 (1.2)	8.82 (2.1)	6.7–10.0 (3.3)
Eye diameter (D _E)	22.36 (2.75)	11.0–22.6	21.48 (3.2)	17.65 (4.2)	14.7–22.5 (6.5)
Interorbital width (W _I)	6.50 (0.8)	5.2–12	6.71 (1.3)	6.30 (1.5)	4.0–6.7 (2.3)
Premaxillary length (L _p)	51.22 (6.3)	50.3–61.2	55.03 (8.2)	53.78 (12.8)	50.2–56.3 (21.8)
Distance from snout to the origin of pelvic fin (Sn-OP _v)	33.62 (13.65)	28.4–35.9	33.92 (17.4)	31.76 (24.2)	31.8–36.4 (41.0)
Distance from snout to the origin of dorsal fin (Sn-OD)	42.61 (17.3)	37.4–43.5	40.94 (21.0)	41.34 (3.15)	36.4–43.1 (53.7)
Distance from snout to the origin of anal fin (Sn-OA)	67.49 (27.4)	61.4–70.2	67.45 (34.6)	63.25 (48.2)	60.5–67.7 (79.5)
Distance from origin of dorsal fin to the origin of adipose fin (OD-OA)	33.74* (13.7)	40.3–46.4	44.14 (22.2)	38.06 (29.0)	38.1–46.1 (54.5)
Length of the longest dorsal ray (L _{DR})	17.4 (7.1)	15.8–26.2	19.10 (9.8)	19.69 (15.0)	16.5–21.1 (23.6)
Length of the longest pectoral ray (L _{per})	10.71 (4.35)	10.2–14.0	12.77 (6.55)	11.94 (9.0)	11.6–13.7 (17.0)
Length of the longest pelvic ray (L _{pvr})	26.97 (10.95)	22.2–29.3	25.63 (13.15)	25.07 (19.1)	24.1–29.4 (34.6)
Length of the last dorsal ray (L _{LDR})	10.09 (4.1)	8.7–11.8	11.13 (5.6)	12.86 (9.8)	9.5–12.9 (14.7)
Dorsal-fin base (DB)	15.76 (6.4)	15.0–18.7	15.31 (7.7)	16.08 (12.25)	14.9–17.5 (19.6)
Anal-fin base (AB)	22.41 (9.1)	20.6–26.8	23.46 (11.8)	23.29 (17.75)	22.3–30.5 (30.7)

TABLE 2. Meristic data of three *Trachinocephalus* specimens examined in this study. Data from Polanco *et al.* (2016) is included for comparison.

	<i>T. trachinus</i>		<i>T. gauquini</i>		
	NTUM 11201	Polanco <i>et al.</i> (2016) n=75	NTUM 11085	NTUM 11212	Polanco <i>et al.</i> (2016) n=18
Lateral-line scales	57	53–58	56	59	56–59
Dorsal-fin rays	12	11–14	11	11	11–13
Anal-fin rays	13	13–18	14	15	14–16
Pectoral-fin rays	12	11–13	11	11	11–12
Predorsal scales	17	14–18	18	17	16–18

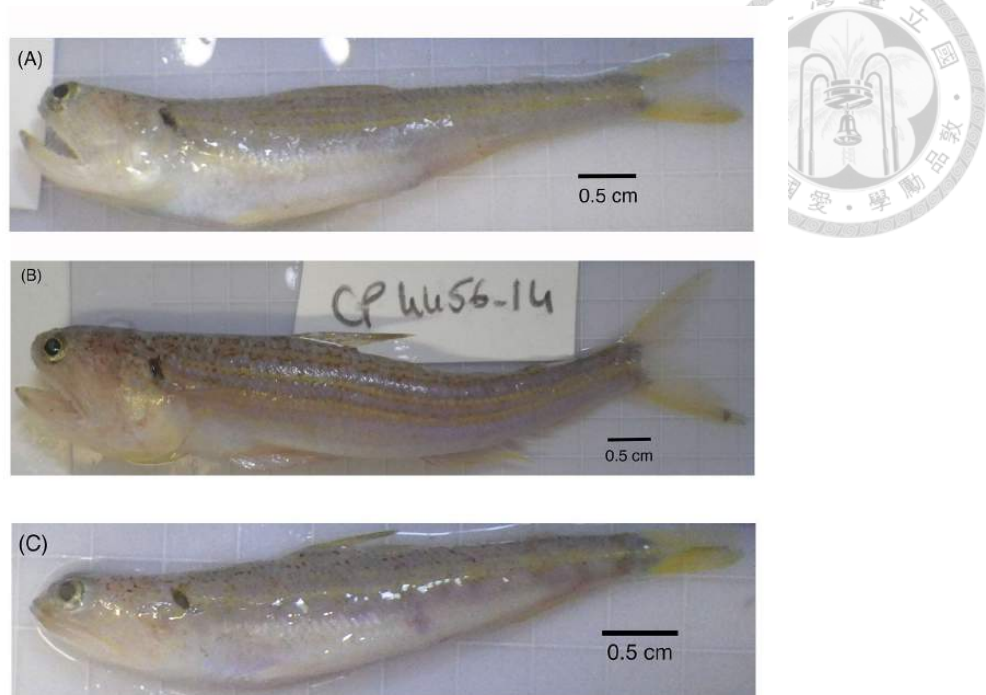


FIGURE 1. Three *Trachinocephalus* specimens collected from Papua New Guinean waters. (A) *T. gauguini*, NTUM 11085, SL = 51.3 mm (B) *T. gauguini*, NTUM 11212, SL = 76.4 mm (C) *T. trachinus*, NTUM 11201, SL = 40.6 mm. (Photographed by J.-N. Chen).

