

**Bukti Korespondensi Jurnal Internasional Bereputasi terakreditasi Q3
(Aquatic Science)**

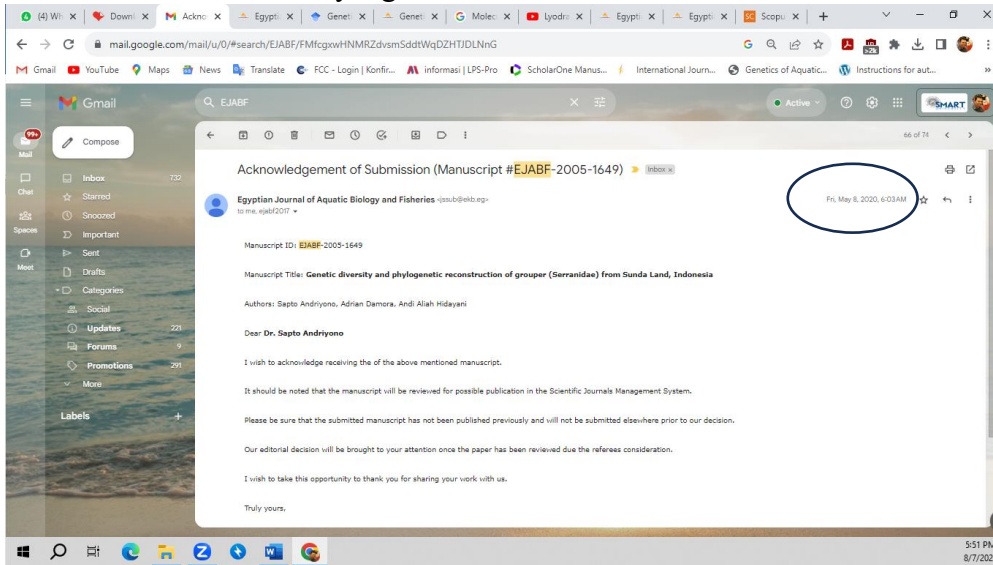
Judul : **Genetic Diversity and Phylogenetic Reconstruction of Grouper (Serranidae)
From Sunda Land, Indonesia**

Jurnal : Egyptian Journal of Aquatic Biology and Fisheries

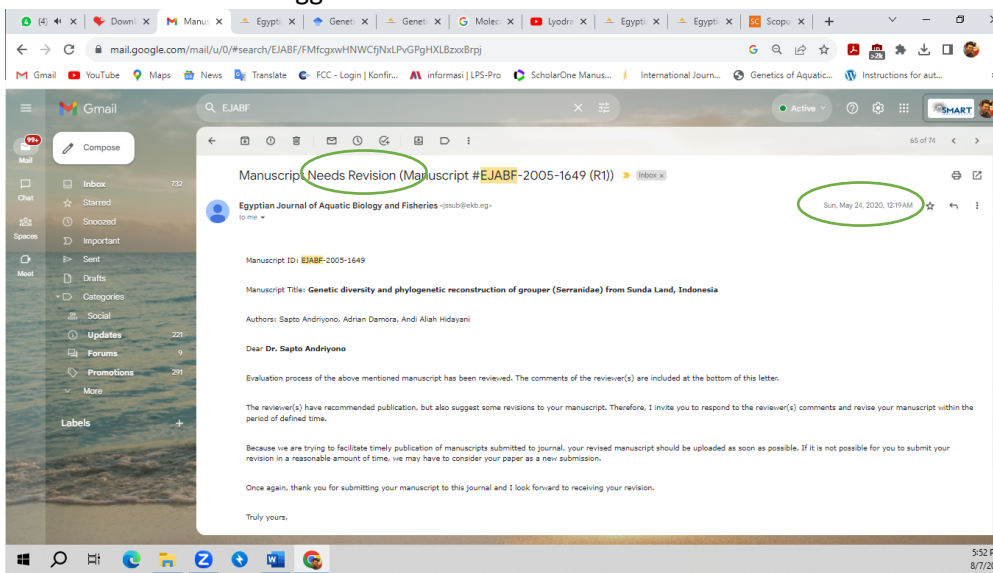
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No.	Perihal	Tanggal	Keterangan
1	Bukti Submit dan Artikel yang di submit	8 Mei 2020	Page 2, Lampiran 1
2	Bukti reviewed minor revision	24 April 2020	Page 2, Lampiran 2
3	Bukti Accepted	25 Mei 2020	Page 3,
4	Link Artikel terpublikasi	29 Mei 2022	Page 3, Lampiran 3

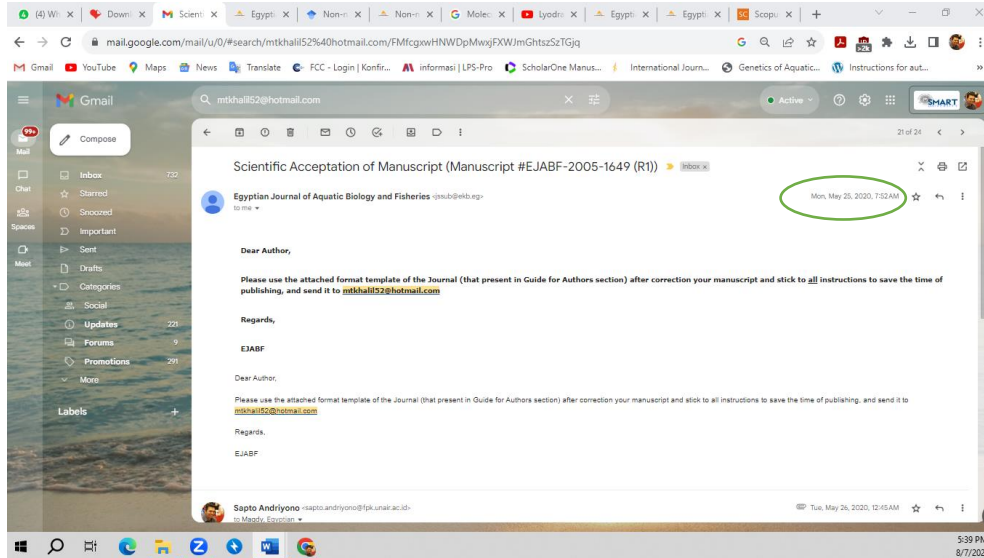
1. Bukti Submit dan Artikel yang disubmit 8 Mei 2020 melalui OJS



2. Revisi Minir Revision tanggal 24 Mei 2020



3. Accepted tanggal 25 Mei 2020



4. Artikel terpublished tanggal melalui link https://journals.ekb.eg/article_92320.html

Genetic diversity and phylogenetic reconstruction of grouper (Serranidae) from Sunda Land, Indonesia

Abstract

Groupers are coral reefs associated and favored in the aquaculture industry. Aquaculture system has been successfully carried out with a floating cage system as well as in an aquaculture system in a pond. Lately, breeding activities in groupers have produced hybrid species that are expected to increase production and fulfillment the demand of groupers in live fish market in Singapore, Taiwan, and China. The study of biology has supported the success of many of groupers, but information on genetic variation in commercial groupers is still very limited. This report is a preliminary study of genetic diversity in commercial groups from Java, Bali, and Aceh, which is the Sunda land region in western Indonesia. Eleven specimens have been identified with the barcode region (Cytochrome c Oxidase subunit I gene region). As a result, two species identified as Indonesian haplotypes, namely *Epinephelus merra* and *Cephalopholis cyanostigma*. Phylogenetic tree analysis produces two large clades, namely Clade I (*Epinephelus*) and Clade II (*Cephalopholis* and *Variola*), which are clearly separated in the subfamily Epinephelinae. However, in-depth studies of genetic variation need to be more accurate by increasing the number of specimens from various regions in Indonesia to describe genetic diversity comprehensively.

Keywords: commercial grouper, genetic study, Sunda land, Indonesia

Introduction

Groupers is a group of fish that make coral reef ecosystems and rocky shallow waters as their primary habitat. Several species found in shallow waters that have sandy mud substrate, which makes the grouper habitat variation quite diverse. The diversity of grouper habitat also makes groupers have a variety of species. As reported in previous studies, the waters of Bali have Serranidae diversity of 54 species or about 5.5 % of the composition of reef fish (Allen and Erdmann 2013). Other studies reported that the Epinephelinae subfamily has 159 species including 15 genera of *Cephalopolis* and 31 genera of *Epinephelus* (Allen and Adrim 2003).

Groupers is a favorite group in aquaculture industry, because it is able to reach significant size in weight of up to 400 kg and total length of 2.5 meters (Heemstra 1993), this fish became an essential commodity of aquaculture in Asia and some countries in the world (Chiu et al. 2008), both with floating net systems and in ponds that show an increase of 8-16 % starting in the 1900s (Pomeroy 2002). The high demand for grouper, both for consumption and for ornamental fisheries, makes grouper aquaculture more attractive with high market prices and export-oriented (Halim 2001). The Indo-Malayan Archipleago region plays a vital role in the grouper supply chain worldwide, and it has been estimated that about 80 % of the world's

production of groupers was reported from Asia, especially from Indonesia, the Philippines and Malaysia with a steady increasing numbers of production every year (Alcantara and Yambot 2016, Craig et al. 2011, Kadir et al. 2018, Sadovy de Mitcheson et al. 2013, Yulianto et al. 2015). Increased export values have been felt since 1980, with export values to several Asian countries (Singapore, Hong Kong, and China) (Nuraini and Hartati 2006), United States, and Europe (Halim 2001). The high level of human exploitation of groupers causes at least one-third of the genus of the subfamily Epinephelinae, especially the *Epinephelus* and *Mycteroperca* genera listed as endangered species (Morris et al. 2000) and requires very strict licensing and approval. For example, the giant groupers (*E. lanceolatus*) and the Napoleon wrasse (*C. undulatus*), have become vulnerable fish since they were established in 1996 by IUCN (Halim 2001). In addition, out of 163 grouper species across the globe, 12 % (20 species) are at a risk of extinction and 13 % (22 species) are considered to be nearly threatened based on the IUCN Red List criteria (Craig et al. 2011).

The limitations of the study of phylogenetic relationships between fish in subfamily Epinephelinae (*Epinephelus*, Serranidae) are still vital, given the complexity of the members of this family (Craig and Hastings 2007). *Epinephelus* distribution is quite extensive, around the Indo-west Pacific and Indo-Pacific (Heemstra and Randall 1993, Unsworth et al. 2007, Van Herwerden et al. 2002). In general, people only mention groupers, which are indicated by the spots on their body parts. The fish have a brownish to attractive red color associated with their diverse habitats from shallow water areas and very colorful coral reef ecosystems (Unsworth et al. 2007).

