

Molecular identification and phylogenetic reconstruction of marine fish from Kutaradja fish landing Station, Banda Aceh

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ADDITIONAL KEYWORDS

Molecular.
Barcoding.
Diversity.
Marine fish.
Indonesia.

PALABRAS CLAVE ADICIONALES

Molecular.
Códigos de barras.
Diversidad.
Peces marinos.
Indonesia.

INFORMATION

Cronología del artículo.
Recibido/Received: 06.10.2021
Aceptado/Accepted: 01.02.2024
On-line: 15.07.2024
Correspondencia a los autores/Contact e-mail:
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SUMMARY

The large potential of marine resources possessed by Banda Aceh Province is expected to be utilized optimally. Complete identification of marine fish resources is an important requirement in order to support their utilization and preservation in Banda Aceh Province. In this study, a molecular identification approach is carried out in addition to conducting a morphological identification that has been commonly used. In this molecular identification study, the target DNA is the Cytochrome c oxidase subunit I (COI) region located in the mitochondria. The extraction method used a DNA Kit that was adjusted to the manufacturer's guidelines, then continued with PCR to duplicate the extracted DNA. The PCR results were carried out by direct sequencing and sequence analysis was performed using Chromas and Mega7 software. The results obtained were 47 COI sequences were generated representing 33 genera, 19 families, and 5 orders. Perciformes was the most predominant group of fish, and several fish species with important economic value were identified such as the Scombridae group including *Thunnus albacares*, *Auxis thazard*, and *Katsuwonus pelamis*. From the resulting sequence, there are one haplotype from the Scombridae family, two haplotypes from the Carangidae family, and two haplotypes from the Serranidae family. This study is essential in fisheries biology studies and other fisheries studies to support the sustainable utilization of marine fisheries potential in Banda Aceh.

Identificación molecular y reconstrucción filogenética de peces marinos de la estación de desembarco de pescado de Kutaradja, Banda Aceh.

RESUMEN

Se espera que el gran potencial de los recursos marinos que posee la provincia de Banda Aceh se utilice de manera óptima. La identificación completa de los recursos de peces marinos es un requisito importante para apoyar su utilización y preservación en la provincia de Banda Aceh. En este estudio, se lleva a cabo un enfoque de identificación molecular, además de realizar una identificación morfológica que ha sido comúnmente utilizada. En este estudio de identificación molecular, el ADN objetivo es la región de la subunidad I de la citocromo c oxidasa (COI) ubicada en las mitocondrias. El método de extracción utilizó un Kit de ADN que se ajustó a las directrices del fabricante, luego continuó con PCR para duplicar el ADN extraído. Los resultados de la PCR se llevaron a cabo mediante secuenciación directa y el análisis de secuencias se realizó utilizando los software Chromas y Mega7. Los resultados obtenidos fueron 47 secuencias de COI generadas representando 33 géneros, 19 familias y 5 órdenes. Los Perciformes fueron el grupo de peces más predominante, y se identificaron varias especies de peces con importante valor económico como el grupo Scombridae, incluyendo *Thunnus albacares*, *Auxis thazard* y *Katsuwonus pelamis*. A partir de la secuencia resultante, hay un haplotipo de la familia Scombridae, dos haplotipos de la familia Carangidae y dos haplotipos de la familia Serranidae. Este estudio es esencial en estudios de biología pesquera y otros estudios de pesquerías para apoyar la utilización sostenible del potencial de pesquerías marinas en Banda Aceh.

INTRODUCTION

Banda Aceh is the western tip province on the mainland of Sumatra (Indonesia), which has considerable fishery potential with waters reaching 295,370 km² and with a coastline length reaching 2,666.3 km² (Mukhtar, 2017). From the 2003 fisheries statistics report that Banda Aceh's capture fisheries activities support community activities (55% of the population of Aceh) and one of the largest fish landing centers in Banda Aceh is Kutardja fish landing (Yeni and Naufal, 2017, Yusuf, 2003). The Kutardja fish landing suffered heavy damage due to the tsunami that struck Aceh Province and was rebuilt in 2004 (Zulmaidah et al., 2015). The rebuilding of the Kutardja fish landing has revived the economy and fisheries activities in the region. Fishing catchment areas in the Banda Aceh region are included in WPP 572 based on KEPMEN KP N^o.50 / 2017 reported to have experienced fully exploited so that the need for management of capture fisheries activities in this region (Salmarika and Wisudo, 2019).

