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DNA Barcoding of Commercially Important Snappers (Genus *Lutjanus* (Pisces: Lutjanidae)) from Aceh Waters, Indonesia

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ABSTRACT

Snappers (Lutjanidae) are a group of reef fishes with high commercial importance in Indonesia. However, there is currently a lack of available information on the bioecology and genetics of these snappers. The present identification of snapper species relies primarily on morphological differences, frequently leading to misidentification due to the high similarity among members of this fish group. Molecular data has emerged as a crucial tool in validating and supporting fisheries management plans. Therefore, this study uses a DNA barcoding approach to analyze and validate the taxonomic status of commercially important snappers harvested from Aceh water. DNA barcoding is a species identification method that uses a DNA base sequence system, typically mitochondrial DNA (mtDNA) "cytochrome oxidase subunit I" (COI) in animals, with a standard length of 648 bp. The fish samples were collected from January to August 2022 at several landing sites across Aceh, namely Weh Island, Aceh Besar, Banda Aceh, Langsa, Simeulue, and Tapak Tuan. A total of 78 sequences belonging to 15 species were successfully generated. The genetic distance and phylogenetic analyses showed that *L. decussatus* and *L. lemniscatus* had a close relationship (genetic distance: 4.90%), while the farthest genetic distance was found between *L.gibbus* and *L. lemniscatus* (16.97%). In addition, this study provided a reliable DNA barcode reference library of significant snappers from Aceh for fisheries management through precise species identification for conservation strategies.

1. INTRODUCTION

Aceh Province is located in the westernmost part of Indonesia within the Indo-Malaya Archipelago (IMA) region of Southeast Asia. This region is renowned as a hotspot for tropical marine biodiversity [1]. Therefore, capture fisheries play an important role in Aceh, which has steadily increased in production. According to the Department of Marine and Fisheries of Aceh, the annual catch of marine fisheries was 209,642 tons in 2017 and increased to 283,676 tons in 2021 [2]. Coral reef fish constitute a significant portion of the catchment composition [3-6], with snappers (family Lutjanidae) being predominant [7]. The annual snapper catches in Aceh were 18,786.8 tons in 2017, increasing to 20,998.8 tons in 2021 [2].

The Lutjanidae family comprises at least 113 species of 17 genera [8]. This fish lives in the tropics and subtropical regions, with a wide distribution in Indonesian waters from Aceh to Papua Province [9, 10]. To date 58 species have been reported in Indonesian waters [8]. While most snappers live in the oceans and inhabit depths less than 100 m, some can live at depths of 100 to 200 m with a maximum depth of up to 450 m [11]. Several species have also been reported foraging and spawning in freshwater habitats [8, 12]. Snappers are mostly carnivorous, feeding on small fish and crustaceans [8].

The current identification of snapper species relies primarily on morphological differences, which often leads to misidentification due to the high similarity among members of this fish group. This lack of accurate taxonomic status for fish at landing sites hinders effective capture fisheries management [7, 13]. Accurate species identification is crucial for stock assessment and the allocation of catchment quotas. In Indonesia, fish landing data are typically recorded without precise species information and often registered under local names. Moreover, local names can differ among regions, and multiple snapper species may be recorded in a particular

common group. As mentioned earlier, snappers are difficult to distinguish among closely related species due to highly similar morphology and overlapping characteristics [14]. This difficulty in differentiation has led to the discovery of cryptic diversity and new snapper species [15]. Therefore, molecular tools such as DNA barcoding have become a necessary complementary approach to address these problems by using the mitochondrial COI gene to rapidly and accurately identify species based on their unique genetic fingerprints, overcoming the limitations of traditional taxonomy [16]. DNA barcoding is an appropriate method of classifying and identifying a species that is difficult to identify based solely on morphology. Thus, this research can be used as a basis for information and a conservation strategy in the future [17, 18].

