Species composition of hairtails (Trichiuridae) in Myanmar

Short title: Species composition of Trichiuridae in Myanmar

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ABSTRACT

Hairtails (family Trichiuridae) are an important group of fish for coastal fisheries worldwide. In the view to reiterate the need of management of hairtails found in the Republic of the Union of Myanmar, the species composition of hairtails was investigated according to the morphological characteristics and DNA barcoding of mitochondrial cytochrome *c* oxidase subunit I gene. A total of 95 individual landed fish were sampled from fish markets in Yangon and Myeik. The hairtails were treated similarly to the group without species distinction at the fish markets, which consisted of five species from three genera, namely *Trichiurus* sp., *Lepturacanthus savala*, *Lepturacanthus* sp., *Eupleurogrammus* sp., and *Eupleurogrammus muticus*. Further studies on the biological characteristics and taxonomies are needed to establish improved approach of identifying with such fishery species in Myanmar.

Keywords: taxonomy; cutlassfish; DNA barcoding; cryptic species; Andaman Sea

1. Introduction

The Republic of the Union of Myanmar is among important fishing countries of the globe, with its catch increasing dramatically since the late 1990s. Its annual catch was approximately a million tons in 2003 (FAO, 2014) increasing to 2.4 million tons by 2013 (FAO, 2016). the heavy exploitation of coastal resources is attributed to increase in demand for fish products from Myanmar (Raitzer et al., 2015). Furthermore, the landings of such commercial species as conger eels, croakers, sardines, herrings, and hairtails (cutlassfish, family Trichiuridae) have decreased (Khin-Maung-Soe, 2008).

In particular, hairtails are among commercially important fish group found within the world's ocean. According to Nakamura and Parin (1993), hairtails belong to 32 species in nine genera. However, some new species, such as *Trichiurus japonicus* (Chakraborty et al., 2006) and *Trichiurus russelli* (Burhanuddin et al., 2002), have been found as cryptic species recently. The taxonomy of hairtails seems undeveloped (Tzeng et al., 2007; Hsu et al., 2009; Wang et al., 2017). Given such taxonomic problems, any attempt to catch hairtails may well include a catch of other species.

In Myanmar, hairtails (locally called ribbonfish) are an important resource, but their overall catch appears not well reported, making them to be considered as a single group without species identification at fish markets. In addition, taxonomic and biological information of hairtails in Myanmar is scarce. In other localities, the biological characteristics of hairtails such as feeding (Martins et al., 2005; Chiou et al., 2006; Yan et al., 2011; Niino et al., 2017), age, growth (Kwok and Ni, 2000; Shih et al., 2011), and reproduction (Kwok and Ni, 1999) have been documented also. To establish sustainable fisheries of hairtails, it is essential to understand the biological characteristics of each species. Taxonomic studies should precede such biological investigations.

The objective of the present study was to identify the species composition of hairtails in Myanmar. Morphological characteristics and DNA barcoding (Hebert et al., 2003; Steinke and Hanner, 2011) will then be used to identify the taxon.

2. Materials and Methods

2.1. Study site and sampling protocol

Hairtails landed at fish markets (Myo Thint Market and Tat Pyin Market) in Myeik City (Fig. 1) and a fish market (Ngwe Pin Lae Jetty) in Yangon City were sampled (Table 1). Forty-two samples caught by drifting gill net or set net fisheries were collected in Myeik. The fishing ground was supposed to be located nearshore around Myeik. At a market in Yangon, 53 samples were collected from hairtails caught by the driftnet fishery (approximately 3,390 kg of landings on the survey date). The location of the fishing ground was provided by the fishermen (14°49'50"N, 96°23'50"E; 85 to 90 m deep; Fig. 1). Because landed hairtails were classified into two size groups (large, 124 kg and small, 3,267 kg) at a market in Yangon, samples were selected randomly from each group.

To examine the taxonomic relationship of hairtails between Myanmar and Japan, we also collected one individual *Trichiurus japonicus* (234 mm pre-anal length [PAL]) sample landed in Ehime (34°04'22"N, 133°00'08"E) in May 2015, one individual *Trichiurus* sp. 1 (565 mm PAL) and two individual *Trichiurus* sp. 2 (213 and 234 mm PAL) landed in Okinawa (26°58'34"N, 127°98'11"E and 26°32'39"N, 127°83'78"E) in October 2015.

2.2. Measurements

The PAL (mm) and wet weight (g) of each individual hairtail were measured on the collection day. The total length was not used because some specimens had lost part of their caudal fin. After the measurements, a muscle tissue sample of approximately 1 cm^3 was sampled from the left side of each individual fish and was preserved in 99% ethanol for the molecular analysis.