Previous research on the types of fish landed by many traditional fishermen in Kutardja fish landing is still being done conventionally. From the inventory carried out at the Kutardja fish landing, 11 species have been identified (Munawwarah et al., 2016). However, another report on the types of marine fish species in Banda Aceh (Simeuleu Island) identified around 77 marine fish species included in 54 genus, 26 families, and seven orders (Batubara et al., 2017). The morphological approach is the most widely used method in many regions in Indonesia, including in Banda Aceh. This research identifies molecular marine fish in the Cytochrome C Oxidase subunit I (COI) region of the mitochondrial gene to complete the morphological identification that was also carried out. This COI Region is the region that some gene markers have agreed on in molecular identification globally. Research on barcoding in several aquatic biota has been carried out such as marine fish in Australia (Ward et al., 2005), marine fish in India (Lakra et al., 2011), marine fish in Turkey (Keskin and Atar, 2013), marine fish in China (Wang et al., 2012, Zhang and Hanner, 2012), and marine fish in Taiwan (Bingpeng et al., 2018, Chang et al., 2017). Whereas research on molecular identification of fish in Aceh has carried out on some species such as grouper fish (Kamal et al., 2019), and Scomber spp (Edwaryah et al., 2019). This research on the identification of marine fish landed at the Kutardja fish landing is the first study to carry out molecular identification.

The purpose of this research is to identify species of marine fish to species level by using a molecular approach to minimize identification errors. Besides, the research carried out identification of Aceh's haplotype in the Scombridae, Serranidae, and Carangidae groups which are pelagic fish resources that have important economic value.

MATERIAL AND METHODS

SAMPLING SITE

A total of 47 fish samples were collected from the Kutardja traditional fish market close to the Ku-

taradja fish landing on 19 July 2019. Morphologically, identification and species confirmation have been carried out with molecular identification carried out in this study. No specific permit was required for this study, and a digital camera has taken the individual photograph. All samples have collected from the local traditional fish market were dead upon purchasing.

DNA EXTRACTION AND PCR

Each specimen has been collected based on the morphological characters and after collection directly preserved in 90% ethanol for further experimental purposes. Genomic DNA extracted using an Accuprep® Genomic DNA Extraction Kit (Bioneer) according to the manufacturer's guidelines. The anal fin, around 1 cm tissues, was dissected and mix with 6X lysis buffer, which was further homogenized by the TissueLyser II (Qiagen). Quantification of purified genomic DNA performed by nanoDrop (ThermoFisher Scientific D1000), aliquoted and stored at the -70oC for further analysis.

PCR CONDITION AND DATA ANALYSIS

One set universal fish primer targeting cytochrome c oxidase I (COI) region, BCL-BCH (Baldwin et al., 2009, Handy et al., 2011) used to obtain the partial sequences of each 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: 95oC for 5 min in initial denaturation, followed by denaturation at 95oC for 30 s in 40 cycles, 50oC for 30 s in annealing and 72oC for 45 s in extension step, and a final extension at 72oC for 5 min. The PCR products purified with the AccuPrep®Gel purification kit (Bioneer, Korea).

PHYLOGENETIC ANALYSIS

All sequences were aligned and submitted to GenBank (**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 Mega 7 (Kumar et al., 2016).

RESULTS

SPECIES IDENTIFICATION

A total of 47 COI sequences generated representing 33 genera, 19 families, and five orders. Common names, taxonomic designation, habitat, IUCN list, as well as the GenBank accession number for all specimens in **Table 1**. The sequencing of the COI gene produced more than 600 nucleotide base pairs per taxon. The unambiguity and simplicity observed among all the sequences, and no stop codons, deletions and insertions were observed in all the sequences. Here, we cluster into two groups are Perciformes and another order.

PERCIFORMES

The nucleotide frequencies of COI sequences are 29.65% (T/U), 23.95% (A), 28.80% (C), and 17.6% (G).

Table 1. The marine fish species list was identified by COI region from Lampulo marine fish landing station, Banda Aceh, Indonesia (La lista de especies de peces marinos fue identificada por la región del COI en la estación de desembarque de peces marinos de Lampulo, Banda Aceh, Indonesia).