In the regional context, there have been limited studies on DNA barcoding of snappers. Allen et al. [19] used barcoding to describe two new species of snappers, namely *L. indicus* from the Indo-West Pacific and *L. papuensis* from Cenderawasih Bay, West Papua, Indonesia. Iwatsuki et al. [20] barcoded and described a new snapper species (*L. xanthopinnis*) from the Indo-West Pacific based on the same approach. In another study, da Silva et al. [11] barcoded 18 snappers' species from the Western Atlantic and Eastern Pacific, while Bakar et al. [15], identified 17 species in Malaysia using the COI gene. Furthermore, Velamala et al. [14] barcoded ten species of snappers from Visakhapatnam, Central Eastern coast of India. Sala et al. [10] also successfully barcoded nine species of snappers from Yapen, Papua, Indonesia.

Although snappers have high economic value and market demand in Aceh, detailed investigation on the species is still limited. The majority of studies were focused on inventory analysis using the traditional taxonomy approach. For example, Muchlisin et al. [21] recorded four snappers species namely *L. argentimaculatus, L. johnii, L. russelli,* and *Lutjanus* sp. in the estuary of Tripa Peat Swamp, Aceh Province. In another study, Batubara et al. [3] found 77 commercial marine fishes on Simeulue Island, including 13 Lutjanidae species. Furthermore, Dekar et al. [12] documented three snappers species namely *L. argentimaculatus, L. monostigma*, and *L. russelli* in the estuary of Aceh River. Batubara et al. [22] reported three Lutjanidae species including *L. ehrenbergii*, *L. johnii*, and *L. fulviflamma* in the estuary area of Simeulue Island. In another study, Fadli et al. [9], recorded five Lutjanidae species namely *L. decussatus, L. johnii, L. bengalensis, L. lutjanus,* and *L. rufolineatus* on Weh Island. This was the first molecular taxonomic study of fishes on this island creating the initial and detailed COI sequences repository of important snapper in Aceh, thus establishing a foundational dataset for a fisheries management plan in Aceh.

Therefore, this study aims to expand the DNA barcoding data and validate the taxonomic status of *Lutjanus*, the major commercially important snappers in Aceh waters, Indonesia.

2. MATERIAL AND METHODS

2.1 Sample collection

The fish samples were collected from January to August 2022 at several landing sites across Aceh, namely Weh Island (5°53'9.74" N 95°19'21.49" E), Aceh Besar (5°42′0″N 95°4′0″ E), Banda Aceh (5°35'7.80" N95°18'59.31″ E), Langsa (4.47° N 97.95° E), Simeuleu (2°29′00″ N 96°22′30″ E), and Tapak Tuan (3°15'12.16″ N 97°11'47.16″ E) (Figure 1). The fish was morphologically identified based on Froese and Pauly [8]. The tissue sample was taken from the pectoral fin of each individual with at least five samples for each presumed taxon and stored in 96% ethanol in a 2 mL tube. Whole specimens were transported to the Genetics and Aquatic Biodiversity Laboratory, Faculty of Marine and Fisheries, Universitas Syiah Kuala, at Banda Aceh, Indonesia, for documentation, laboratory work, and storage.

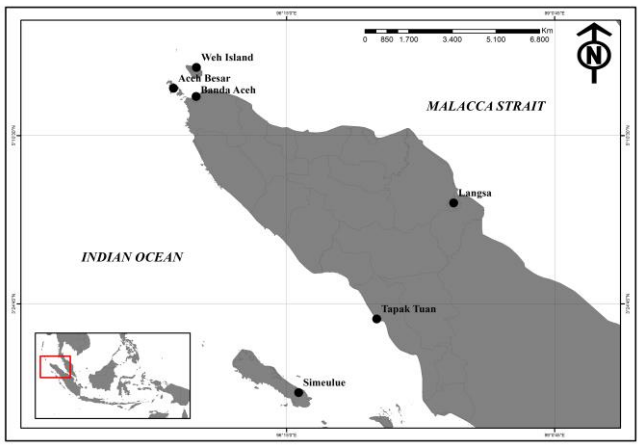

Figure 1. The map of Aceh province showed sampling sites of snappers along the coast of Aceh (black dots)