Diagnosis. Morphometric and meristic data for the Papua New Guinea specimen is in Table 1 and 2 respectively. According to the diagnosis provided in Polanco et al. (2016), this species can be distinguished from other two *Trachinocephalus* species by the following meristic characteristics: L_{Sn} 50.89% of D_E ; L_{Sn} 19.71% of D_B ; W_1 6.5% of HL; D_E 22.36% of HL; length of the last dorsal ray 10.09% of L_S ; anal rays 13; pectoral rays 12; predorsal scales 17. This specimen is a transitional juvenile with black peritoneum spots still faintly visible. The pectoral, caudal and anal fin yellow, while dorsal fin dark yellow. Several yellow stripes along the trunk longitudinally, with the most obvious one across the middle part of the body. An oval black spot above the dorsal border of the operculum. Indistinct dark spot below the eye. The morphological data of the Papua New Guinea specimen matches the description of *T. trachinus* (Table 1, 2; Fig. 1C).

The genetic pairwise distance analysis based on *COI* sequences shows high interspecific variation between *T. gauguini* and *T. trachinus* (p -distance: 0.13944–0.14053) while low intraspecific variation within *T. gauguini* specimens (p -distance: 0–0.00157) (Table 3). This result supports the morphological diagnosis of the three specimens and confirms their species status.

Remarks. In a checklist of the marine and estuarine fishes of the Madang District, Papua New Guinea (Fricke et al. 2014), recorded eight synodontid species. One of these was identified as *Trachinocephalus* “*myops*” based on material deposited in the Australian Museum (AMS) and Western Australian Museum (WAM). It should be noted that *T. myops* is a species complex and following Polanco et al. (2016) we apply the name *T. trachinus* for *T. “myops”* populations from the Indo-West Pacific. Our study additionally records *T. trachinus* from New Ireland, and extends the distribution of *T. gauguini* from its previously reported area (Marquesas Archipelago) to the western Pacific (Papua New Guinea). Our work shows that *Trachinocephalus trachinus* and *T. gauguini* occur sympatrically in Papua New Guinea waters, and as both were collected from the station CP4455, we can confirm that these two species share the same habitat.

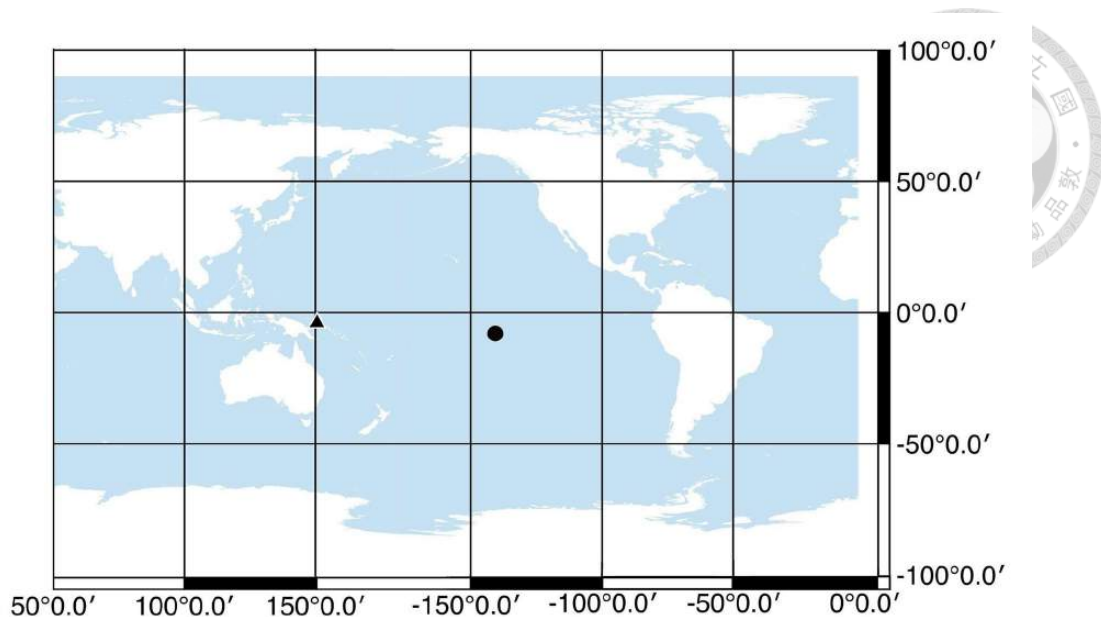


FIGURE 2. Distribution records of *Trachinocephalus gauguini*. Open circle, occurrence described in Polanco *et al.* (2016); triangle, new record from Papua New Guinea (this study).

TABLE 3. Matrix of pairwise genetic distances (*p*-distance) of *COI* sequences.

Sample				Sample			
No.	Species	Tissue no.	GenBank access. no.	1	2	3	4
1	<i>T. trachinus</i>	PNG3126	MG751097	-			
2	<i>T. gauguini</i>	PNG3127	MG751098	0.14053	-		
3	<i>T. gauguini</i>	PNG3163	MG751099	0.13944	0.00155	-	
4	<i>T. gauguini</i>	MARQ-221	KP099622	0.13996	0.00157	0.00000	-

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