Nº.	ID (AC).	Species Name	Family	GenBank Acc No.	Order	Common name	Habitat	IUCN list
1	16	Myripristis berndti	Holocentridae	MN257521	Beryciformes	Blotcheye soldierfish	Indo-Pacific and Eastern Pacific	LC
2	17	Myripristis berndti	Holocentridae	MN257522	Beryciformes	Blotcheye soldierfish	Indo-Pacific and Eastern Pacific	LC
3	36	Sardinella jussieu	Clupeidae	MN257539	Clupeiformes	Mauritian sardinella	Western Indian Ocean	DD
4	37	Sardinella jussieu	Clupeidae	MN257540	Clupeiformes	Mauritian sardinella	Western Indian Ocean	DD
5	38	Stolephorus commersonii	Engraulidae	MN257541	Clupeiformes	Commerson's anchovy	Indo-West Pacific	LC
6	39	Stolephorus commersonii	Engraulidae	MN257542	Clupeiformes	Commerson's anchovy	Indo-West Pacific	LC
7	40	Thryssa baelama	Engraulidae	MN257543	Clupeiformes	Baelama anchovy	Indo-Pacific	LC
8	41	Thryssa baelama	Engraulidae	MN257544	Clupeiformes	Baelama anchovy	Indo-Pacific	LC
9	1	Scolopsis xenochroa	Nemipteridae	MN257509	Perciformes	Oblique-barred monocle bream	Indo-West Pacific	NE
10	4	Lutjanus bengalensis	Lutjanidae	MN257511	Perciformes	Bengal snapper	Indo-West Pacific:	NE
11	5	Upeneus sulphureus	Mullidae	MN257512	Perciformes	Sulphur goatfish	Indo-West Pacific	LC
12	7	Pristipomoides filamentosus	Lutjanidae	MN257513	Perciformes	Crimson jobfish	Indo-Pacific	LC
13	8	Parascolopsis eriomma	Nemipteridae	MN257514	Perciformes	Rosy dwarf monocle bream	Indo-West Pacific	NE
14	9	Epinephelus areolatus	Serranidae	MN257515	Perciformes	Areolate grouper	Indo-Pacific	LC
15	10	Variola albimarginata	Serranidae	MN257516	Perciformes	White-edged lyretail	Indo-Pacific	LC
16	11	Cephalopholis sonnerati	Serranidae	MN257517	Perciformes	Tomato hind	Indo-Pacific	LC
17	12	Parastromateus niger	Carangidae	MN257518	Perciformes	Black pomfret	Indo-West Pacific	LC
18	14	Parupeneus macronemus	Mullidae	MN257519	Perciformes	Long-barbel goatfish	Indo-West Pacific	LC
19	15	Parupeneus macronemus	Mullidae	MN257520	Perciformes	Long-barbel goatfish	Indo-West Pacific	LC
20	18	Priacanthus tayenus	Priacanthidae	MN257523	Perciformes	Purple-spotted bigeye	Indo-West Pacific	LC
21	19	Lethrinus rubrioperculatus	Lethrinidae	MN257524	Perciformes	Spotcheek emperor	Indo-Pacific	LC
22	25	Megalaspis cordyla	Carangidae	MN257528	Perciformes	Torpedo scad	Indo-West Pacific	LC
23	26	Pomadasy argyreus	Haemulidae	MN257529	Perciformes	Bluecheek silver grunt	Indo-West Pacific	NE
24	27	Terapon jarbua	Terapontidae	MN257530	Perciformes	Jarbua terapon	Indo-Pacific	LC
25	28	Equulites leuciscus	Leiognathidae	MN257531	Perciformes	Whipfin ponyfish	Indo-West Pacific	LC
26	29	Gazza minuta	Leiognathidae	MN257532	Perciformes	Toothpony	Indo-Pacific	LC