2.2 Extraction, PCR, and DNA sequencing

DNA was extracted based on the modified cetyl trimethylammonium bromide (CTAB) protocol [23]. The fish fin was finely chopped inside a sterile 1.5 mL tube. Subsequently, CTAB solution was added to the tube, totalling 700 µL, along with 3 µL of Proteinase K. It was uniformly mixed using a vortex for 15 seconds and then incubated at 60°C for 3 hours. After incubation, 700 µL of chloroform isoamyl alcohol (CIA) was added, mixed thoroughly for 30 seconds, and centrifuged at 11000 rpm for 15 minutes. The clear supernatant was then transferred to a new 1.5 mL sterile tube. A volume of 100% ethanol was added, and the solution was vortexed for 30 seconds. The solution was centrifuged at a speed of 12000 rpm for 15 minutes. The supernatant was discarded and the tube cleaned with 70% ethanol. The tube was inverted and tapped several times on tissue paper to remove residual ethanol. Then, 60 µL of deionized water was added and DNA stored at -20°C.

Partial COI gene (DNA barcoding gene) was then amplified using the set of primers FishF1: 5'TCA-ACC-AAC-CAC-AAA-GAC-ATT-GGG-AC3' and FishR1:5'TAG-ACT-TCT-GGG-TGG-CCA-AAG-AAT-CA3'), according to Ward et al. [24]. PCR was run in a 25 µL master mix containing 12.5 µL MyTaq Red Mix, 2.0 µL DNA template, 1 µL each primer, and 8.5 µL ddH_2O water on a Sensoquest gradient Thermal Cycler (https://www.sensoquest.de/). The thermocycling conditions consisted of initial denaturation at 95°C (2 min) followed by denaturation at 94°C (30 cycles, 45 s), annealing at 49.7 – 60°C (45 s); elongation at 72°C (1 min), and final extension at 72°C (10 min) before termination of the reaction at 4°C [9, 15]. The FishF1 primer region is typically short enough to be easily amplified using this PCR method, and its sequencing is technically feasible and facilitates efficient DNA barcoding workflow [25].

PCR products that met the standards were sent to Apical

Scientific Sdn Bhd, Malaysia, for sequencing using BigDye Terminator v3.1 Cycle Sequencing Kit and ABI PRISM 3730xl DNA Analyzer (Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

2.3 Data analysis

The results of COI gene sequencing were synchronized and edited using MEGA 6.06 software [26]. The sequences were compared with BLAST (http://www.ncbi.nlm.nih.gov/BLAST) and BOLD (www.boldsystems.org) to confirm the species' identity. The genetic distance was estimated with the Kimura-2-parameter (K2P) model using MEGA 6.06 [26]. Nearest-neighbor analysis was carried out by applying a Barcoding Gap Analysis. In addition, the MEGA 6.06 software was also used to cluster COI haplotypes into a Neighbor-Joining (NJ) phylogeny, employing 1000 bootstrap replicates. *Caranx ignobilis* sequence (Accession No. MW 498554) was used as outgroup. The conservation status of the observed snappers was determined based on the International Union for Conservation of Nature (IUCN) website (http://www.iucnredlist.org, accessed on 28 May 2023).

3. RESULTS AND DISCUSSION

A total of 78 sequences belonging to 15 species were successfully generated in this study. In contrast to Langsa, where only one species was found, Aceh Besar recorded the highest number of species (nine), followed by Banda Aceh and Weh Island (both with six), as shown in Table 1.

Table 1. List of commercially important snapper species from Aceh, Indonesia

Species	Sample Locality						Total Sample
	WI	BA	AB	LG	TT	SML	
Lutjanus argentimaculatus				4			4
Lutjanus bengalensis	5	1	1				7
Lutjanus decussatus	3		1				4
Lutjanus fulviflamma	2	12					14
Lutjanus fulvus			2				2
Lutjanus gibbus			3				3
Lutjanus johnii	2	1			2		5
Lutjanus kasmira		1	1			3	5
Lutjanus lemniscatus			1				1
Lutjanus lunulatus			3				3
Lutjanus Lutjanus	6	3					9
Lutjanus rufolineatus	8				4	2	14
Lutjanus russelli			4				4
Lutjanus vitta			1				1
Lutjanus xanthopinnis		2					2
	26	20	17	4	6	5	78

Note: WI= Weh Island; BA= Banda Aceh; AB= Aceh Besar; LG= Langsa; TT= Tapak Tuan; and SML= Simeulue

3.1 Nucleotide diversity

The sequence read lengths were 612 bp with an average nucleotide composition of A = 25.03%, T = 28.17%, C = 29.07%, and G = 17.73%. There were 388 conserved sites and 224 variable sites, of which 213 were parsimony informative, and 11 were singletons. The base composition showed that the AT content (53.20%) was higher than the GC content (46.80%), as depicted in Table 2.