DNA barcoding believed to be one of the methods used globally to identify molecular approaches for animals and plants. This identification, the DNA in mitochondrial, becomes an important sequence that is considered capable of being a marker and has been accepted as a global bio-identification system for animals (Hebert et al. 2003, Ward et al. 2005). This identification is beneficial in specimens that are difficult to identify morphologically, such as larval stage, and organ fragments or morphologically incomplete specimens (Hebert et al. 2003). Various advantages of DNA coding are straightforward and useful universal tools that include all the animals both in the form of fresh and processed product samples (Giusti et al. 2017, Pepe et al. 2007). The accuracy of DNA-based identification is nearly 100 %, which indicates that this method can prove the identification of specimens under different environmental conditions

(Meyer and Paulay 2005). The barcoding system uses sequences that have a diversity in the single region of mitochondrial DNA, cytochrome c oxidase subunit I gene (COI), and then deposited to the GenBank database. The GenBank has become central to deposit diverse taxa from all parts of the world. With the increase of molecular databases, scientists have demonstrated their effectiveness in conducting DNA barcoding from freshwater fish to deep-sea fish (Lakra et al. 2011, Ward et al. 2005). Previous research has shown that mitochondrial DNA has a higher mutation rate compared to nuclear DNA by inheriting the maternal gene. Thus, researchers can obtain handy data for studying evolution between species, even within the same species (Waugh 2007). In this research, we performed the molecular identification of several Grouper from seven sampling sites (Java, Bali Island, and Aceh) with the COI gene region to understand the diversity and measure the genetic distance of each species, especially in the genus *Epinephelus*, *Cephalopholis*, and *Variola*.

MATERIALS AND METHODS

Sampling site

A total of 8 fish samples were collected from the five traditional fish markets around the Jawa Island during July 2019. In the northern part of Java, samples were obtained from the Banten (6°0'50.00'S-106°10'21.00"E), and Gresik (6°52'56.65'S-112°12'15.87"), while Southern Java was represented samples from Malang (8°26'06.65'S-112°40'55.31"), the Banyuwangi (8°12'07.52'S-114°23'07.18"E), and Bali (8°45'23.00'S-115°10'05.68"E). Here, we also collected a specimen from the Kutaradja fish traditional market in Aceh, the westernmost province of Sumatera (5°35'07.00'N-95°19'07.00"E). Morphologically identification conducted according to the guideline from FAO (Heemstra 1993), and species confirmation has been carried out with molecular identification carried out in this study using the COI gene region. No specific permit was required for this study due to collect from the local traditional fish market were dead upon purchasing. Before dissected, all specimen has been photographed by the digital camera.

DNA extraction and PCR

Each specimen has been collected and directly preserved in 90 % ethanol for further experimental purposes. Around one cm tissues was taken from the anal fin of each specimen, dissected and mix with 6X lysis buffer, which was further homogenized by the TissueLyser II (Qiagen). Genomic DNA extracted using an Accuprep® Genomic DNA Extraction Kit (Bioneer) according to the manufacturer's guidelines. Quantification of purified genomic DNA performed by Nanodrop (ThermoFisher Scientific D1000), aliquoted and stored at -70°C for further analysis.

PCR condition and Data Analysis

One set of universal fish primer targeting cytochrome c oxidase I (COI) region, FISH-BCL (5'-TCA ACY AAT CAY AAA GAT ATY GGC AC-3') and FISH-BCH (5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3') (Baldwin et al. 2009, Handy et al. 2011), used to obtain the partial sequences of COI gene. The PCR mixture (20µL) included 11.2 µL ultra-pure water, 1 µL primer forward and reverse (0.5 µM), 0.2 µL Ex Taq DNA polymerase (TaKaRa, Japan), 2 µL 10X ExTag Buffer, 2 µL dNTPs (1 µM, TaKaRa, Japan), and 2 µL genomic DNA as template. The PCR condition carried out under the following setting: 95°C for 5 min in initial denaturation, followed by denaturation at 95°C for 30 s in 40 cycles, 50°C for 30 s in annealing, and 72°C for 45 s in extension step, and a final extension at 72°C for 5 min. The PCR products were purified with the AccuPrep®Gel purification kit (Bioneer, Korea).

Phylogenetic analysis

All sequences were aligned, including reference sequences from the GenBank database (Table 1). The pairwise evolutionary distance among the family determined by the Kimura 2-Parameter method. The Neighbor-joining (NJ) tree constructed, and 1000 bootstrap analysis was carried by Mega7 program (Kumar et al. 2016).

Results

A total of 11 successful identification samples consisted of 3 genera, *Epinephelus* (5), *Cephalopholis* (3), *Variola* (1). In this study, the genus *Epinephelus* was more dominated the general catches of fishers, including *E. coioides*, *E. ongus*, *E. poecilonotus*, *E. areolatus*, *E. merra*. Meanwhile, other types are only in small quantities.

Genetic distance

Genetic distance analysis was carried out using Mega 7, which aligned all obtained queries (Table 1). The results of this analysis provide a description of the distance between species (interspecific) and in the same species (intraspecific). *Epinephelus areolatus* obtained from Aceh is not different from the reference sequences originating from Saudi Arabia (KU499597) by the genetic distance is zero. The same thing also happens to other genus *Epinephelus*, which also has genetic distance 0 with reference in the GenBank database except in *E. merra*. In *E. merra* there is a slight difference, although identification still refers to the same species. Genetic distance with specimens originating from Japan (AP005991) is only 0.004, indicating that *E.merra* species is an Indonesian haplotype. Whereas in *Cephalopholis* species, only *C. cyanostigma* was found in Indonesian haplotypes with a genetic distance of 0.002 with reference specimens from the Philippines (KU668647).

Table 1. The genetic distance of Epinephelinae compare to the reference from GenBank database

Species name	Genetic distance within species	Genetic distance between species
Clade I <i>Epinephelus</i>		
<i>E. areolatus</i>	0.000	0.152-0.181
<i>E. merra</i>	0.004	0.157-0.185
<i>E. ongus</i>	0.000	0.107-0.184
<i>E. poecilonotus</i>	0.000	0.107-0.119
<i>E. oioides</i>	0.000	0.119-0.181
Clade II <i>Cephalopholis</i> and <i>Variola</i>		
<i>C. miniata</i>	0.000	0.089-0.216
<i>C. sonnerati</i>	0.000	0.089-0.174
<i>C. cyanostigma</i>	0.002	0.150-0.202
<i>V. albimarginata</i>	0.000	0.173-0.206

Phylogenetic reconstruction

In the phylogenetic tree produced, two clades have been formed consisting of the genus *Epinephelus*, and the other clade consists of *Cephalopholis* and *Variola* (Figure 1). Morphologically, the *Epinephelus* group is dark gray to dark brown, while *Cephalopholis* and *Variola* are bright red body color (Figure 2). Although morphologically, the two clades show

differences, sometimes it is challenging for researchers and the public to distinguish each species. Besides, the giving of a variety of regional names also adds to the complexity of the naming so that molecular identification is expected to help in ensuring the types of fish that are identified and traded in traditional markets in some regions. The certainty of the name in the specie here is also essential in various scientific writings because it deals with scientific information that will be read by the general public, especially in academic purposes.

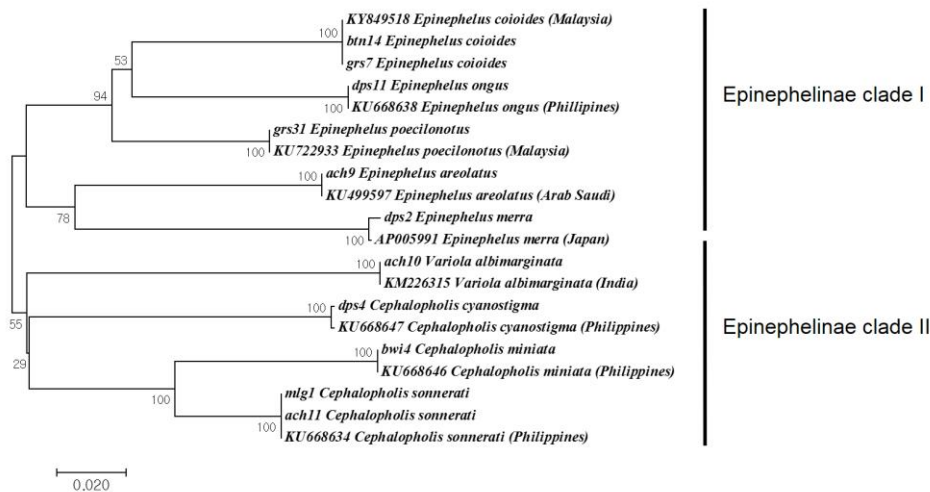


Figure 1. Phylogenetic tree of Epinephelinae including references from the GenBank database

Epinephelinae status in IUCN and CITES

Almost all grouper species in this study have the status of Least Concern (LC), while the grouper in international trade (CITES) is not evaluated (Table 2). However, *E. merra* has been reported as a causative agent of Ciguatera fish poisoning in several countries (Lewis 1986). This fish poisoning occurs in some countries such as Thailand (Toyoda et al. 1981), the Philippines (Montejo et al. 2020), Hong Kong (Sadovy 1997), Australia (Gillespie et al. 1986), and other countries (Chan 2015, Gaboriau et al. 2014, Randall 1958). However, there have been no reports of ciguatera in Indonesia (Chan 2015).

Tabel 2. IUCN and CITES status of all grouper specimens

Species name	English name	Distribution	IUCN	CITES	Threat to humans
<i>E. areolatus</i>	Areolate grouper	Indo-Pacific	LC	NE	Harmless
<i>E. merra</i>	Honeycomb grouper	Indo-Pacific	LC	NE	Reports of ciguatera poisoning
<i>E. ongus</i>	White-streaked grouper	Indo-West Pacific	LC	NE	Harmless
<i>E. poecilnotus</i>	Dot-dash grouper	Indo-West Pacific	LC	NE	Harmless
<i>E. oioides</i>	Orange-spotted grouper	Indo-West Pacific	LC	NE	Harmless
<i>C. miniata</i>	Coral hind	Indo-Pacific	LC	NE	Harmless
<i>C. sonnerati</i>	Tomato hind	Indo-Pacific	LC	NE	Harmless
<i>C. cyanostigma</i>	Blue-spotted hind	Western Pacific	LC	NE	Harmless
<i>V. albimarginata</i>	White-edged lyre tail	Indo-Pacific	LC	NE	Harmless

LC: Least Concern

NE: Not Evaluated

Discussion

Grouper has become a leading commodity in aquaculture in several Asian countries and several other continents (Halim 2001). The success of aquaculture is demonstrated by many studies on the reproductive biology that are sufficient detailed (Andamari et al. 2007, Andrade et al. 2003), hatchery (Rimmer 2000, Sugama et al. 2012), larval rearing to a variety of grow-up system (Fukuhara 1989, Pomeroy 2002). Several studies have shown good results in hatching several species of groupers such as *E. coioides*, *E. fuscoguttatus*, *Plectropomus leopardus*, and *Cromileptes altivelis* (Rimmer 2000), *E. fuscoguttatus* (Sugama et al. 2017). Research on the grow-up system also showed excellent results both in the floating net system (Baliao et al. 2000) and in the aquaculture system in pond (Baliao et al. 1998).