27	30	<i>Leiognathus striatus</i>	Leiognathidae	MN257533	Perciformes	Toothpony	Western Indian Ocean	NE
28	31	<i>Photopectoralis bindus</i>	Leiognathidae	MN257534	Perciformes	Orangefin ponyfish	Indo-West Pacific	NE
29	32	<i>Gerres filamentosus</i>	Gerreidae	MN257535	Perciformes	Whipfin silver-biddy	Indo-Pacific	LC
30	33	<i>Equulites leuciscus</i>	Leiognathidae	MN257536	Perciformes	Whipfin ponyfish	Indo-West Pacific	LC
31	34	<i>Gazza minuta</i>	Leiognathidae	MN257537	Perciformes	Toothpony	Indo-Pacific	LC
32	35	<i>Megalaspis cordyla</i>	Carangidae	MN257538	Perciformes	Torpedo scad	Indo-West Pacific	LC
33	43	<i>Lutjanus lutjanus</i>	Lutjanidae	MN257545	Perciformes	Bigeye snapper	Indo-West Pacific	LC
34	46	<i>Caranx sexfasciatus</i>	Carangidae	MN257546	Perciformes	Bigeye trevally	Indo-Pacific	LC
35	47	<i>Siganus sutor</i>	Siganidae	MN257547	Perciformes	Shoemaker spinefoot	Indian Ocean	LC
36	48	<i>Siganus sutor</i>	Siganidae	MN257548	Perciformes	Shoemaker spinefoot	Indian Ocean	LC
37	49	<i>Nemipterus bipunctatus</i>	Nemipteridae	MN257549	Perciformes	Delagoa threadfin bream	Indian Ocean	NE
38	50	<i>Terapon jarbua</i>	Terapontidae	MN257550	Perciformes	Jarbua terapon	Indo-Pacific	LC
39	51	<i>Terapon jarbua</i>	Terapontidae	MN257551	Perciformes	Jarbua terapon	Indo-Pacific	LC
40	52	<i>Coryphaena hippurus</i>	Coryphaenidae	MN257552	Perciformes	Common dolphinfish	Atlantic, Indian and Pacific	LC
41	53	<i>Auxis thazard</i>	Scombridae	MN257553	Perciformes	Frigate tuna	Atlantic, Indian and Pacific (Western Central)	LC
42	54	<i>Auxis thazard</i>	Scombridae	MN257554	Perciformes	Frigate tuna	Atlantic, Indian and Pacific (Western Central)	LC
43	55	<i>Thunnus albacares</i>	Scombridae	MN257555	Perciformes	Yellowfin tuna	Worldwide in tropical and subtropical seas	NT
44	56	<i>Decapterus macarellus</i>	Carangidae	MN257556	Perciformes	Mackerel scad	Circumglobal	LC
45	57	<i>Katsuwonus pelamis</i>	Scombridae	MN257557	Perciformes	Skipjack tuna	Cosmopolitan in tropical and warm-temperate waters	LC
46	24	<i>Psettodes erumei</i>	Psettodidae	MN257527	Pleuronectiformes	Indian halibut	Indo-West Pacific	NE
47	20	<i>Platycephalus sp.</i>	Platycephalidae	MN257525	Scorpaeniformes	Bartail flathead	Indo-West Pacific	DD

Least Concern (LC); Not Evaluated (NE); Data deficient (DD); Near Threatened (NT).

The average of transitional pair ($si=5.07$) and was lower than the average of transversional pair ($sv=14.86$) with an overall transition/transversion ratio bias is 1.57. The phylogenetic tree was constructed the COI sequences for the Perciformes and shown the average K2P distance within taxonomic levels measured for COI sequences is 0.226 (Figure 1).

CLUPEIFORMES AND OTHERS

The nucleotide frequencies of COI sequences are 28.17% (T/U), 23.04% (A), 30.11% (C), and 18.68% (G). The average of transitional pair ($si=1.43$) was lower

than the average of transversional pair ($sv=22.13$) with an average transition/transversion bias is 8.71. The phylogenetic tree was constructed the COI sequences for small number order including the Clupeiformes, Beryciformes, Pleuronectiformes, and Scorpaeniformes (Figure 2). The average K2P distance within taxonomic levels measured for COI sequences is 0.214.

THE HAPLOTYPE OF SCOMBRIDAE, SERRANIDAE, AND CARANGIDAE FROM ACEH

In this study, the sample from Aceh had several unique haplotypes compared to the same species from the