Table 2. Summary statistics for the nucleotide frequency distribution of COI sequences of snappers in Aceh

	Min.	Mean	Max.
G%	15.31	17.73	19.22
C%	27.29	29.07	31.05
A%	23.98	25.03	26.14
T%	25.65	28.17	29.90
AT%	50.49	53.20	55.23
GC%	44.77	46.80	49.51

Other studies about DNA barcoding of reef fish in northern Aceh of Fadli et al. [9] also showed results which were similar for the genetic diversity dan nucleotide composition values of A = 24.15%, T = 29.56%, C = 28.14% and G = 18.14%. However, assessment of fish diversity in the South China Sea of Xu et al. [27] showed the average base composition was A = 23.76%, C = 28.88%, G = 18.64%, and T = 28.71%. This shows that nucleotide diversity and population composition may depend on geographic distribution [28].

3.2 Species delimitation

The current data showed 98–100% identity with BOLD and BLAST searches, implying the effectiveness of COI sequences for species identification. The results of the Barcoding Gap Analysis also indicated that the maximum intraspecies distance was less than 2% among all putative species. The nearest neighbor (NN) distance ranged from 4.90% to 13.56%. This analysis also showed that all specimens exhibited high distance values to their nearest neighbor, indicating the presence of a "barcode gap" among the 15 presumed species (Figure 2, Table 3). Furthermore, the NJ tree revealed that all the presumed species formed monophyletic clusters without any overlap (Figure 3). The pairwise comparisons of the COI gene based on K2P distances (%) within species and between snapper species are presented in Table 4.

Based on the IUCN conservation status, most observed snappers were categorized as Least Concern (LC) with unknown population trends. Only *L. xanthopinnis* was considered Data Deficient (DD), while *L. decussatus* showed a decreasing population trend, as depicted in Table 5.

Table 3. The average and maximum intraspecific values for each species to the distance to a nearby species

No.	Species	Mean Intra-Species (K2P%)	Max Intra-Species (K2P%)	Nearest Neighbor	Distance to Nearest Neighbor (K2P%)
1	*Lutjanus argentimaculatus*	0.01	0.02	*Lutjanus fulvus*	12.54
2	*Lutjanus bengalensis*	0.00	0.01	*Lutjanus kasmira*	5.37
3	*Lutjanus decussatus*	0.00	0.00	*Lutjanus lemniscatus*	4.90
4	*Lutjanus fulviflamma*	0.00	0.01	*Lutjanus decussatus*	8.34
5	*Lutjanus fulvus*	0.00	0.00	*Lutjanus kasmira*	8.93
6	*Lutjanus gibbus*	0.00	0.00	*Lutjanus Lutjanus*	13.56
7	*Lutjanus johnii*	0.01	0.01	*Lutjanus Lutjanus*	12.52
8	*Lutjanus kasmira*	0.01	0.02	*Lutjanus bengalensis*	5.37
9	*Lutjanus lemniscatus*	N/A	0.00	*Lutjanus decussatus*	4.90
10	*Lutjanus lunulatus*	0.00	0.00	*Lutjanus decussatus*	5.10
11	*Lutjanus Lutjanus*	0.00	0.01	*Lutjanus vitta*	7.58
12	*Lutjanus rufolineatus*	0.01	0.02	*Lutjanus kasmira*	5.75
13	*Lutjanus russelli*	0.00	0.00	*Lutjanus fulviflamma*	9.29
14	*Lutjanus vitta*	N/A	0.00	*Lutjanus lemniscatus*	6.91
15	*Lutjanus xanthopinnis*	0.00	0.01	*Lutjanus vitta*	6.99

N/A is represented by a single specimen

Table 4. COI gene pairwise comparisons based on mean K2P distances (%) between snapper species and within species (in bold)