Trade-in grouper in the live fish becomes a superior commodity because the price is quite high when compared to fresh dead fish. The demand for live fish forms continues to increase, so fishers prefer to sell live fish (Halim 2001). However, many aquaculture activities are currently conducting such as breeding between species, which are expected to produce variants that have growth and other good traits such as disease resistance, good growth, resistance to extreme environments, and at the same time, making sterile fish (Hickling 1968). For example, the crossing of tiger grouper and *E. fuscoguttatus* and *E. polyphkadion* grouper, which produce hybrid grouper with excellent growth performance (James et al. 1999). However, please note that the pure parent lines that will be breeding must be well known so that the study of this breeding

effect can be done well. Other breeding was also developed on *E. costae* with *E. marginatus* (Glamuzina et al. 2001), *Plectropomus leopardus* with *Plectropomus maculatus* (Frisch and Hobbs 2007), and *E. coioides* with *E. lanceolatus* (Kiryakit et al. 2011, Sutthinon et al. 2015).

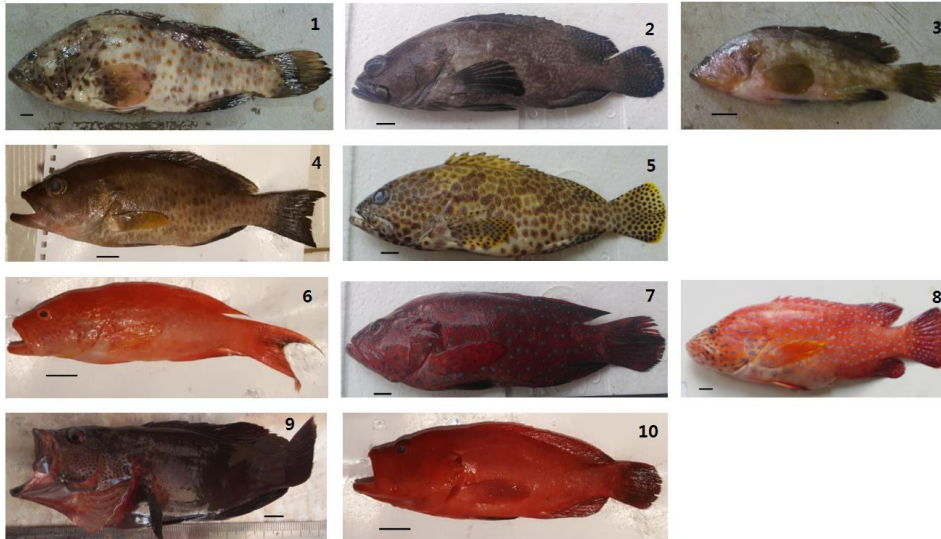


Figure 2. grs7 *E. coioides*(1); dps11 *E.ongus* (2); grs31 *E. poecilonotus* (3); ach9 *E. areolatus* (4); dps2 *E. merra* (5); ach10 *Variola albimarginata* (6); dps4 *Cephalopholis cyanostigma* (7); bwi4 *C. miniata* (8); mlg11 *C. sonnerati* (9) ; ach11 *C. sonnerati* (10)

Some breeding activities between *Epinephelus* species have been carried out in Indonesia. One of them is a hybrid between *E. microdon* (male) and *E. fuscoguttatus* (female) by producing seeds that have the title grouper cantik (Ismi 2014). Another type of hybrid is the grouper cantang, which is a hybrid of *E. fuscoguttatus* and *E. lanceolatus* (Shapawi et al. 2019). Another hybrid type is the kustang grouper, which is breeding of *Cromileptes altivelis* with *E. coioides* (Yu et al. 2004). Breeding between *E. microdon* and *E. lanceolatus* has been carried out, which produces a new type of hybrid grouper (Sutarmat and Yudha 2016). Also, back-cross hybrids have also been carried out between hybrids (*E. coioides* x *E. lanceolatus*) breeding with *E. lanceolatus* (Luan et al. 2016). Back-cross breeding efforts are carried out to produce seeds that are more productive and have the advantage of better traits such as a high survival rate than the previous generation.

Due to the intensive exploitation of grouper species in the world, only a small number of studies on the genetic diversity of the species have been carried out. In Indonesia, although intensive aquaculture activities are carried out, only a few types of grouper have been reported about genetic studies such as *E. coioides* (Antoro et al. 2006), *E. siullus* (Parenrengi and Tenriulo 2008), *Cromileptes altivelis* (Sugama et al. 2017, Susanto et al. 2011) and several other types of grouper *E. areolatus*, *E. merra*, *E. ongus*, *E. fasciatus*, *E. coioides*, *E. coeruleopunctatus*, and *E. longispinis* (Jefri et al. 2015). Nevertheless, barcoding studies of several types of grouper have been carried out from some regions in Java and Bali (Andriyono et al. 2020), Makassar (Parenrengi and Tenriulo 2008), Lampung and Papua (Jefri et al. 2015). This report is the first report involving specimens from Aceh and at the same time comparing with references from the GenBank database.

The use of genetic information from the GenBank database provides a picture of the similarities between species groups, even though the species has a large habitat distribution in the Indo-Pacific region (Randall and Heemstra 1991, Unsworth et al. 2007). It is estimated, the grouper included in coral reef fish associated has experienced speciation that allow it to have variations in its genetic composition (Rocha and Bowen 2008). Specialization of reef fishes has illustrated that open access sea also has its boundaries and niches so that many species will be different and adapt to each type of coral reef ecosystem. In this study, only two types (*E. merra* and *C. cyanostigma*) were found to be Indonesian haplotypes and differ from the same species from the alignment of the DNA reference sequence.

The distribution of *E. merra* is quite extensive with major habitats found in the Indo-Pacific region including South Africa to French Polynesia and even in the central Pacific (Craig et al. 2011, Muths and Bourjea 2011, Randall and Heemstra 1991) which generally inhabit waters bring (<20 m depth). Its natural habitat is a coral reef area and becomes important in artisanal fisheries as a source of protein and food for coastal communities (Heemstra 1993). Studies on *E. merra* diversity also indicate genetic variation in Madagascar, the Maldives, and small islands in the West Indian Ocean (Muths et al. 2015).

Meanwhile, *C. cyanostigma* was also identified in Maluku waters, which has a fairly high diversity of the genus *Cephalopolis* with 11 species inhabiting the waters of this region (Pattikawa 2017) and North Sulawesi (Tokeshi et al. 2013). Based on previous reports, the genus *Cephalopolis* consists of 22 species that have habitat distribution in the Pacific Ocean region

(Heemstra 1993), which tend to have a cryptic habit on coral reef ecosystems (Shpigel and Fishelson 1989). Of the 22 known species of *Cephalopholis*, only nine species have been studied in terms of their biology. Many studies on several aspects of biology, including sexual maturity (Shapiro 1987), spawning (Donaldson 1989), territoriality and their ecology (Shpigel and Fishelson 1991), and sex change and population structure of *Cephalopholis* (Siau 1994). Meanwhile, this report is the first report on genetic distance in *C. cyanostigma* in Indonesia based on the COI sequences that show the existence of different haplotypes with the same species in the Philippines. The haplotype was formed due to geographical different, the Philippine species is an Indo West-pacific species, while the sample in this study is a species of the Indian ocean. This result needs to get attention for further research on genetic variation of *Cephalopholis* in Indonesian regions with a larger number of samples.

The haplotypes found in *E. merra* and *C. cyanostigma* can be known by phylogenetic tree analysis, which shows a slight distance with sequence reference (Figure 1). This study is quite helpful in giving an idea of the haplotype formed. Also, through this phylogenetic tree, it is known that the genus *Epinephelus* forms a separate clade separating from *Cephalopolis* and *Variola*. In this study, *Cephalopholis* and *Variola* are in the same clade, but separated in several branches. Morphologically, these two genera can be easily distinguished by observing the caudal fin (**Figure 2**). In *Variola* species have caudal fin lunate (Baldwin 2003), than *Cephalopholis* have rounded caudal fin (Allen 2015). Thus, the phylogenetic tree places the two genera in separate branches (**Figure 1**). Although the number of samples is still small, this report reinforces that the Epinephelinae group has several clades, which are genetic variations in the grouper.

Conclusion

In this study, we found genetic variation in *E. merra* and *C. cyanostigma* that showed the existence of Indonesian haplotypes. This result was figure-out genetic distance of some species in this report. The genetic distance of *E. merra* and *C. cyanostigma* are 0.004 and 0.002, which is slightly different from sequences from Japan and the Philippines, respectively. It is necessary more in-depth studies of *C. cyanostigma*, due to the limited study of genetic variation, especially in Indonesia. The study of *C. cyanostigma* is very supportive in efforts to develop this species as

an aquaculture commodity in the future, such as *Epinephelus*. An in-depth study of biological characteristics, including reproductive biology, ecology, and other specific characteristics, will be beneficial in both conservation and domestication.

Acknowledgments

The authors would like to express our sincere gratitude for the initiation of collaborative research between Airlangga University (Surabaya), Syiah Kuala University (Aceh), and Hasanuddin University (Makassar) which have given great importance to the development of studies in Indonesia. Fisheries studies in Java, Sumatra, Sulawesi, Kalimantan, and Papua require the support of many collaborators to produce quality and beneficial research for Indonesia.