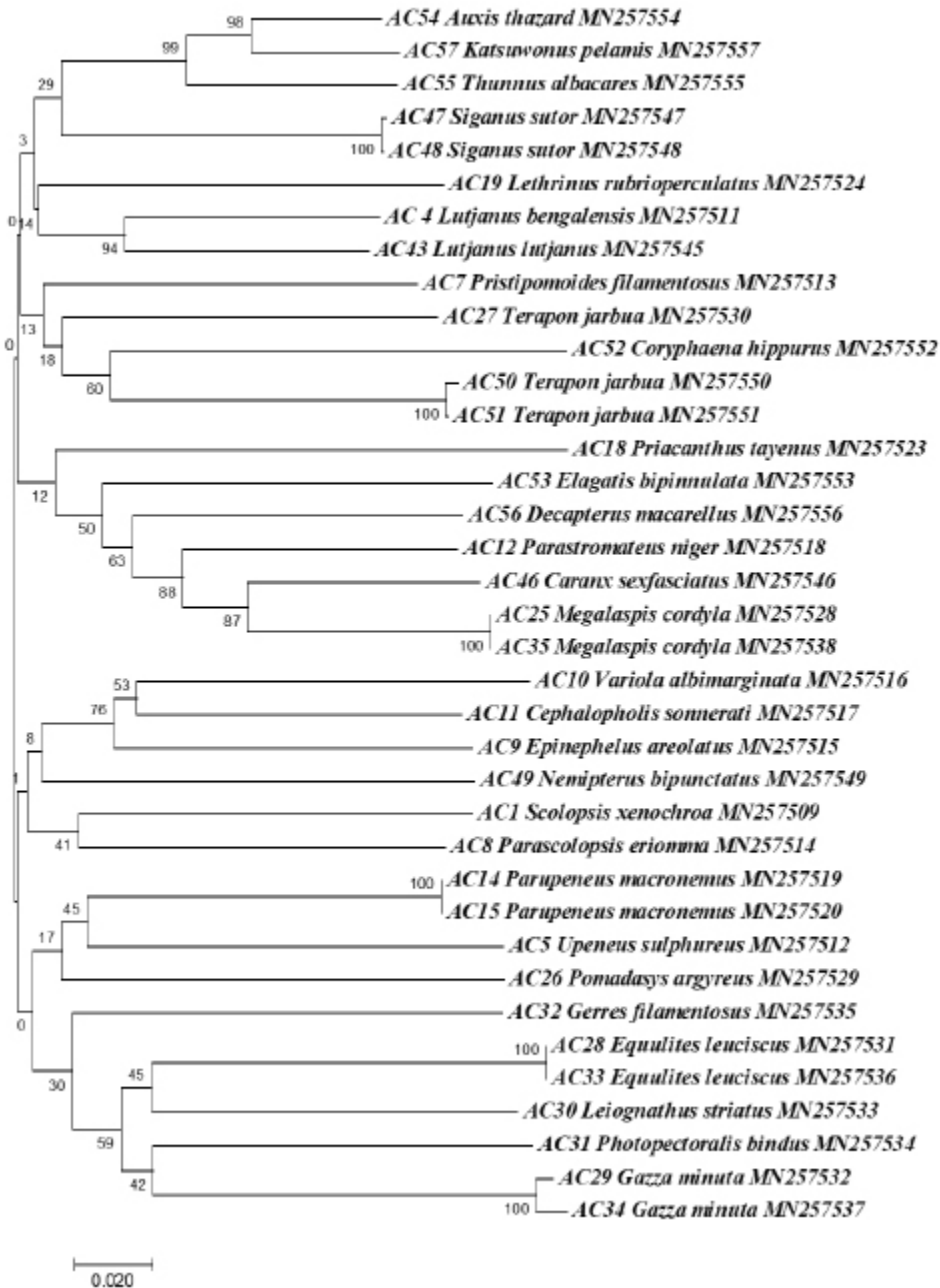


Figure 1. Phylogenetic tree of Perciformes order by Neighbor-Joining tree algorithm using Mega7 (Árbol filogenético del orden Perciformes mediante el algoritmo de árbol de unión de vecinos utilizando Mega7).

GenBank database. By aligning the sequence generated with the reference sequence, some different nucleotides produce genetic variations (**Table 2**). The phylogenetics reconstruction of those sequences shown that several haplotypes found in this study (**Figure 3**). The identified haplotype in the Carangid group was found in the *Decapterus macarellus* species (MN257556) which had similarities with sequences from China and Malaysia, and had a genetic distance with an Indian sequence is 0.002. In addition, *Elagatis bipinnulata* (MN257553) is closer to the similarity of the sequence owned by the same type of fish (KF461174) from Alabama, USA. While the genetic distance of *Elagatis bipinnulata* with the same species is 0.003 (Philippines) and 0.02 (India and

China). In the Carangid group, *Caranx sexfasciatus* (MN257546) and *Megalaspis cordyla* (MN257528 and MN257538) species were not found polymorphic in the sequences obtained.

In the Scombridae family group, haplotypes found in *Auxis thazard* fish (MN257554) which differed from Chinese, Indian, and Spanish haplotypes with a genetic distance of 0.002. While in the Serranidae family, haplotypes found in *Variola albimarginata* fish (MN257516) and *Cephalopholis sonnerati* (MN257517). This *Variola albimarginata* species (MN257516) has similarities with sequences from India but is different from Chinese