No.	Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	*Lutjanus argentimaculatus*	**0.01**														
2	*Lutjanus bengalensis*	13.91	**0.00**													
3	*Lutjanus decussatus*	12.96	12.24	**0.00**												
4	*Lutjanus fulviflamma*	15.12	13.45	8.34	**0.00**											
5	*Lutjanus fulvus*	12.54	10.69	12.89	14.86	**0.00**										
6	*Lutjanus gibbus*	15.91	16.45	15.25	15.76	16.77	**0.00**									
7	*Lutjanus johnii*	14.98	15.51	13.06	14.90	17.42	17.12	**0.01**								
8	*Lutjanus kasmira*	12.60	5.37	12.18	14.18	8.93	15.35	15.28	**0.01**							
9	*Lutjanus lemniscatus*	13.57	11.28	4.90	9.02	13.61	16.97	14.44	11.99	**N/A**						
10	*Lutjanus lunulatus*	13.18	12.15	5.10	9.15	14.23	14.59	14.10	10.91	6.59	**0.00**					
11	*Lutjanus Lutjanus*	14.14	12.59	8.44	9.87	13.89	13.56	12.52	11.49	8.46	9.25	**0.00**				
12	*Lutjanus rufolineatus*	12.70	6.37	13.30	13.37	9.97	15.83	14.47	5.75	13.30	12.11	11.34	**0.01**			
13	*Lutjanus russelli*	15.57	14.73	9.30	9.29	15.04	14.90	14.89	14.30	10.75	10.59	10.99	13.88	**0.00**		
14	*Lutjanus vitta*	14.95	12.15	8.56	9.54	13.42	17.16	15.15	11.97	6.91	9.92	7.58	11.82	10.74	**N/A**	
15	*Lutjanus xanthopinnis*	13.63	13.53	8.92	10.35	14.92	16.09	14.79	13.09	8.74	9.20	8.55	13.58	11.82	6.99	**0.00**

N/A is represented by a single specimen

Table 5. List of the studied snapper species from Aceh, Indonesia and their IUCN status

No.	Species	Common Name	IUCN status	Population Trend
1	*Lutjanus argentimaculatus*	Mangrove Red Snapper	LC	Unknown
2	*Lutjanus bengalensis*	Bengal Snapper	LC	Unknown
3	*Lutjanus decussatus*	Checkered Snapper	LC	Decreasing
4	*Lutjanus fulviflamma*	Dory Snapper	LC	Unknown
5	*Lutjanus fulvus*	Blacktail Snapper	LC	Unknown
6	*Lutjanus gibbus*	Humpback Red Snapper	LC	Unknown
7	*Lutjanus jhonii*	John's Snapper	LC	Unknown
8	*Lutjanus kasmira*	Common Bluestripe Snapper	LC	Unknown
9	*Lutjanus lemniscatus*	Yellow Streaked Snapper	LC	Unknown
10	*Lutjanus lunulatus*	Lunartail Snapper	LC	Unknown
11	*Lutjanus Lutjanus*	Bigeye Snapper	LC	Unknown
12	*Lutjanus rufolineatus*	Yellow-Lined Snapper	LC	Unknown
13	*Lutjanus russelli*	Russell's Snapper	LC	Unknown
14	*Lutjanus vitta*	Brown Stripe Red Snapper	LC	Unknown
15	*Lutjanus xanthopinnis*	Yellowfin Snapper	DD	Unknown
Total				

(LC= Least Concern, DD= Data Deficient) (http://www.iucnredlist.org, accessed on 28 May 2023)

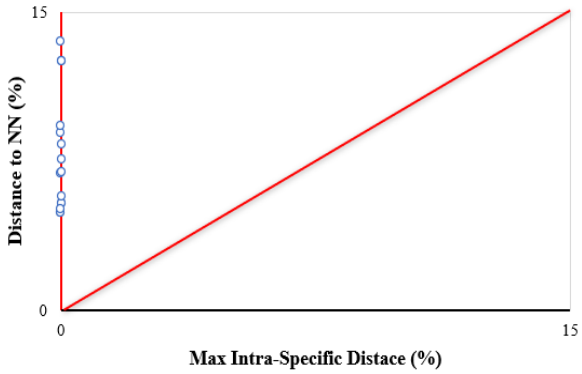

Figure 2. Maximum intraspecific divergence (% K2P) in the barcode region of the COI displayed versus the distance to the nearest neighbor (% K2P) for the 15 species
A barcode gap was present based on the locations of all spots above the red line in each comparison