2.3. Species identification

We observed the morphological characteristics of samples based on previous reports (Nakamura and Parin, 1993; Nakabo and Doiuchi, 2013). Four of the nine genera were selected based on the tail morphology. Importantly, the *Tentoriceps* species were excluded from this selection because their head shape and pectoral fins did not reach the lateral line. The remaining three genera, *Trichiurus*, *Lepturacanthus*, and *Eupleurogrammus* were identified by the following key features. When the free margin of the subopercle was concave, and the lateral line slope sharply declined near the operculum, the genus was assigned as *Trichiurus* or *Lepturacanthus*.

Furthermore, when the first anal-fin spine was remarkably large (with a length equivalent to half the eye diameter), the genus was considered as *Lepturacanthus*. When the margin of the subopercle was convex, and the lateral line slope was small (Fig. 2), the genus was determined to be *Eupleurogrammus*. When the genus could not be identified based on the margin of subopercle and the slope of the lateral line, the shape of the teeth was observed. If the teeth in upper jaw were canine, the genus was considered as *Trichiurus* or *Lepturacanthus*; otherwise, the genus was considered as *Eupleurogrammus*. The presence of pelvic fins was also useful for distinguishing the *Eupleurogrammus* from other genera.

The muscle tissues of hairtails were used for DNA barcoding based on the mitochondrial cytochrome *c* oxidase subunit I (*COI*) gene (Ivanova et al., 2007). When the sample sizes of the same morphological types and similar sizes at each site exceeded 20, 10–15 specimens were chosen as subsamples and used for the DNA barcoding. Genomic DNA was prepared using the HotSHOT method (Truett et al., 2000; Meeker et al., 2007). A small portion of the muscle sample preserved in ethanol was digested in 50 mM sodium hydroxide (NaOH) at 95ºC for 20 min, chilled at 4ºC for 15 min, and then 10 μL 1 M Tris-hydrochloride (HCl, pH 8.0) was added to neutralize the solution. The supernatant was used for the subsequent polymerase chain reaction (PCR).

A partial fragment of the mitochondrial DNA (mtDNA) *COI* gene was amplified using the following universal fish primers (Ward et al., 2005): FishF1 (5'-TCA ACC AAC CAC AAA GAC ATT GGC AC-3') and FishR1 (5'-TAG ACT TCT GGG TGG CCA AAG AAT CA-3'). The PCR was performed in a total volume of 10 μL, containing 0.05 μL TaKaRa ExTaq HS polymerase, 1 μL 10 × ExTaq Buffer, 0.8 μL dNTP, 0.1 μL 20 μM of each forward and reverse primer, 0.5 μL template DNA, and 7.45 μL hyper pure water. The thermal cycling schedule was as follows: an initial activation at 95ºC for 5 min followed by 35 cycles of denaturation at 95ºC for 30 s, annealing at 54.5ºC for 30 s, and extension at 72ºC for 1 min with a final extension for 7 min at 72ºC. The PCR products were purified using the Affymetrix ExoSAP-IT and then sequenced using the BigDye Terminator v.3.1 cycle sequencing kit on an ABI 3130 xl genetic analyzer (Applied Biosystems).

The reference sequences of hairtails (family Trichiuridae) were downloaded from GenBank. The references used from a previous report (Tzeng and Chiu, 2012) were *Assurger anzac* (JN990845), *Benthodesmus elongatus* (JN990841), *Evoxymetopon poeyi* (JN990846), *Evoxymetopon taeniatus* (JN990843), *Lepidopus caudatus* (JN990842), *Lepturacanthus savala* (JN990857-61), *Lepturacanthus roelandti* (JN990847-51), *Tentoriceps cristatus* (JN990844),

Trichiurus brevis (JN990852-56), *Trichiurus japonicus* (JN990867-71), *Trichiurus lepturus* (JN990872-76), *Trichiurus nanhaiensis* (JN990862-66), and *Lepidocybium flavobrnneum* (KP244580, used as an outgroup). In addition, *Trichiurus gangeticus* (KP641596) and *Trichiurus russelli* (FJ265829) were included from GenBank because of their high homology (>98%) with the other species investigated in this study that was detected using the Basic Local Alignment Search Tool (BLAST) in GenBank.

These references together with the investigated species in this study were aligned using ClustalW in Bioedit (Hall, 1999). Preliminarily, specimens with sequences that could not be read clearly (four out of 447 individuals) were excluded from any further analysis. Pairwise genetic distance was calculated based on Kimura's two-parameter (K2P) model (Kimura, 1980). A neighbor-joining (NJ) phylogenetic tree was constructed using the MEGA ver. 5.0 (Tamura et al., 2011). The robustness of NJ tree was assessed by performing a bootstrap analysis with 1,000 replicates (Tzeng and Chiu, 2012; Wang et al., 2017). The K2P values of intraspecific difference were assumed to be lower than 0.05 in hairtails (Tzeng and Chiu, 2012). The sequences we obtained from the hairtail specimens in Myanmar and Japan were submitted to the DNA Data Bank of Japan (LC269196 to LC269241).