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Egyptian Journal of Aquatic Biology & Fisheries
 Zoology Department, Faculty of Science,
 Ain Shams University, Cairo, Egypt.
 ISSN 1110 – 6131
 Vol. XX(X): XXX – XXX (2020)
 www.ejabf.journals.ekb.eg



Genetic diversity and phylogenetic reconstruction of grouper (Serranidae) from Sunda Land, Indonesia

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ARTICLE INFO

Article History:

Received: xx, 2020

Accepted: xx, 2020

Online: xx, 2020

Keywords:

commercial grouper, Serranidae, genetic study, Sunda land, Indonesia

ABSTRACT

Groupers are coral reefs associated and favored in the aquaculture industry. Aquaculture system has been successfully carried out with a floating cage system as well as in an aquaculture system in a pond. Lately, breeding activities in groupers have produced hybrid species that are expected to increase production and fulfillment the demand of groupers in live fish market in Singapore, Taiwan, and China. The study of biology has supported the success of many of groupers, but information on genetic variation in commercial groupers is still very limited. This report is a preliminary study of genetic diversity in commercial groups from Java, Bali, and Aceh, which is the Sunda land region in western Indonesia. Eleven specimens have been identified with the barcode region (Cytochrome c Oxidase subunit I gene region). As a result, two species identified as Indonesian haplotypes, namely *Epinephelus merra* and *Cephalopholis cyanostigma*. Phylogenetic tree analysis produces two large clades, namely Clade I (*Epinephelus*) and Clade II (*Cephalopholis* and *Variola*), which are clearly separated in the subfamily Epinephelinae. However, in-depth studies of genetic variation need to be more accurate by increasing the number of specimens from various regions in Indonesia to describe genetic diversity comprehensively.

INTRODUCTION

A grouper is a group of fish that inhabit in the coral reef ecosystems and rocky shallow waters as their primary habitat. Several species found in shallow waters that have sandy mud substrate, which makes the grouper habitat variation quite diverse. The diversity of grouper habitat also makes groupers have a variety of species. As reported in previous studies, the waters of Bali have Serranidae diversity of 54 species or about 5.5 % of the composition of reef fish (Allen and Erdmann, 2013). Other studies reported

that the Epinephelinae subfamily has 159 species, including 15 genera of *Cephalopolis* and 31 genera of *Epinephelus* (Allen and Adrim, 2003).

Groupers are an intimate group in the aquaculture industry because it can reach a significant size in weight of up to 400 kg and the total length of 2.5 meters (Heemstra, 1993), this fish became an essential commodity of aquaculture in Asia and some countries in the world (Chiu et al., 2008), both with floating net systems and in ponds that show an increase of 8-16 % starting in the 1900s (Pomeroy, 2002). The high demand for grouper, both for consumption and for ornamental fisheries, makes grouper aquaculture more attractive with high market prices and export-oriented (Halim, 2001). The Indo-Malayan Archipelago region plays a vital role in the grouper supply chain worldwide. It has been estimated that about 80 % of the world's production of groupers was reported from Asia, mainly from Indonesia, the Philippines and Malaysia with a steadily increasing number of products every year (Craig et al., 2011; Sadovy de Mitcheson et al., 2013; Yulianto et al., 2015; Alcantara and Yambot, 2016; and Kadir et al., 2018). Increased export values have been felt since 1980, with export values to several Asian countries (Singapore, Hong Kong, and China) (Nuraini and Hartati, 2006), United States, and Europe (Halim, 2001). The high level of human exploitation of groupers causes at least one-third of the genus of the subfamily Epinephelinae, especially the *Epinephelus* and *Mycteroperca* genera listed as endangered species (Morris et al., 2000) and requires very strict licensing and approval. For example, the giant groupers (*E. lanceolatus*) and the Napoleon wrasse (*C. undulatus*), have become vulnerable fish since they were established in 1996 by IUCN (Halim, 2001). In addition, out of 163 grouper species across the globe, 12 % (20 species) are at risk of extinction, and 13 % (22 species) are considered to be nearly threatened based on the IUCN Red List criteria (Craig et al., 2011).

The limitations of the study of phylogenetic relationships between fish in subfamily Epinephelinae (*Epinephelus*, Serranidae) are still vital, given the complexity of the members of this family (Craig and Hastings, 2007). *Epinephelus* distribution is quite extensive, around the Indo-west Pacific and Indo-Pacific (Heemstra and Randall, 1993; Van Herwerden et al., 2002; and Unsworth et al. 2007). In general, people only mention groupers, which are indicated by the spots on their body parts. The fish have a brownish to attractive red colour associated with their diverse habitats from shallow water areas and very colourful coral reef ecosystems (Unsworth et al., 2007)

DNA barcoding believed to be one of the methods used globally to identify molecular approaches for animals and plants. This identification, the DNA in mitochondrial, becomes a remarkable sequence that is considered capable of being a marker and has been accepted as a global bio-identification system for animals (Hebert et al., 2003 and Ward et al., 2005). This identification is beneficial in specimens that are difficult to identify morphologically, such as larval stage, and organ fragments or morphologically incomplete specimens (Hebert et al., 2003). Various advantages of DNA coding are straightforward and useful universal tools that include all the animals both in the form of fresh and processed product samples (Pepe et al., 2007 and Giusti et al. 2017). The accuracy of DNA-based identification is nearly 100 %, which indicates that this method can prove the identification of specimens under different environmental conditions (Meyer and Paulay, 2005). The barcoding system uses sequences that have a diversity in the single region of mitochondrial DNA, cytochrome c oxidase subunit I gene

(COI), and then deposited to the GenBank database. The GenBank has become central to deposit diverse taxa from all parts of the world. With the increase of molecular databases, scientists have demonstrated their effectiveness in conducting DNA barcoding from freshwater fish to deep-sea fish (Ward et al., 2005 and Lakra et al., 2011). Previous research has shown that mitochondrial DNA has a higher mutation rate compared to nuclear DNA by inheriting the maternal gene. Thus, researchers can obtain handy data for studying evolution between species, even within the same species (Waugh, 2007). In this research, we performed the molecular identification of several grouper from seven sampling sites (Java, Bali Island, and Aceh) with the COI gene region to understand the diversity and measure the genetic distance of each species, especially in the genus *Epinephelus*, *Cephalopholis*, and *Variola*.

MATERIALS AND METHODS

Sampling site

A total of 8 fish samples were collected from the five traditional fish markets around Jawa Island during July 2019. In the northern part of Java, samples were obtained from the Banten (6°0'50.00'S-106°10'21.00"E), and Gresik (6°52'56.65"S-112°12'15.87"), while Southern Java was represented samples from Malang (8°26'06.65"S-112°40'55.31"), the Banyuwangi (8°12'07.52"S-114°23'07.18"E), and Bali (8°45'23.00"S-115°10'05.68"E). Here, we also collected a specimen from the Kutaradja fish traditional market in Aceh, the westernmost province of Sumatera (5°35'07.00"N-95°19'07.00"E). Morphologically identification conducted according to the guideline from FAO (Heemstra, 1993), and species confirmation has been carried out with molecular identification carried out in this study using the COI gene region. No specific permit was required for this study due to collect from the local traditional fish market were dead upon purchasing. Before dissected, all specimen has been photographed by the digital camera.

DNA extraction and PCR

Each specimen has been collected and directly preserved in 90 % ethanol for further experimental purposes. Around one cm tissues was taken from the anal fin of each specimen, dissected and mix with 6X lysis buffer, which was further homogenized by the TissueLyser II (Qiagen). Genomic DNA extracted using an Accuprep® Genomic DNA Extraction Kit (Bioneer) according to the manufacturer's guidelines. Quantification of purified genomic DNA performed by Nanodrop (ThermoFisher Scientific D1000), aliquoted and stored at -70°C for further analysis.

PCR condition and Data Analysis

One set of universal fish primer targeting cytochrome c oxidase I (COI) region, FISH-BCL (5'-TCA ACY AAT CAY AAA GAT ATY GGC AC-3') and FISH-BCH (5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3') (Baldwin et al., 2009 and Handy et al., 2011), used to obtain the partial sequences of COI gene. The PCR mixture (20µL) included 11.2 µL ultra-pure water, 1 µL primer forward and reverse (0.5 µM), 0.2 µL Ex Taq DNA polymerase (TaKaRa, Japan), 2 µL 10X ExTag Buffer, 2 µL dNTPs (1 µM, TaKaRa, Japan), and 2 µL genomic DNA as template. The PCR condition carried out

under the following setting: 95°C for 5 min in initial denaturation, followed by denaturation at 95°C for 30 s in 40 cycles, 50°C for 30 s in annealing, and 72°C for 45 s in extension step, and a final extension at 72°C for 5 min. The PCR products were purified with the AccuPrep®Gel purification kit (Bioneer, Korea).

Phylogenetic analysis

All sequences were aligned, including reference sequences from the GenBank database (**Table 1**). The pairwise evolutionary distance among the family determined by the Kimura 2-Parameter method. The Neighbor-joining (NJ) tree constructed, and 1000 bootstrap analysis was carried by Mega7 program (**Kumar et al., 2016**).

RESULTS

A total of 11 successful identification samples consisted of three genera, *Epinephelus* (5), *Cephalopholis* (3), *Variola* (1). In this study, the genus *Epinephelus* was more dominated the general catches of fishers, including *E. coioides*, *E. ongunus*, *E. poecilonotus*, *E. areolatus*, *E. merra*. Meanwhile, other types are only in small quantities.

Table 1. The genetic distance of Epinephelinae compare to the reference from GenBank database

Species name	Genetic distance within species	Genetic distance between species
Clade I (<i>Epinephelus</i>)		
<i>E. areolatus</i>	0.000	0.152-0.181
<i>E. merra</i>	0.004	0.157-0.185
<i>E. ongunus</i>	0.000	0.107-0.184
<i>E. poecilonotus</i>	0.000	0.107-0.119
<i>E. coioides</i>	0.000	0.119-0.181
Clade II (<i>Cephalopholis</i> and <i>Variola</i>)		
<i>C. miniata</i>	0.000	0.089-0.216
<i>C. sonnerati</i>	0.000	0.089-0.174
<i>C. cyanostigma</i>	0.002	0.150-0.202
<i>V. albimarginata</i>	0.000	0.173-0.206

Genetic distance

Genetic distance analysis was carried out using Mega 7, which aligned all obtained queries (**Table 1**). The results of this analysis provide a description of the distance between species (interspecific) and in the same species (intraspecific). *Epinephelus areolatus* obtained from Aceh is not different from the reference sequences originating from Saudi Arabia (KU499597) by the genetic distance is zero. The same thing also happens to another genus *Epinephelus*, which also has genetic distance 0 with reference in the GenBank database except in *E. merra*. In *E. merra* there is a slight difference, although identification still refers to the same species. Genetic distance with specimens originating from Japan (AP005991) is only 0.004, indicating

that *E. merra* species is an Indonesian haplotype. Whereas in *Cephalopholis* species, only *C. cyanostigma* was found in Indonesian haplotypes with a genetic distance of 0.002 with reference specimens from the Philippines (KU668647).

Phylogenetic reconstruction

In the phylogenetic tree produced, two clades have been formed consisting of the genus *Epinephelus*, and the other clade consists of *Cephalopholis* and *Variola* (**Figure 1**). Morphologically, the *Epinephelus* group is dark grey to dark brown, while *Cephalopholis* and *Variola* are bright red body-colour (**Figure 2**). Although morphologically, the two clades show differences, sometimes it is challenging for researchers and the public to distinguish each species. Besides, the giving of various regional names also adds to the complexity of naming. So that the molecular identification carried out in this study is expected to help ensure the types of fish identified and traded in traditional markets in several areas. The certainty of the name in the specie here is also essential in various scientific writings because it deals with scientific information that will be read by the general public, especially in academic purposes.