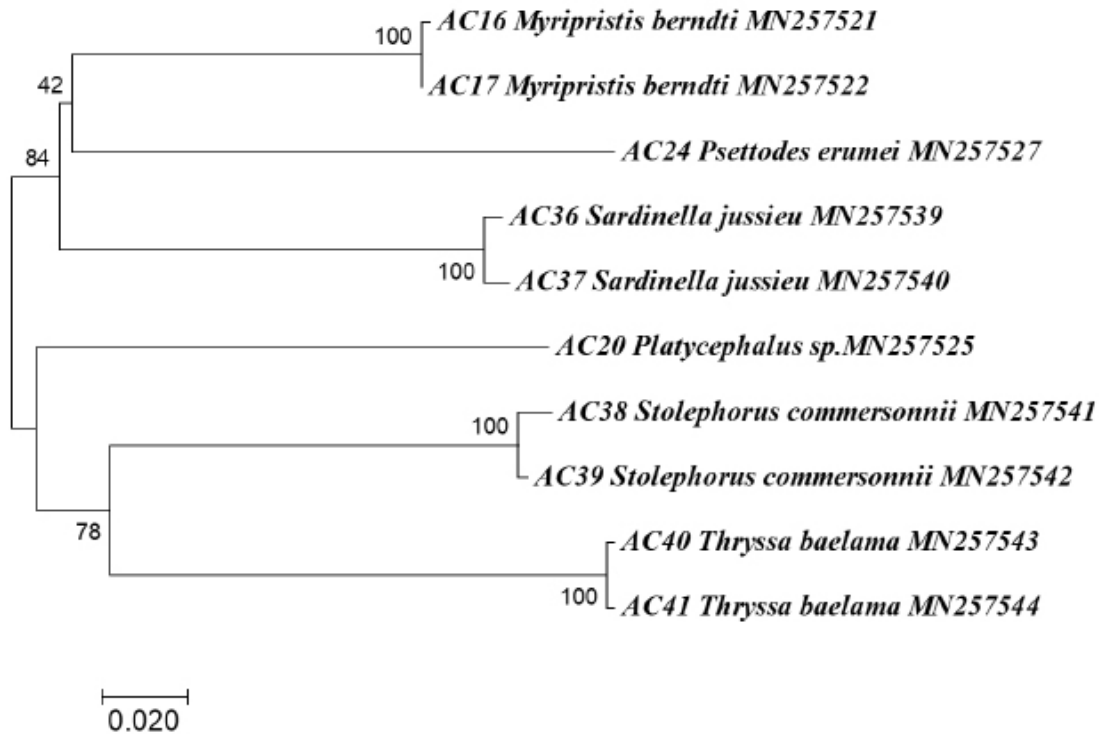


Figure 2. Phylogenetic tree of small number others order in this study including the Clupeiformes, Beryciformes, Pleuronectiformes, and Scorpaeniformes by Neighbor-Joining tree algorithm using Mega7 (Árbol filogenético de un pequeño número de otros órdenes en este estudio, incluidos los Clupeiformes, Beryciformes, Pleuronectiformes y Scorpaeniformes mediante el algoritmo de árbol de unión de vecinos utilizando Mega7).

haplotypes with a genetic distance of 0.007. While species of *Cephalopholis sonnerati* (MN257517) differ only from Chinese haplotypes, this species merged in one clade with samples of the Philippines, Australia, and Indonesia with genetic distance 0.00-0.002. In *Epinephelus arelatus* species, there are no haplotypes and sequences obtained from samples from China and Saudi Arabia.

DISCUSSION

Research on molecular identification is now very broad in the field of fisheries and marine sciences. In this study, molecular identification used to completing the morphological identification and at the same time, determine the position of the species identified in the phylogenetic tree created. Conventional identification that has been done at this time still finds obstacles with the difficulty of getting taxonomists in determining species, in addition to the long enough time in the identification process, errors in identification also still occur in some cases. By doing a combination of identification, it is expected to be more valid in getting the results of fish species obtained.

In this study, several marine fish landed at the Kutardja became an important fishery commodity in

Banda Aceh. After the 2004 tsunami disaster in this province, a number of activities capable of mobilizing economic activities continue to be carried out including capture fisheries activities in this Kutardja fish port (Zulmaidah et al., 2015). Previous studies have also reported the identification of marine fish species from Kutardja. There is still inaccurate information regarding marine fish identification in some reports. Besides, an identification that is only based on morphological characteristics that are not done by taxonomists, then the results in the identification may be incorrect on species justification. In an earlier report, the species *Sardinella sirin* (Serranidae) was reported to exist in this Kutardja port (Munawwarah et al., 2016), but an inaccurate in determining taxonomy made the identification results unreliable. The genus *Sardinella spp* is a group of fish in the family Clupeidae, order Clupeiformes (www.fishbase.org), not include in Serranidae.