3. Results and Discussion

Based on the morphological observation, hairtails in Myeik and the large group in Yangon were considered to closely resemble *Trichiurus* or *Lepturacanthus* species with respect to the shape of their subopercles and lateral line slopes, but their genus seemed not clearly identifiable by morphological observations particularly because the remarkable first anal-fin spine could not be confirmed. Small hairtails in Yangon seemed to belong to two genera, *Lepturacanthus* in terms of the shape of its subopercle, slope of lateral line, and remarkable first anal-fin spine and *Eupleurogrammus* in terms of the shape of subopercle and slope of lateral line.

The DNA barcoding showed that specimens of this study as obtained in Myanmar could be classified into five groups (A, B, C, D, and E) based on the high bootstrap probability (Fig. 3). The K2P values of the same group members appeared lower than the typical intraspecific difference of 0.05 in hairtails (Tzeng & Chiu, 2012), and the inter-group values exceeded 0.05. For future research, it may be useful to analyse 16S rRNA gene together with the COI gene, following Wang et al. (2017), to identify at the species level and reveal the species composition of hairtails in Myanmar.

Group A, including *T. gangeticus* and *T. russelli*, which had contained most of the hairtails from Myeik and Yangon (large group). This group could not be identified at the species level and was therefore assigned as *Trichiurus* sp. Moreover, dominant species of *Trichiurus* in the waters of Myanmar were regarded as *T. lepturus* (Chakraborty and Iwatsuki, 2006; Thapanand-Chaidee et al., 2010). Hsu et al. (2009) suggested that *T. lepturus* from the Indo-Pacific region and *Trichiurus* sp. 2 are the same species, but this study revealed that group A is a different species from *Trichiurus* sp. 2.

Group B that contained only small hairtails landed in Yangon was assigned as *Lepturacanthus* sp. This group also could not be identified at the species level. However, a few individuals (Y-121, 122, 123, and 127) had an anus with a black margin (Fig. 2), which is the species characteristics of *Lepturacanthus pantului* (Nakamura and Parin, 1993).

Group C that contained only one individual collected from Myeik, which subsequently has been identified as *Lepturacanthus savala* (K2P = 0.0253). This species is common and abundant in the waters of Myanmar (Strømme et al., 1981), although only one individual was available in this study.

Groups D and E that consisted of two species of small hairtails from Yangon, which has been morphologically identified as belonging to the genus *Eupleurogrammus* (Table 1). Group E was assigned as *Eupleurogrammus muticus* because four of the seven individuals in this group had a black spot around the base of the pectoral fin. The other (group D) was assigned as *Eupleurogrammus* sp. Although the black line on the pectoral fin was unclear, group D may be *E. glossodon* (Iwatsuki, Y., pers. comm.).

This study first revealed that hairtails consisted of multiple species with at least five identified in two regions in Myanmar. They were traded without species distinction. The species composition in the landings of hairtails at the market in Yangon was estimated: dominant species was *Lepturacanthus* sp. (75.0% in number and 79.2% in weight), followed by *E. muticus* (17.1% in number and 10.1% in weight), *Eupleurogrammus* sp. (7.5% in number and 7.0% in weight), and *Trichiurus* sp. (0.3% in number and 3.7% in weight). It should be noted that this study investigated the species composition only in May before the rainy season. It may be necessary to investigate species composition during other seasons because primary production in Myanmar shows seasonal fluctuation (Maung-Saw-Htoo-Thaw et al., 2017), which may affect the abundance of higher trophic levels. Further studies on the species composition and biological characteristics of hairtails in many localities in Myanmar are expected. Such studies would contribute to the development of fishery management of hairtails

in Myanmar.

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References

Burhanuddin, A.I., Iwatsuki, Y., Yoshino, T., Kimura, S., 2002. Small and valid species of *Trichiurus brevis* Wang and You, 1992 and *T. russelli* Dutt and Thankam, 1966, defined as the "*T. russelli* complex" (Perciformes: Trichiuridae). Ichthyol. Res. 49, 211–223. doi:10.1007/s102280200030

Chakraborty, A., Iwatsuki, Y., 2006. Genetic variation at the mitochondrial 16S rRNA gene among *Trichiurus lepturus* (Teleostei:Trichiuridae) from various localities: preliminary evidence of a new species from West coast of Africa. Hydrobiologia 563, 501–513. doi:10.1007/s10750-006-0105-4

Chakraborty, A., Aranishi, F., Iwatsuki, Y., 2006. Genetic differentiation of *Trichiurus japonicus* and *T. lepturus* (Perciformes: Trichiuridae) based on mitochondrial DNA analysis. Zool. Stud. 45, 419–427.