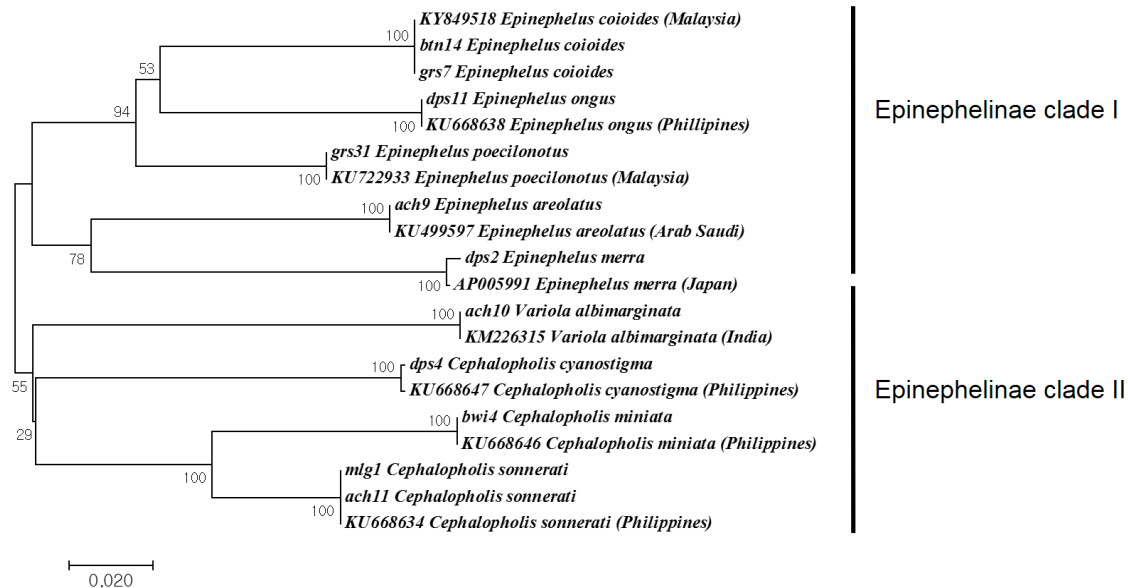


Figure 1. Phylogenetic tree of Epinephelinae including references from the GenBank database

Epinephelinae status in IUCN and CITES

Almost all grouper species in this study have the status of Least Concern (LC), while the grouper in international trade (CITES) is not evaluated (**Table 2**). However, *E. merra* has been reported as a causative agent of Ciguatera fish poisoning in several countries (**Lewis, 1986**). This fish poisoning occurs in some countries such as Thailand (**Toyoda et al., 1981**), the Philippines (**Montejo et al., 2020**), Hong Kong (**Sadovy, 1997**), Australia (**Gillespie et al., 1986**), and other countries (**Randall, 1958; Chan 2015; and Gaboriau et al., 2014, .**). However, there have been no reports of ciguatera in Indonesia (**Chan, 2015**).

Tabel 2. IUCN and CITES status of all grouper specimens

Species name	English name	Distribution	IUCN	CITES	Threat to humans
<i>E. areolatus</i>	Areolate grouper	Indo-Pacific	LC	NE	Harmless
<i>E. merra</i>	Honeycomb grouper	Indo-Pacific	LC	NE	Reports of ciguatera poisoning
<i>E. ongus</i>	White-streaked grouper	Indo-West Pacific	LC	NE	Harmless
<i>E. poecilonotus</i>	Dot-dash grouper	Indo-West Pacific	LC	NE	Harmless
<i>E. oioides</i>	Orange-spotted grouper	Indo-West Pacific	LC	NE	Harmless
<i>C. miniata</i>	Coral hind	Indo-Pacific	LC	NE	Harmless
<i>C. sonnerati</i>	Tomato hind	Indo-Pacific	LC	NE	Harmless
<i>C. cyanostigma</i>	Blue-spotted hind	Western Pacific	LC	NE	Harmless
<i>V. albimarginata</i>	White-edged lyre tail	Indo-Pacific	LC	NE	Harmless

LC: Least Concern

NE: Not Evaluated

DISCUSSION

Grouper has become a leading commodity in aquaculture in several Asian countries and several other continents (Halim, 2001). The success of aquaculture is demonstrated by many studies on the reproductive biology that are sufficient detailed (Andrade et al., 2003 and Andamari et al., 2007,), hatchery (Rimmer, 2000, and Sugama et al. 2012), larval rearing to a variety of grow-up system (Fukuhara, 1989 and Pomeroy, 2002). Several studies have shown good results in hatching several species of groupers such as *E. coioides*, *E. fuscoguttatus*, *Plectropomus leopardus*, and *Cromileptes altivelis* (Rimmer, 2000), *E. fuscoguttatus* (Sugama et al., 2017). Research on the grow-up system also showed excellent results both in the floating net system (Baliao et al., 2000) and in the aquaculture system in the pond (Baliao et al., 1998).

Trade-in grouper in the live fish becomes a superior commodity because the price is quite high when compared to fresh dead fish. The demand for live fish forms continues to increase, so fishers prefer to sell live fish (Halim, 2001). However, many aquaculture activities are currently conducting such as breeding between species, which are expected to produce variants that have growth and other good traits such as disease resistance, good growth, resistance to extreme environments, and at the same time, making sterile fish (Hickling, 1968). For example, the crossing of tiger grouper and *E. fuscoguttatus* and *E. polyphkadion* grouper, which produce hybrid grouper with excellent growth performance (James et al., 1999). However, please note that the pure parent lines that will be breeding must be well known so that the study of this breeding effect can be done well. Other breeding was also developed on *E. costae* with *E. marginatus* (Glamuzina et al., 2001), *Plectropomus leopardus* with *Plectropomus maculatus* (Frisch and Hobbs, 2007), and *E. coioides* with *E. lanceolatus* (Kiryakit et al., 2011 and Sutthinon et al., 2015).

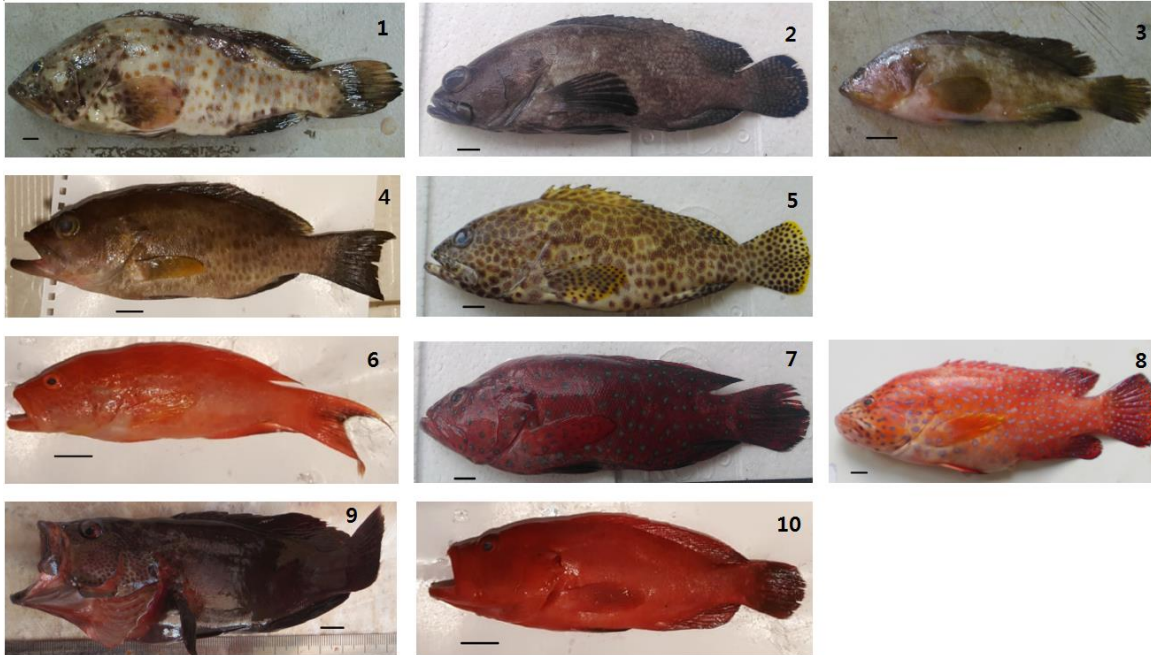


Figure 2. grs7 *E. coioides*(1); dps11 *E.ongus* (2); grs31 *E. poecilonotus* (3); ach9 *E. areolatus* (4); dps2 *E. merra* (5); ach10 *Variola albimarginata* (6); dps4 *Cephalopholis cyanostigma* (7); bwi4 *C. miniata* (8); mlg11 *C. sonnerati* (9) ; ach11 *C. sonnerati* (10)

Some breeding activities between *Epinephelus* species have been carried out in Indonesia. One of them is a hybrid between *E. microdon* (male) and *E. fuscoguttatus* (female) by producing seeds that have the title grouper cantik (Ismi, 2014). Another type of hybrid is the grouper cantang, which is a hybrid of *E. fuscoguttatus* and *E. lanceolatus* (Shapawi et al., 2019). Another hybrid type is the kustang grouper, which is breeding of *Cromileptes altivelis* with *E. coioides* (Yu et al., 2004). Breeding between *E. microdon* and *E. lanceolatus* has been carried out, which produces a new type of hybrid grouper (Sutarmat and Yudha, 2016). Also, back-cross hybrids have also been carried out between hybrids (*E. coioides* x *E. lanceolatus*) breeding with *E. lanceolatus* (Luan et al., 2016). Back-cross breeding efforts are carried out to produce seeds that are more productive and have the advantage of better traits such as a high survival rate than the previous generation.

Due to the intensive exploitation of grouper species in the world, only a small number of studies on the genetic diversity of the species have been carried out. In Indonesia, although intensive aquaculture activities are carried out, only a few types of grouper have been reported about genetic studies such as *E. coioides* (Antoro et al., 2006), *E. siullus* (Parenrengi and Tenriulo, 2008), *Cromileptes altivelis* (Susanto et al., 2011 and Sugama et al., 2017,) and several other types of grouper *E. areolatus*, *E. merra*, *E. ongus*, *E. fasciatus*, *E. coioides*, *E. coeruleopunctatus*, and *E. longispinis* (Jefri et al. 2015). Nevertheless, barcoding studies of several types of grouper have been carried out from some regions in Java and Bali (Andriyono et al., 2020), Makassar (Parenrengi and Tenriulo, 2008), Lampung and Papua (Jefri et al., 2015). This report is the first report involving specimens from Aceh and at the same time comparing with references from the GenBank database.