In this report, family Perciformes are identified as a group that dominates the caught by fishermen in Banda Aceh who landed at the Kutardja. These fish are consumption fish that are important export commodities with high economic value such as Skipjack tuna (57%) followed by yellowfin tuna (23%) (Lubis et al., 2016). The results of identification, the Scombridae family is a group of pelagic fish that is quite commonly

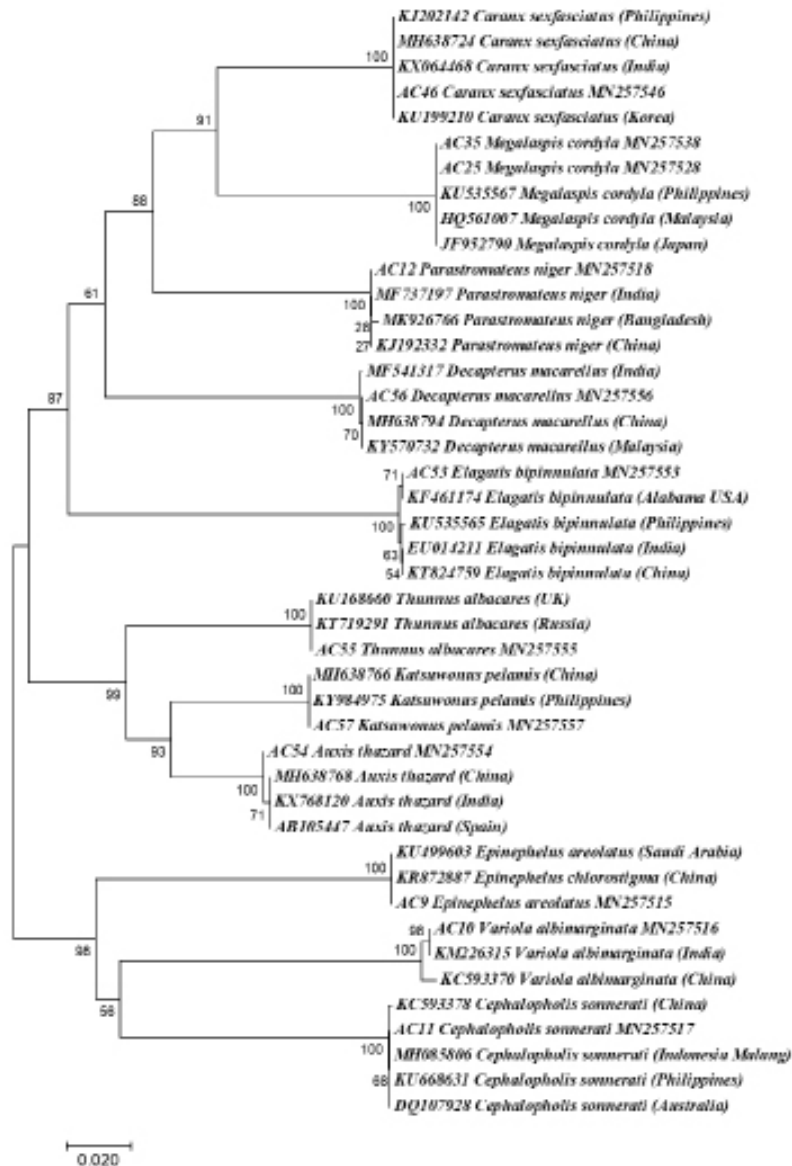


Figure 3. Phylogenetic reconstruction of three families (Carangidae, Scombridae, and Serranidae) by Neighbor-Joining algorithm using Mega7 (Reconstrucción filogenética de tres familias (Carangidae, Scombridae y Serranidae) mediante el algoritmo de unión de vecinos utilizando Mega7)..

found. The types identified in this report include *Thunnus albacares*, *Auxis thazard*, and *Katsuwonus pelamis*. In addition, the genus Lutjanidae (snapper) found three species, namely *Lutjanus bengalensis*, *Lutjanus lutjanus*, and *Lethrinus rubrioperculatus*. Other groups that are targeted by fishermen are reef fish that have important economic value, such as Grouper and Carangid. The groups identified in this study include *Epinephelus areolatus*, *Variola albimarginata*, and *Cephalopholis sonnerati*, whereas the Carangids group includes *Parastromateus niger*, *Megalaspis cordyla*, *Caranx sexfasciatus* and *Decapterus macarellus* (Table 1).

In another group on the Clupeiformes order, two families found in the Kutaradja namely Clupeidae (*Sardinella jussieu*) and Engraulidae (*Stelephorus commersonii* and *Thryssa baelama*). In connection with the types of fish caught by fishermen, it is shown that capture fisheries in Banda Aceh use purse seine which catches a group of pelagic fish in large quantities. Previous studies have explained that the fishermen in Banda Aceh mostly use purse seine (Hariati, 2017, Wiryawan et al., 2016). The purse-seine also generally fishing gear to catch fish of *Euthynnus affinis*, *Auxis thazard*, and *Auxis rochei* (Salmarika and Wisudo, 2019).