Chiou, W.D., Chen, C.Y., Wang, C.M., Chen, C.T., 2006. Food and feeding habits of ribbonfish *Trichiurus lepturus* in coastal waters of south-western Taiwan. Fish. Sci. 72, 373–381. doi:10.1111/j.1444-2906.2006.01159.x

FAO, 2014. The state of world fisheries and aquaculture. Food and Agriculture Organization of the United Nations, Rome: 10–11.

FAO, 2016. The state of world fisheries and aquaculture. Food and Agriculture Organization of the United Nations, Rome: 11–18.

Hall, T.A., 1999. BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp. Ser. 41, 95–98.

Hebert, P.D.N., Cywinska, A., Ball, S.L., deWaard, J.R., 2003. Biological identifications through DNA barcodes. Proc. Royal Soc. B: Biol. Sci. 270, 313–321. doi:10.1098/rspb.2002.2218

Hsu, K.C., Shih, N.T., Ni, I.H., Shao, K.T., 2009. Speciation and population structure of three *Trichiurus* species based on mitochondrial DNA. Zool. Stud. 48, 835–849.

Ivanova, N.V., Zemlak, T.S., Hanner, R.H., Hebert, P.D.N., 2007. Universal primer cocktails for fish DNA barcoding. Mol. Ecol. Notes 7, 544–548. doi:10.1111/j.1471-8286.2007.01748.x

Khin-Maung-Soe, 2008. Trends of development of Myanmar fisheries: with references to Japanese experience. Institute of Developing Economies Japan External Trade Organization. pp. 58.

241 Kimura, M., 1980. A simple method for estimating evolutionary rates of base substitutions
242 through comparative studies of nucleotide sequences. J. Mol. Evol. 16, 111–120.
243 doi:10.1007/BF01731581
244 Kwok, K.Y., Ni, I.H., 1999. Reproduction of cutlassfishes *Trichiurus* spp. from the South
245 China Sea. Mar. Ecol. Prog. Ser. 176, 39–47. doi:10.3354/meps176039
246 Kwok, K.Y., Ni, I.H., 2000. Age and growth of cutlassfishes, *Trichiurus* spp., from the South
247 China Sea. Fish. Bull. 98, 748–758.
248 Martins, A.S., Haimovici, M., Palacios, R., 2005. Diet and feeding of the cutlassfish
249 *Trichiurus lepturus* in the Subtropical Convergence Ecosystem of southern Brazil. J. Mar.
250 Biol. Assoc. UK 85, 1223–1229.
251 Maung-Saw-Htoo-Thaw, Ohara, S., Matsuoka, K., Yurimoto, T., Higo, S., Khin-Ko-Lay, Win-
252 Kyaing, Myint-Shwe, Sein-Thaung, Yin-Yin-Htay, Nang-Mya-Han, Khin-Maung-Cho,
253 Si–Si-Hla-Bu, Swe-Thwin, Koike, K., 2017. Seasonal dynamics influencing coastal
254 primary production and phytoplankton communities along the southern Myanmar coast.
255 J. Oceanogr. 73, 345–364. doi:10.1007/s10872-016-0408-7
256 Meeker, N.D., Hutchinson, S.A., Ho, L., Trede, N.S., 2007. Method for isolation of PCR-
257 ready genomic DNA from zebrafish tissues. Biotechniques 43, 610–614.
258 doi:10.2144/000112619
259 Nakabo, T., Doiuchi, R., 2013. Family Trichiuridae. In: Nakabo, T. (ed) Fishes of Japan with
260 pictorial keys to the species (3rd ed). Tokai University Press, Hadano, 1644–1647. (in
261 Japanese)
262 Nakamura, I., Parin, N.V., 1993. FAO species catalogue, vol. 15. Snake mackerels and
263 cutlassfish of the world (Families Gempylidae and Trichiuridae): An annotated and
264 illustrated catalogue of the snake mackerels, snoeks, escolars, gemfishes, sackfishes,
265 domine, oilfish, cutlassfishes, scabbardfishes, hairtails, and frostfishes known to date.
266 FAO Fish Synopsis 125, pp. 136.
267 Niino, Y., Shibata, J., Tomiyama, T., Sakai, Y., Hashimoto, H., 2017. Feeding habits of the
268 cutlassfish *Trichiurus japonicus* around Hiuchi-Nada, central Seto Inland Sea, Japan.
269 Nippon Suisan Gakkaishi 83, 34–40. (in Japanese with English abstract)
270 doi:10.2331/suisan.16-00032
271 Raitzer, D.A., Samson, J.N.G., Nam, K.Y., 2015. Achieving environmental sustainability in
272 Myanmar. Asian Develop. Bank Economics Work Paper Ser. 467, 19–21.
273 Shih, N.T., Hsu, K.C., Ni, I.H., 2010. Age, growth and reproduction of cutlassfishes
274 *Trichiurus* spp. in the southern East China Sea. J. Appl. Ichthyol. 27, 1307–1315.
275 doi:10.1111/j.1439-0426.2011.01805.x
276 Steinke, D., Hanner, R., 2011. The FISH-BOL collaborators' protocol. Mitochondrial DNA 22
277 Suppl. 1, 10–14. doi:10.3109/19401736.2010.536538
278 Strømme, T., Nakken, O., Aung, S., Sætersdal, G., 1981. Surveys of the marine fish resources
279 of Burma September-November 1979 and March-April 1980. Institute of Marine
280 Research, Bergen. pp. 90.
281 Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S., 2011. MEGA5:
282 Molecular evolutionary genetics analysis using maximum likelihood, evolutionary
283 distance, and maximum parsimony methods. Mol. Biol. Evol. 28, 2731–2739.
284 doi:10.1093/molbev/msr121
285 Thapanand-Chaidee, T., Myint P.U., Chanrachkij, I., 2010. Status of marine fisheries
286 resources in Myanmar waters: estimates from bottom trawl survey. Kasetsart Univ. Fish.
287 Res. Bull. 34, 35–48.
288 Truett, G.E., Heeger, P., Mynatt, R.L., Truett, A.A., Walker, J.A., Warman, M.L., 2000.
289 Preparation of PCR-quality mouse genomic DNA with hot sodium hydroxide and tris
290 (HotSHOT). BioTechniques 29, 52–54.