The use of genetic information from the GenBank database provides a picture of the similarities between species groups, even though the species has a large habitat distribution in the Indo-Pacific region (**Randall and Heemstra, 1991** and **Unsworth et al. 2007**). It is estimated, the grouper included in coral reef fish associated has experienced speciation that allows it to have variations in its genetic composition (**Rocha and Bowen, 2008**). Specialization of reef fishes has illustrated that open access sea also has its boundaries and niches so that many species will be different and adapt to each type of coral reef ecosystem. In this study, only two types (*E. merra* and *C. cyanostigma*) were found to be Indonesian haplotypes and differ from the same species from the alignment of the DNA reference sequence.

The distribution of *E. merra* is quite extensive with significant habitats found in the Indo-Pacific region including South Africa to French Polynesia and even in the central Pacific (**Randall and Heemstra, 1991; Craig et al., 2011; and Muths and Bourjea, 2011**) which generally inhabit waters bring (<20 m depth). Its natural habitat is a coral reef area and becomes essential in artisanal fisheries as a source of protein and food for coastal communities (**Heemstra, 1993**). Studies on *E. merra* diversity also indicate genetic variation in Madagascar, the Maldives, and small islands in the West Indian Ocean (**Muths et al., 2015**).

Meanwhile, *C. cyanostigma* was also identified in Maluku waters, which has a reasonably high diversity of the genus *Cephalopholis* with 11 species inhabiting the waters of this region (**Pattikawa, 2017**) and North Sulawesi (**Tokeshi et al., 2013**). Based on previous reports, the genus *Cephalopholis* consists of 22 species that have habitat distribution in the Pacific Ocean region (**Heemstra, 1993**), which tend to have a cryptic habit on coral reef ecosystems (**Shpigel and Fishelson, 1989**). Of the 22 known species of *Cephalopholis*, only nine species have been studied in terms of their biology. Many studies on several aspects of biology, including sexual maturity (**Shapiro 1987**), spawning (**Donaldson, 1989**), territoriality and their ecology (**Shpigel and Fishelson, 1991**), and sex change and population structure of *Cephalopholis* (**Siau, 1994**). Meanwhile, this report is the first report on genetic distance in *C. cyanostigma* in Indonesia based on the COI sequences that show the existence of different haplotypes with the same species in the Philippines. The haplotype was formed due to geographical different, the Philippine species is an Indo West-pacific species, while the sample in this study is a species of the Indian ocean. This result needs to get attention for further research on genetic variation of *Cephalopholis* in Indonesian regions with a more significant number of samples.

The haplotypes found in *E. merra* and *C. cyanostigma* can be known by phylogenetic tree analysis, which shows a slight distance with sequence reference (**Figure 1**). This study is quite helpful in giving an idea of the haplotype formed. Also, through this phylogenetic tree, it is known that the genus *Epinephelus* forms a separate clade separating from *Cephalopholis* and *Variola*. In this study, *Cephalopholis* and *Variola* are in the same clade but separated in several branches. Morphologically, these two genera can be easily distinguished by observing the caudal fin (**Figure 2**). In *Variola* species have caudal fin lunate (**Baldwin, 2003**), than *Cephalopholis* have rounded caudal fin (**Allen, 2015**). Thus, the phylogenetic tree places the two genera in separate branches (**Figure 1**). Although the number of samples is still small, this report

reinforces that the Epinephelinae group has several clades, which are genetic variations in the grouper.

CONCLUSION

In this study, we found genetic variation in *E. merra* and *C. cyanostigma* that showed the existence of Indonesian haplotypes. This result was figure-out genetic distance of some species in this report. The genetic distance of *E. merra* and *C. cyanostigma* are 0.004 and 0.002, which is slightly different from sequences from Japan and the Philippines, respectively. It is necessary more in-depth studies of *C. cyanostigma*, due to the limited study of genetic variation, especially in Indonesia. The study of *C. cyanostigma* is very supportive in efforts to develop this species as an aquaculture commodity in the future, such as *Epinephelus*. An in-depth study of biological characteristics, including reproductive biology, ecology, and other specific characteristics, will be beneficial in both conservation and domestication.

ACKNOWLEDGMENTS

The authors would like to express our sincere gratitude for the initiation of collaborative research between Airlangga University (Surabaya), Syiah Kuala University (Aceh), and Hasanuddin University (Makassar) which have given great importance to the development of studies in Indonesia. Fisheries studies in Java, Sumatra, Sulawesi, Kalimantan, and Papua require the support of many collaborators to produce quality and beneficial research for Indonesia.

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Egyptian Journal of Aquatic Biology & Fisheries
 Zoology Department, Faculty of Science,
 Ain Shams University, Cairo, Egypt.
 ISSN 1110 – 6131
 Vol. 24(3): 403 – 415 (2020)
 www.ejabf.journals.ekb.eg



Genetic diversity and phylogenetic reconstruction of grouper (Serranidae) from Sunda Land, Indonesia

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ARTICLE INFO

Article History:

Received: May 7, 2020

Accepted: May 25, 2020

Online: May 29, 2020

Keywords:

Commercial groupers,
 Serranidae,
 Genetic study,
 Sunda land,
 Indonesia

ABSTRACT

Groupers are coral reefs associated and favored in the aquaculture industry. Aquaculture system has been successfully carried out with a floating cage system as well as in an aquaculture system in a pond. Lately, breeding activities in groupers have produced hybrid species that are expected to increase production and fulfillment of the demand of groupers in the live fish market in Singapore, Taiwan, and China. The study of biology has supported the success of many of groupers, but information on genetic variation in commercial groupers is still very limited. This report is a preliminary study of genetic diversity in commercial groups from Java, Bali, and Aceh, which is the Sunda land region in western Indonesia. Eleven specimens have been identified with the barcode region (Cytochrome c Oxidase subunit I gene region). As a result, two species were identified as Indonesian haplotypes, namely *Epinephelus merra* and *Cephalopholis cyanostigma*. Phylogenetic tree analysis produces two large clades, namely Clade I (*Epinephelus*) and Clade II (*Cephalopholis* and *Variola*), which are clearly separated in the subfamily Epinephelinae. However, in-depth studies of genetic variation need to be more accurate by increasing the number of specimens from various regions in Indonesia to describe genetic diversity comprehensively.

INTRODUCTION

A grouper is a group of fish that inhabit in the coral reef ecosystems and rocky shallow waters as their primary habitat. Several species found in shallow waters that have sandy mud substrate, which makes the grouper habitat variation quite diverse. The diversity of grouper habitat also makes groupers have a variety of species. As reported in previous studies, the waters of Bali have Serranidae diversity of 54 species or about 5.5 % of the composition of reef fish (Allen and Erdmann, 2013). Other studies reported

that the Epinephelinae subfamily has 159 species, including 15 genera of *Cephalopolis* and 31 genera of *Epinephelus* (Allen and Adrim, 2003).

Groupers are an intimate group in the aquaculture industry because it can reach a significant size in weight of up to 400 kg and the total length of 2.5 meters (Heemstra, 1993), this fish became an essential commodity of aquaculture in Asia and some countries in the world (Chiu *et al.*, 2008), both with floating net systems and in ponds that show an increase of 8-16 % starting in the 1900s (Pomeroy, 2002). The high demand for grouper, both for consumption and for ornamental fisheries, makes grouper aquaculture more attractive with high market prices and export-oriented (Halim, 2001). The Indo-Malayan Archipelago region plays a vital role in the grouper supply chain worldwide. It has been estimated that about 80 % of the world's production of groupers was reported from Asia, mainly from Indonesia, the Philippines and Malaysia with a steadily increasing number of products every year (Craig *et al.*, 2011; Sadovy de Mitcheson *et al.*, 2013; Yulianto *et al.*, 2015; Alcantara and Yambot, 2016; and Kadir *et al.*, 2018). Increased export values have been felt since 1980, with export values to several Asian countries (Singapore, Hong Kong, and China) (Nuraini and Hartati, 2006), United States, and Europe (Halim, 2001). The high level of human exploitation of groupers causes at least one-third of the genus of the subfamily Epinephelinae, especially the *Epinephelus* and *Mycteroperca* genera listed as endangered species (Morris *et al.*, 2000) and requires very strict licensing and approval. For example, the giant groupers (*E. lanceolatus*) and the Napoleon wrasse (*C. undulatus*), have become vulnerable fish since they were established in 1996 by IUCN (Halim, 2001). In addition, out of 163 grouper species across the globe, 12 % (20 species) are at risk of extinction, and 13 % (22 species) are considered to be nearly threatened based on the IUCN Red List criteria (Craig *et al.*, 2011).

The limitations of the study of phylogenetic relationships between fish in subfamily Epinephelinae (*Epinephelus*, Serranidae) are still vital, given the complexity of the members of this family (Craig and Hastings, 2007). *Epinephelus* distribution is quite extensive, around the Indo-west Pacific and Indo-Pacific (Heemstra and Randall, 1993; Van Herwerden *et al.*, 2002; and Unsworth *et al.* 2007). In general, people only mention groupers, which are indicated by the spots on their body parts. The fish have a brownish to attractive red colour associated with their diverse habitats from shallow water areas and very colourful coral reef ecosystems (Unsworth *et al.*, 2007)

DNA barcoding believed to be one of the methods used globally to identify molecular approaches for animals and plants. This identification, the DNA in mitochondrial, becomes a remarkable sequence that is considered capable of being a marker and has been accepted as a global bio-identification system for animals (Hebert *et al.*, 2003 and Ward *et al.*, 2005). This identification is beneficial in specimens that are difficult to identify morphologically, such as larval stage, and organ fragments or morphologically incomplete specimens (Hebert *et al.*, 2003). Various advantages of DNA coding are straightforward and useful universal tools that include all the animals both in the form of fresh and processed product samples (Pepe *et al.*, 2007 and Giusti *et al.*, 2017). The accuracy of DNA-based identification is nearly 100 %, which indicates that this method can prove the identification of specimens under different environmental conditions (Meyer and Paulay, 2005). The barcoding system uses sequences that have a diversity in the single region of mitochondrial DNA, cytochrome c oxidase subunit I gene

(COI), and then deposited to the GenBank database. The GenBank has become central to deposit diverse taxa from all parts of the world. With the increase of molecular databases, scientists have demonstrated their effectiveness in conducting DNA barcoding from freshwater fish to deep-sea fish (Ward *et al.*, 2005 and Lakra *et al.*, 2011). Previous research has shown that mitochondrial DNA has a higher mutation rate compared to nuclear DNA by inheriting the maternal gene. Thus, researchers can obtain handy data for studying evolution between species, even within the same species (Waugh, 2007). In this research, we performed the molecular identification of several grouper from seven sampling sites (Java, Bali Island, and Aceh) with the COI gene region to understand the diversity and measure the genetic distance of each species, especially in the genus *Epinephelus*, *Cephalopholis*, and *Variola*.