The small number of fish collected in this study are fish that are associated with coral reefs such as grouper fish groups that make coral reef areas as a nursery ground, feeding ground, and spawning ground. The diversity of reef fish around Banda Aceh experiences a natural gradient, which shows an increase in the area far from the mainland of the island of Sumatra. Diversity in the area of small islands around Banda Aceh still shows good conditions when compared to the condition of coral reefs in the mainland, Sumatra (Edrus et al., 2016). The species of *Epinephelus areolatus*, *Variola albimarginata*, and *Cephalopholis sonnerati* are a group of fish that become coral reefs as their habitat. However, pelagic fish around the shallow seas of Banda Aceh remain the main target such as skipjack tuna *Rastrellinger kanagurta* (Hariati and Fauzi, 2017, Hariati et al., 2015), yellowfin tuna *Thunnus albacares* (Neliyana et al., 2014), Mackerel scad *Decapterus macrosoma*, dan anchovy *Stolephorus spp* (Kurnia et al., 2016) were also obtained in this study.

In this report, several Acehnese fish sequences also have similarities in some previous studies, and some are unique to other sequences. Species *Auxis Thazard*, identified from the port of Kutaradja, may have been collected from the area around the sea waters of Western of Banda Aceh Province with a catch distance of about 50-190 nautical miles (Salmarika and Wisudo, 2019). Although it is still in the Indian Ocean region, there may be specialization in this species so that the Aceh haplotype separated from the same species in the resulting phylogenetic tree analysis.

In this study, a phylogenetic tree analysis of 3 important marine fish families, namely Scombridae, Serranidae, and Carangidae, was carried out. The results of the analysis found that the Scombridae *Auxis thazard* (Aceh) which separates from the same clade species even though it only has a genetic distance of only 0.002. This haplotype appears likely to occur due to differences in species populations analyzed from India, China (Xu et al., 2019), and Spain (Catanese et al., 2008). While other haplotypes found in reef fish are *Variola albimarginata* and *Cephalopholis sonnerati*, the *Variola albimarginata* from Aceh may be a population with the results of a study conducted in India that allows the sharing of habitats in the Indian Ocean in the Western part of Sumatra Island. Previous studies on molecular identification of *Variola albimarginata* species have carried out in the Andaman Islands and Nicobar Island (Basheer et al., 2017). This area is Indian sea waters which have the potential to have reef fish which are almost the same as the species in Aceh. While *Cephalopholis sonnerati* fish species also have similarities with populations from Australia and the Philippines, but slightly different from populations from China (Zhuang et al., 2013). The study of *Cephalopholis sonnerati* shows the possibility of differences in the structure of coral fish populations in the South China Sea with Indian Ocean, especially in Aceh waters. Although integrated with Indian Ocean waters, no similarities with Indian populations found in the *Cephalopholis sonnerati* species only in previous studies conducted in the Philippines (Alcantara and Yambot, 2016), and Australia (Ward et al., 2005). The speciation process that occurs in coral reef ecosystems

occurs with an allopathic pattern that makes geographic isolation the main cause for the emergence of different species. However, the presence of pelagic larvae in reef fish species also becomes a big question even though it is believed that the allopatric pattern is a speciation pattern on the main coral reefs (Rocha and Bowen, 2008).

CONCLUSIONS

From this study, identification of marine fish landed at the fishing port of Kutaradja confirmed 47 specimens (33 genera) of marine fish that became fishery commodities and became the main target of the Province of Banda Aceh's exports, including Tuna fish (*Thunnus albacares*) and Cakalang fish (*Katsuwonus pelamis*). In this study, the Scombridae group, found one Aceh haplotype in the *Auxis thazard* species (MN257554), whereas in the Carangids group, it was known that the *Elagatis bipinnulata* species (MN257553) had similar sequences with the same species from Alabama USA (KF461174). Another species in the Carangidae order, namely *Decapterus macarellus* from Aceh, has similarities with the sequence China (MH638794) and Malaysia (KY570732). In this type of reef fish, this study found *Variola albimarginata* species (India KM226315) which had similarities with Aceh samples, while *Cephalopholis sonnerati* (MN257517) had similarities with the same sequence species from the Philippines (KU668631) and Australia (DQ107928). More in-depth research on the haplotypes of the marine fish mentioned above is very much needed to maintain genetic biodiversity in the waters of Banda Aceh which is a very valuable asset for Indonesia

ACKNOWLEDGMENTS

This work was supported by an educational grant from the LPDP BUDI-LN batch I 2016 and Molecular Physiology Laboratory, Department of Marine Biology, Pukyong National University, Korea. This paper as the initiation of the first research collaboration between Universitas Airlangga and Syiah Kuala University.

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