291 Tzeng, C.H., Chiu, T.S., 2012. DNA barcode-based identification of commercially caught
292 cutlassfishes (Family: Trichiuridae) with a phylogenetic assessment. Fish. Res. 127–128,
293 176–181. doi:10.1016/j.fishres.2012.01.022
294 Tzeng, C.H., Chen, C.S., Chiu, T.S., 2007. Analysis of morphometry and mitochondrial DNA
295 sequences from two *Trichiurus* species in waters of the western North Pacific: taxonomic
296 assessment and population structure. J. Fish Biol. 70 Suppl. B, 165–176.
297 doi:10.1111/j.1095-8649.2007.01368.x
298 Wang, H.-Y., Dong, C.A., Lin, H.-C., 2017. DNA barcoding of fisheries catch to reveal
299 composition anddistribution of cutlassfishes along the Taiwan coast. Fish. Res. 187, 103–
300 109. doi:10.1016/ j.fishres.2016.11.015
301 Ward, R.D., Zemlak, T.S., Innes, B.H., Last, P.R., Hebert, P.D.N., 2005. DNA barcoding
302 Australia's fish species. Philosophical Trans. Royal Soc. London B 360, 1847–1857.
303 doi:10.1098/rstb.2005.1716
304 Yan, Y., Hou, G., Chen, J., Lu, H., Jin, X., 2011. Feeding ecology of hairtail *Trichiurus*
305 *margarites* and largehead hairtail *Trichiurus lepturus* in the Beibu Gulf, the South China
306 Sea. Chinese J. Oceanol. Limnol. 29, 174–183. doi:10.1007/s00343-011-0004-z
307

Table 1 List of samples in Myanmar examined in this study

Site	Species (group)	Fishing gears	N	PAL (mm)
Myeik	*Trichiurus* sp. (A)	Drifting gill net	41	185–295
Myeik	*Lepturacanthus savala* (C)	Set net	1	227
Yangon	*Trichiurus* sp. (A)	Drift net	33	191–452
Yangon	*Lepturacanthus* sp. (B)	Drift net	10	121–144
Yangon	*Eupleurogrammus* sp. (D)	Drift net	3	103–134
Yangon	*Eupleurogrammus muticus* (E)	Drift net	7	86–129

Hairtails were collected in Myeik and Yangon in May 2015. Capital letters (A–E) behind species corresponds with Fig. 3. PAL: pre-anal length.

312 Figure captions
313

314 **Fig. 1.** Map of study site. Circles show locations of fish markets where hairtails were landed.
315 Location of fishing ground for samples in Yangon is shown by a triangle (14°49'50" N,
316 96°23'50" E).