MATERIALS AND METHODS

Sampling site

A total of 8 fish samples were collected from the five traditional fish markets around Jawa Island during July 2019. In the northern part of Java, samples were obtained from the Banten (6°0'50.00'S-106°10'21.00"E), and Gresik (6°52'56.65'S-112°12'15.87"), while Southern Java was represented samples from Malang (8°26'06.65'S-112°40'55.31"), the Banyuwangi (8°12'07.52'S-114°23'07.18"E), and Bali (8°45'23.00'S-115°10'05.68"E). Here, we also collected a specimen from the Kutaradja fish traditional market in Aceh, the westernmost province of Sumatera (5°35'07.00"N-95°19'07.00"E). Morphologically identification conducted according to the guideline from FAO (Heemstra, 1993), and species confirmation has been carried out with molecular identification carried out in this study using the COI gene region. No specific permit was required for this study due to collect from the local traditional fish market were dead upon purchasing. Before dissected, all specimen has been photographed by the digital camera.

DNA extraction and PCR

Each specimen has been collected and directly preserved in 90 % ethanol for further experimental purposes. Around one cm tissues was taken from the anal fin of each specimen, dissected and mix with 6X lysis buffer, which was further homogenized by the TissueLyser II (Qiagen). Genomic DNA extracted using an Accuprep® Genomic DNA Extraction Kit (Bioneer) according to the manufacturer's guidelines. Quantification of purified genomic DNA performed by Nanodrop (ThermoFisher Scientific D1000), aliquoted and stored at -70°C for further analysis.

PCR condition and Data Analysis

One set of universal fish primer targeting cytochrome c oxidase I (COI) region, FISH-BCL (5'-TCA ACY AAT CAY AAA GAT ATY GGC AC-3') and FISH-BCH (5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3') (Baldwin *et al.*, 2009 and Handy *et al.*, 2011), used to obtain the partial sequences of COI gene. The PCR mixture (20µL) included 11.2 µL ultra-pure water, 1 µL primer forward and reverse (0.5 µM), 0.2 µL Ex Taq DNA polymerase (TaKaRa, Japan), 2 µL 10X ExTag Buffer, 2 µL dNTPs (1 µM, TaKaRa, Japan), and 2 µL genomic DNA as template. The PCR condition carried out

under the following setting: 95°C for 5 min in initial denaturation, followed by denaturation at 95°C for 30 s in 40 cycles, 50°C for 30 s in annealing, and 72°C for 45 s in extension step, and a final extension at 72°C for 5 min. The PCR products were purified with the AccuPrep®Gel purification kit (Bioneer, Korea).

Phylogenetic analysis

All sequences were aligned, including reference sequences from the GenBank database (**Table 1**). The pairwise evolutionary distance among the family determined by the Kimura 2-Parameter method. The Neighbor-joining (NJ) tree constructed, and 1000 bootstrap analysis was carried by Mega7 program (**Kumar *et al.*, 2016**).

RESULTS

A total of 11 successful identification samples consisted of three genera, *Epinephelus* (5), *Cephalopholis* (3), *Variola* (1). In this study, the genus *Epinephelus* was more dominated the general catches of fishers, including *E. coioides*, *E. ongunus*, *E. poecilonotus*, *E. areolatus*, *E. merra*. Meanwhile, other types are only in small quantities.

Tabel 1. The genetic distance of Epinephelinae compare to the reference from GenBank database

Species name	Genetic distance within species	Genetic distance between species
Clade I (<i>Epinephelus</i>)		
<i>E. areolatus</i>	0.000	0.152-0.181
<i>E. merra</i>	0.004	0.157-0.185
<i>E. ongunus</i>	0.000	0.107-0.184
<i>E. poecilonotus</i>	0.000	0.107-0.119
<i>E. oioides</i>	0.000	0.119-0.181
Clade II (<i>Cephalopholis</i> and <i>Variola</i>)		
<i>C. miniata</i>	0.000	0.089-0.216
<i>C. sonnerati</i>	0.000	0.089-0.174
<i>C. cyanostigma</i>	0.002	0.150-0.202
<i>V. albimarginata</i>	0.000	0.173-0.206

Genetic distance

Genetic distance analysis was carried out using Mega 7, which aligned all obtained queries (**Table 1**). The results of this analysis provide a description of the distance between species (interspecific) and in the same species (intraspecific). *Epinephelus areolatus* obtained from Aceh is not different from the reference sequences originating from Saudi Arabia (KU499597) by the genetic distance is zero. The same thing also happens to another genus *Epinephelus*, which also has genetic distance 0 with reference in the GenBank database except in *E. merra*. In *E. merra* there is a slight difference, although identification still refers to the same species. Genetic distance with specimens originating from Japan (AP005991) is only 0.004, indicating that *E.merra* species is an Indonesian haplotype. Whereas in *Cephalopolis* species,

only *C. cyanostigma* was found in Indonesian haplotypes with a genetic distance of 0.002 with reference specimens from the Philippines (KU668647).

Phylogenetic reconstruction

In the phylogenetic tree produced, two clades have been formed consisting of the genus *Epinephelus*, and the other clade consists of *Cephalopholis* and *Variola* (**Figure 1**). Morphologically, the *Epinephelus* group is dark grey to dark brown, while *Cephalopholis* and *Variola* are bright red body-colour (**Figure 2**). Although morphologically, the two clades show differences, sometimes it is challenging for researchers and the public to distinguish each species. Besides, the giving of various regional names also adds to the complexity of naming. So that the molecular identification carried out in this study is expected to help ensure the types of fish identified and traded in traditional markets in several areas. The certainty of the name in the specie here is also essential in various scientific writings because it deals with scientific information that will be read by the general public, especially in academic purposes.

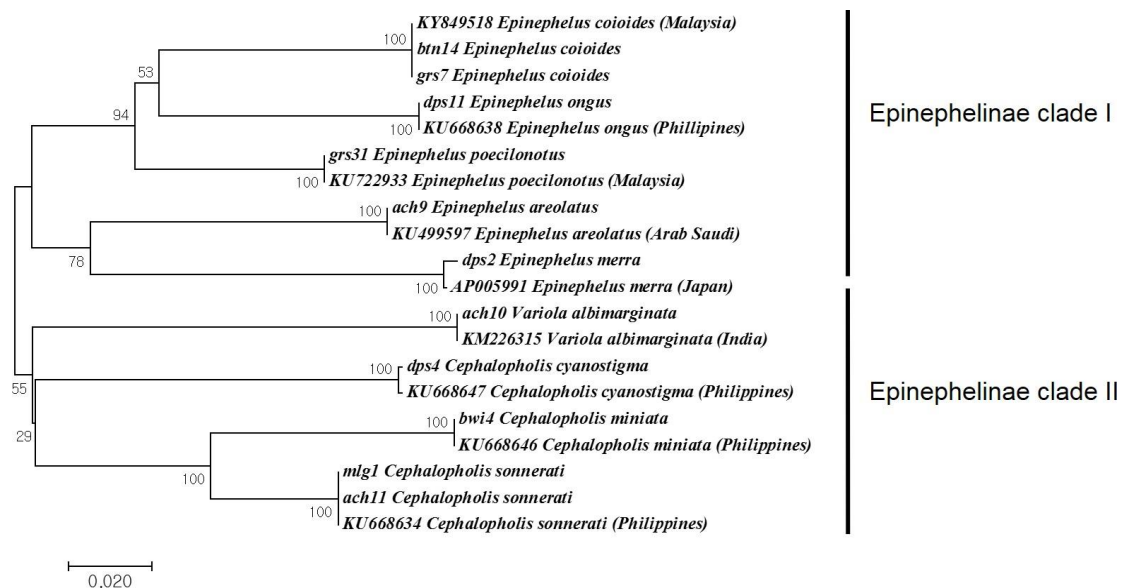


Figure 1. Phylogenetic tree of Epinephelinae including references from the GenBank database

Epinephelinae status in IUCN and CITES

Almost all grouper species in this study have the status of Least Concern (LC), while the grouper in international trade (CITES) is not evaluated (**Table 2**). However, *E. merra* has been reported as a causative agent of Ciguatera fish poisoning in several countries (**Lewis, 1986**). This fish poisoning occurs in some countries such as Thailand (**Toyoda et al., 1981**), the Philippines (**Montejo et al., 2020**), Hong Kong (**Sadovy, 1997**), Australia (**Gillespie et al., 1986**), and other countries (**Randall, 1958; Chan 2015; and Gaboriau et al., 2014,).** However, there have been no reports of ciguatera in Indonesia (**Chan, 2015**).

Tabel 2. IUCN and CITES status of all grouper specimens

Species name	English name	Distribution	IUCN	CITES	Threat to humans
<i>E. areolatus</i>	Areolate grouper	Indo-Pacific	LC	NE	Harmless
<i>E. merra</i>	Honeycomb grouper	Indo-Pacific	LC	NE	Reports of ciguatera poisoning
<i>E. ongus</i>	White-streaked grouper	Indo-West Pacific	LC	NE	Harmless
<i>E. poecilonotus</i>	Dot-dash grouper	Indo-West Pacific	LC	NE	Harmless
<i>E. oioides</i>	Orange-spotted grouper	Indo-West Pacific	LC	NE	Harmless
<i>C. miniata</i>	Coral hind	Indo-Pacific	LC	NE	Harmless
<i>C. sonnerati</i>	Tomato hind	Indo-Pacific	LC	NE	Harmless
<i>C. cyanostigma</i>	Blue-spotted hind	Western Pacific	LC	NE	Harmless
<i>V. albimarginata</i>	White-edged lyre tail	Indo-Pacific	LC	NE	Harmless

LC: Least Concern

NE: Not Evaluated

DISCUSSION

Grouper has become a leading commodity in aquaculture in several Asian countries and several other continents (**Halim, 2001**). The success of aquaculture is demonstrated by many studies on the reproductive biology that are sufficient detailed (**Andrade *et al.*, 2003** and **Andamari *et al.*, 2007**,), hatchery (**Rimmer, 2000**, and **Sugama *et al.* 2012**), larval rearing to a variety of grow-up system (**Fukuhara, 1989** and **Pomeroy, 2002**). Several studies have shown good results in hatching several species of groupers such as *E. coioides*, *E. fuscoguttatus*, *Plectropomus leopardus*, and *Cromileptes altivelis* (**Rimmer, 2000**), *E. fuscoguttatus* (**Sugama *et al.*, 2017**). Research on the grow-up system also showed excellent results both in the floating net system (**Baliao *et al.*, 2000**) and in the aquaculture system in the pond (**Baliao *et al.*, 1998**).