317

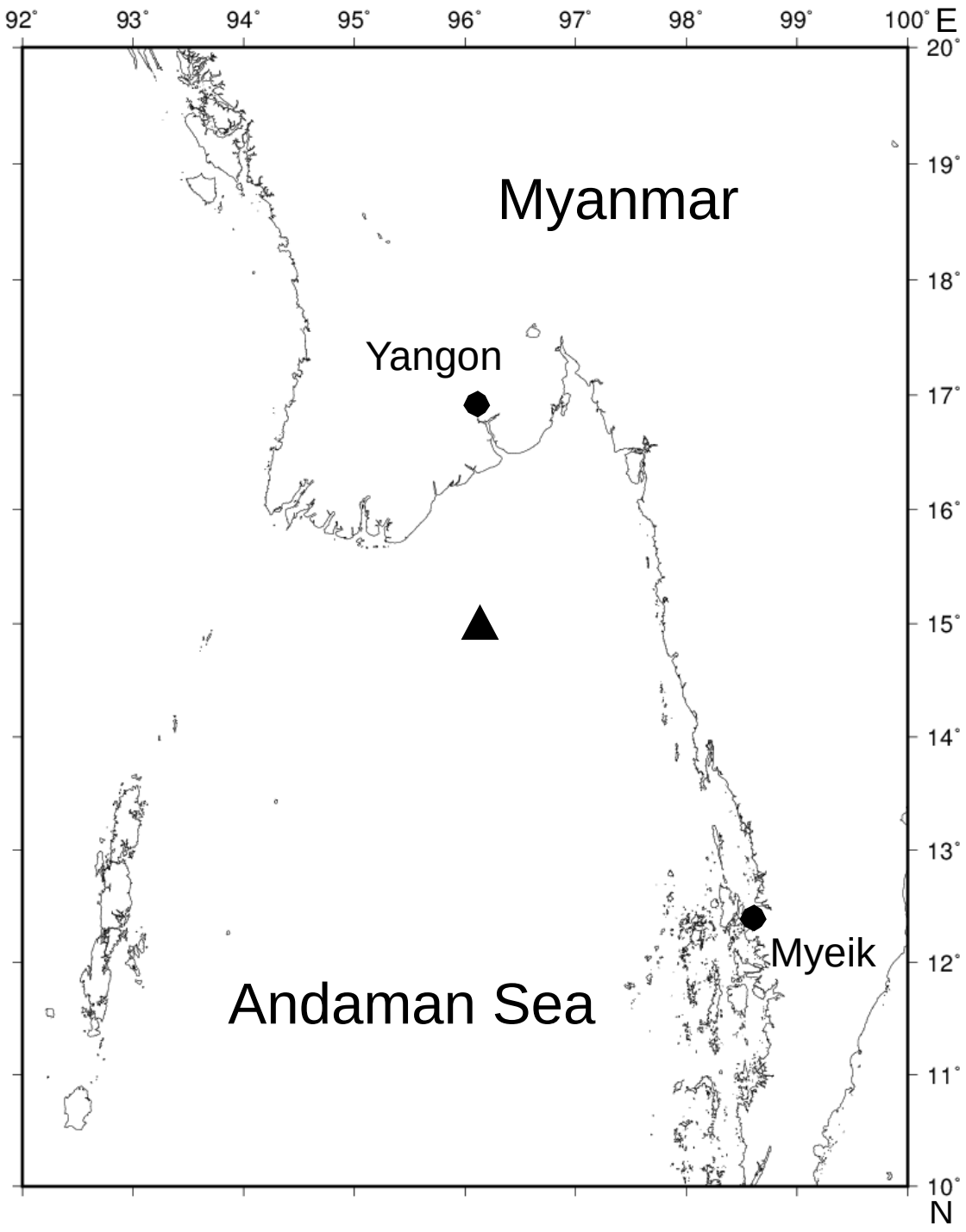
318 **Fig. 2.** Photographs showing head parts of Trichiuridae in Myanmar. (a) *Trichiurus* sp. (group
319 A, M-24), (b) *Trichiurus* sp. (Y-109), (c) *Lepturacanthus* sp. (group B, Y-121), (d)
320 *Lepturacanthus* sp. (Y-122), (e) *Lepturacanthus savala* (group C, M-1), (f) and (g)
321 *Eupleurogrammus* sp. (group D, Y-124), and (h) *Eupleurogrammus muticus* (group E, Y-
322 134). Anus with a black margin is shown by a dashed circle in (d).

323

324 **Fig. 3.** Kimura's two-parameter (K2P) distance neighbor-joining tree of cytochrome *c* oxidase
325 (COI) sequences from the family Trichiuridae and outgroup (*Lepidocybium flavobrnneum*).
326 Bootstrap values >80% are shown near respective branches. Scale bar shows K2P distance.
327 M and Y indicate Myeik and Yangon, respectively.

328

329 Fig. 1



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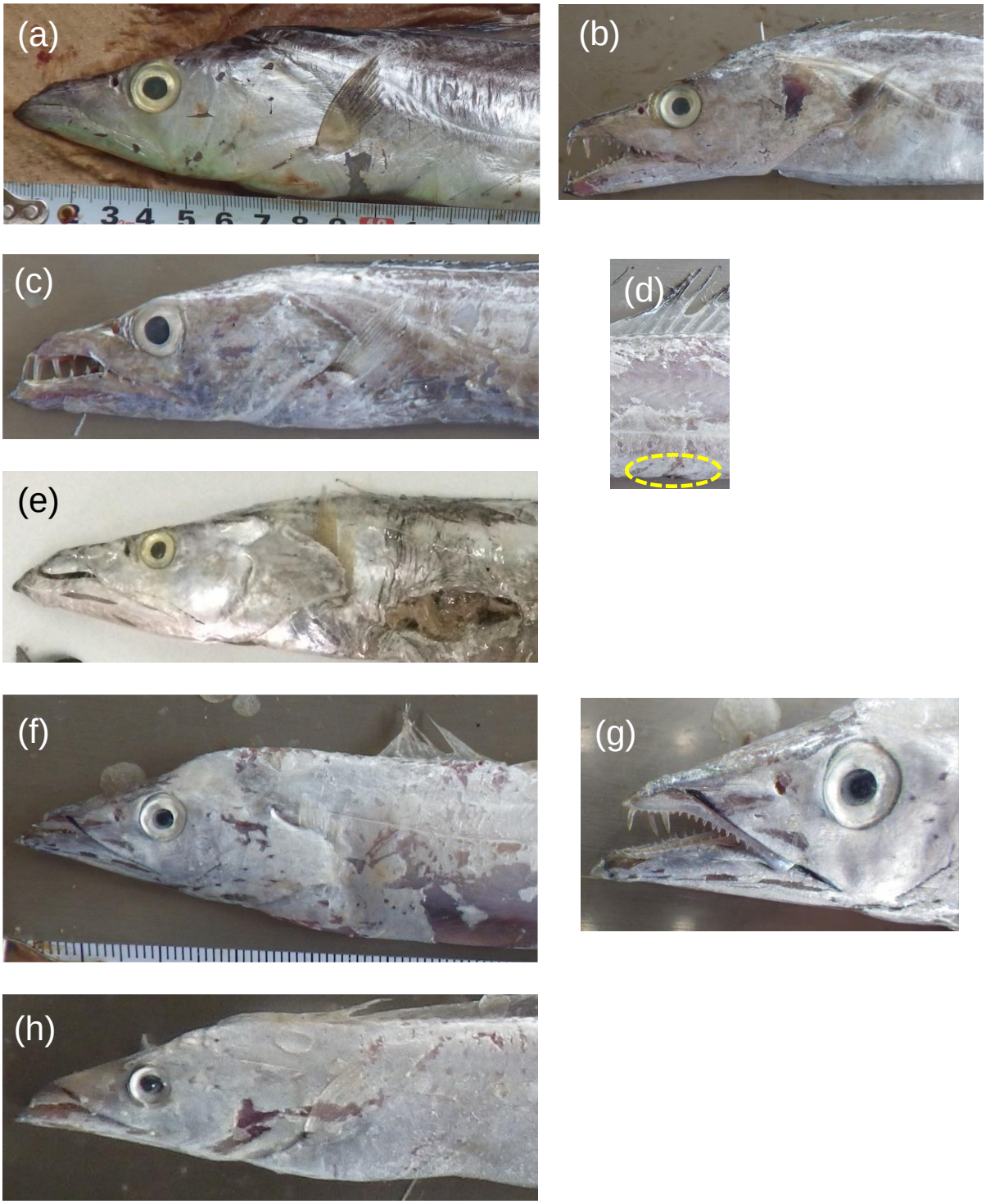
332 Fig. 2