Trade-in grouper in the live fish becomes a superior commodity because the price is quite high when compared to fresh dead fish. The demand for live fish forms continues to increase, so fishers prefer to sell live fish (**Halim, 2001**). However, many aquaculture activities are currently conducting such as breeding between species, which are expected to produce variants that have growth and other good traits such as disease resistance, good growth, resistance to extreme environments, and at the same time, making sterile fish (**Hickling, 1968**). For example, the crossing of tiger grouper and *E. fuscoguttatus* and *E. polyphkadion* grouper, which produce hybrid grouper with excellent growth performance (**James *et al.*, 1999**). However, please note that the pure parent lines that will be breeding must be well known so that the study of this breeding effect can be done well. Other breeding was also developed on *E. costae* with *E. marginatus* (**Glamuzina *et al.*, 2001**), *Plectropomus leopardus* with *Plectropomus maculatus* (**Frisch and Hobbs, 2007**), and *E. coioides* with *E. lanceolatus* (**Kiriyakit *et al.*, 2011** and **Sutthinon *et al.*, 2015**).

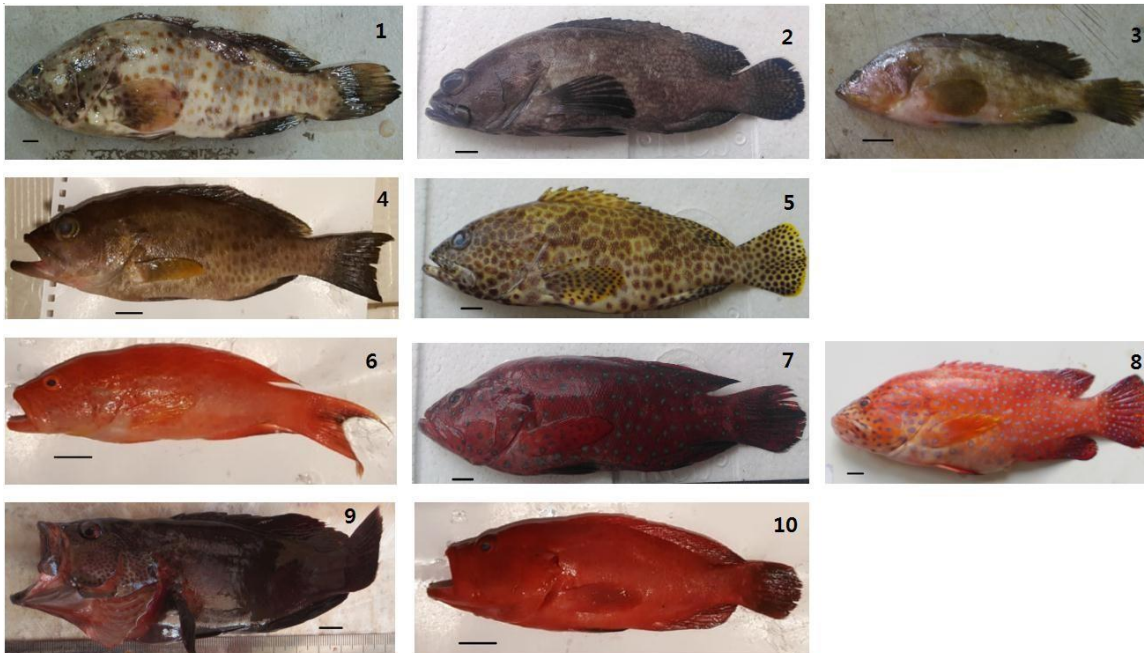


Figure 2. grs7 *E. coioides*(1); dps11 *E.ongus* (2); grs31 *E. poecilonotus* (3); ach9 *E. areolatus* (4); dps2 *E. merra* (5); ach10 *Variola albimarginata* (6); dps4 *Cephalopholis cyanostigma* (7); bwi4 *C. miniata* (8); mlg11 *C. sonnerati* (9) ; ach11 *C. sonnerati* (10)

Some breeding activities between *Epinephelus* species have been carried out in Indonesia. One of them is a hybrid between *E. microdon* (male) and *E. fuscoguttatus* (female) by producing seeds that have the title grouper cantik (Ismi, 2014). Another type of hybrid is the grouper cantang, which is a hybrid of *E. fuscoguttatus* and *E. lanceolatus* (Shapawi *et al.*, 2019). Another hybrid type is the kustang grouper, which is breeding of *Cromileptes altivelis* with *E. coioides* (Yu *et al.*, 2004). Breeding between *E. microdon* and *E. lanceolatus* has been carried out, which produces a new type of hybrid grouper (Sutarmat and Yudha, 2016). Also, back-cross hybrids have also been carried out between hybrids (*E. coioides* x *E. lanceolatus*) breeding with *E. lanceolatus* (Luan *et al.*, 2016). Back-cross breeding efforts are carried out to produce seeds that are more productive and have the advantage of better traits such as a high survival rate than the previous generation.

Due to the intensive exploitation of grouper species in the world, only a small number of studies on the genetic diversity of the species have been carried out. In Indonesia, although intensive aquaculture activities are carried out, only a few types of grouper have been reported about genetic studies such as *E. coioides* (Antoro *et al.*, 2006), *E. siullus* (Parenrengi and Tenriulo, 2008), *Cromileptes altivelis* (Susanto *et al.*, 2011 and Sugama *et al.*, 2017) and several other types of grouper *E. areolatus*, *E. merra*, *E. ongus*, *E. fasciatus*, *E. coioides*, *E. coeruleopunctatus*, and *E. longispinis* (Jefri *et al.*, 2015). Nevertheless, barcoding studies of several types of grouper have been carried out from some regions in Java and Bali (Andriyono *et al.*, 2020), Makassar (Parenrengi and Tenriulo, 2008), Lampung and Papua (Jefri *et al.*, 2015). This report is the first report involving specimens from Aceh and at the same time comparing with references from the GenBank database.

The use of genetic information from the GenBank database provides a picture of the similarities between species groups, even though the species has a large habitat distribution in the Indo-Pacific region (**Randall and Heemstra, 1991** and **Unsworth *et al.*, 2007**). It is estimated, the grouper included in coral reef fish associated has experienced speciation that allows it to have variations in its genetic composition (**Rocha and Bowen, 2008**). Specialization of reef fishes has illustrated that open access sea also has its boundaries and niches so that many species will be different and adapt to each type of coral reef ecosystem. In this study, only two types (*E. merra* and *C. cyanostigma*) were found to be Indonesian haplotypes and differ from the same species from the alignment of the DNA reference sequence.

The distribution of *E. merra* is quite extensive with significant habitats found in the Indo-Pacific region including South Africa to French Polynesia and even in the central Pacific (**Randall and Heemstra, 1991**; **Craig *et al.*, 2011**; and **Muths and Bourjea, 2011**) which generally inhabit waters bring (<20 m depth). Its natural habitat is a coral reef area and becomes essential in artisanal fisheries as a source of protein and food for coastal communities (**Heemstra, 1993**). Studies on *E. merra* diversity also indicate genetic variation in Madagascar, the Maldives, and small islands in the West Indian Ocean (**Muths *et al.*, 2015**).

Meanwhile, *C. cyanostigma* was also identified in Maluku waters, which has a reasonably high diversity of the genus *Cephalopholis* with 11 species inhabiting the waters of this region (**Limmon *et al.*, 2017**) and North Sulawesi (**Tokeshi *et al.*, 2013**). Based on previous reports, the genus *Cephalopholis* consists of 22 species that have habitat distribution in the Pacific Ocean region (**Heemstra, 1993**), which tend to have a cryptic habit on coral reef ecosystems (**Shpigel and Fishelson, 1989**). Of the 22 known species of *Cephalopholis*, only nine species have been studied in terms of their biology. Many studies on several aspects of biology, including sexual maturity (**Shapiro 1987**), spawning (**Donaldson, 1989**), territoriality and their ecology (**Shpigel and Fishelson, 1991**), and sex change and population structure of *Cephalopholis* (**Siau, 1994**). Meanwhile, this report is the first report on genetic distance in *C. cyanostigma* in Indonesia based on the COI sequences that show the existence of different haplotypes with the same species in the Philippines. The haplotype was formed due to geographical different, the Philippine species is an Indo West-pacific species, while the sample in this study is a species of the Indian ocean. This result needs to get attention for further research on genetic variation of *Cephalopholis* in Indonesian regions with a more significant number of samples.

The haplotypes found in *E. merra* and *C. cyanostigma* can be known by phylogenetic tree analysis, which shows a slight distance with sequence reference (**Figure 1**). This study is quite helpful in giving an idea of the haplotype formed. Also, through this phylogenetic tree, it is known that the genus *Epinephelus* forms a separate clade separating from *Cephalopholis* and *Variola*. In this study, *Cephalopholis* and *Variola* are in the same clade but separated in several branches. Morphologically, these two genera can be easily distinguished by observing the caudal fin (**Figure 2**). In *Variola* species have caudal fin lunate (**Baldwin, 2003**), than *Cephalopholis* have rounded caudal fin (**Allen, 2015**). Thus, the phylogenetic tree places the two genera in separate branches (**Figure 1**). Although the number of samples is still small, this report

reinforces that the Epinephelinae group has several clades, which are genetic variations in the grouper.

CONCLUSION

In this study, we found genetic variation in *E. merra* and *C. cyanostigma* that showed the existence of Indonesian haplotypes. This result was figure-out genetic distance of some species in this report. The genetic distance of *E. merra* and *C. cyanostigma* are 0.004 and 0.002, which is slightly different from sequences from Japan and the Philippines, respectively. It is necessary more in-depth studies of *C. cyanostigma*, due to the limited study of genetic variation, especially in Indonesia. The study of *C. cyanostigma* is very supportive in efforts to develop this species as an aquaculture commodity in the future, such as *Epinephelus*. An in-depth study of biological characteristics, including reproductive biology, ecology, and other specific characteristics, will be beneficial in both conservation and domestication.

ACKNOWLEDGMENTS

The authors would like to express our sincere gratitude for the initiation of collaborative research between Airlangga University (Surabaya), Syiah Kuala University (Aceh), and Hasanuddin University (Makassar) which have given great importance to the development of studies in Indonesia. Fisheries studies in Java, Sumatra, Sulawesi, Kalimantan, and Papua require the support of many collaborators to produce quality and beneficial research for Indonesia.

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