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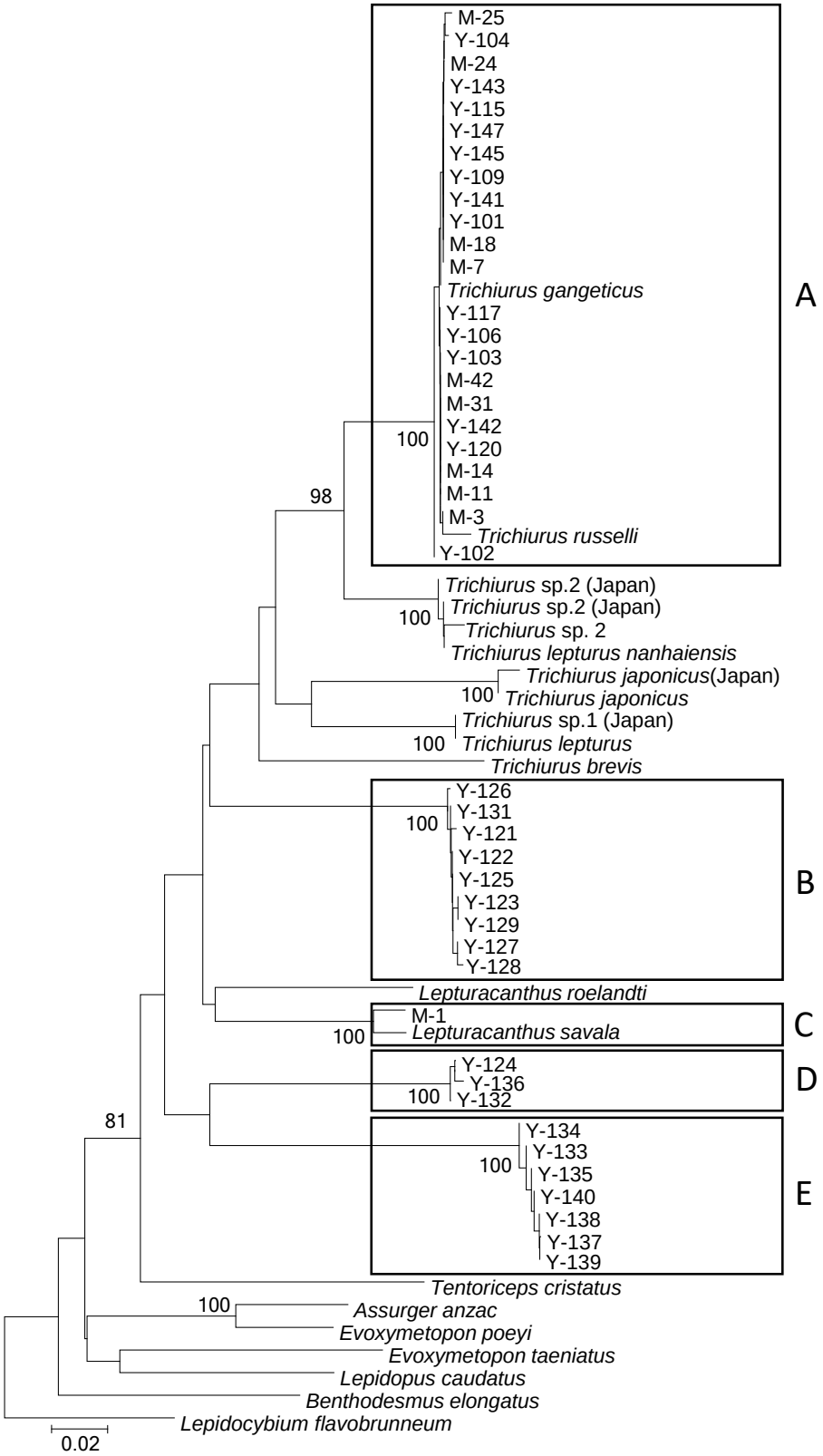
335 Fig. 3


M-25
Y-104
M-24
Y-143
Y-115
Y-147
Y-145
Y-109
Y-141
Y-101
M-18
M-7
Trichiurus gangeticus
Y-117
Y-106
Y-103
M-42
M-31
Y-142
Y-120
M-14
M-11
M-3
Trichiurus russelli
Y-102
A
100
98
Trichiurus sp.2 (Japan)
Trichiurus sp.2 (Japan)
Trichiurus sp. 2
Trichiurus lepturus nanhaiensis
100
Trichiurus japonicus(Japan)
Trichiurus japonicus
100
Trichiurus sp.1 (Japan)
Trichiurus lepturus
100
Trichiurus brevis
Y-126
Y-131
Y-121
Y-122
Y-125
Y-123
Y-129
Y-127
Y-128
B
100
Lepturacanthus roelandti
M-1
Lepturacanthus savala
C
100
Y-124
Y-136
Y-132
D
100
81
Y-134
Y-133
Y-135
Y-140
Y-138
Y-137
Y-139
E
100
Tentoriceps cristatus
Assurger anzac
Evoxymetopon poeyi
Evoxymetopon taeniatus
Lepidopus caudatus
Benthodesmus elongatus
Lepidocybium flavobrunneum
0.02

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