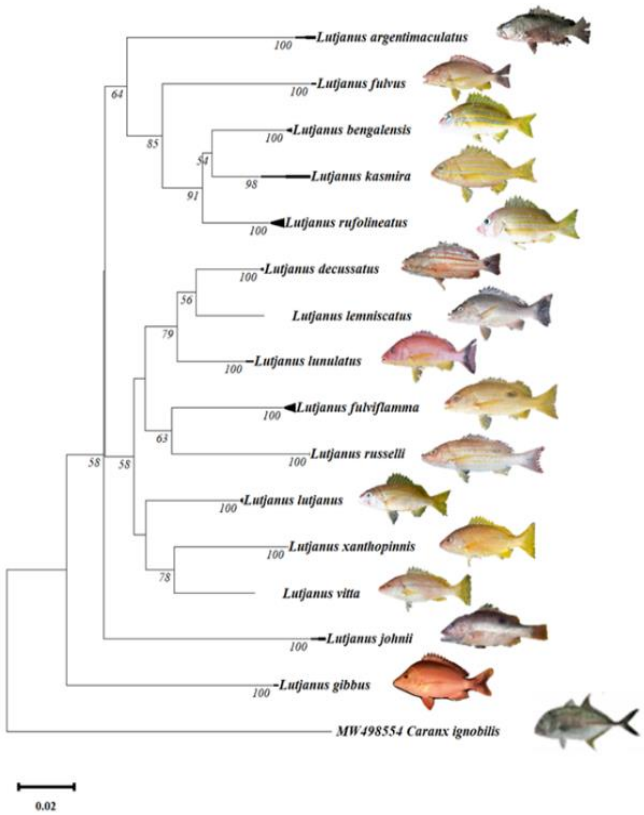

Figure 3. Neighbor-Joining (NJ) tree of COI barcodes for all snapper samples

This study successfully barcoded 15 species of commercially important snappers in Aceh waters, providing genetically based data for precise species identification. The accurate identification of these 15 presumed species was verified by comparing database sequence similarity and genetic distance with voucher references from reference DNA libraries in BLAST and the BOLD Identification System, which showed matches with 98% to 100% identity. In addition, the existence of a "barcoding gap" in this study implied that all the barcoded species were valid independent taxa. All the documented species formed monophyletic clusters without any intersection.

The number of *Lutjanus* species found in this study was consistent with Bakar et al. [15] and da Silva et al. [11], which barcoded 17 and 18 species of *Lutjanus* species in Malaysia, as well as Western Atlantic and Pacific Eastern, respectively. Meanwhile, ten *Lutjanus* species were barcoded from Visakhapatnam, Central Eastern coast of India [14], and nine Lutjanidae species in Yapen, Papua, Indonesia [10]. Most Aceh snappers were found in the northern, south, and west Aceh regions. There were 14 species of snapper successfully identified in northern Aceh waters (Banda Aceh, Aceh Besar, and Weh island), southern Aceh swaters (Aceh Selatan) and western Aceh waters (Simeulue), namely *L. bengalensis*, *L. decussatus*, *L. fulviflamma*, *L. fulvus*, *L. gibbus*, *L. johnii*, *L. kasmira*, *L. lemniscatus*, *L. lunulatus*, *L. lutjanus*, *L. rufolineatus*, *L. russelli*, *L. vitta*, and *L. xanthopinnis*. This is because these regions are dominated by coral reef ecosystems, which are favorable habitats for the snappers [8]. In contrast, only one species was found in the eastern part of Aceh (Langsa), namely the mangrove red snapper (*L. argentimaculatus*) which generally lived in the estuary and mangrove areas [8]. The eastern part of Aceh is dominated by estuaries and mangrove areas [29], thereby providing suitable habitat for *L. argentimaculatus*.

Intraspecies' genetic distances were consistently lower than 2%, supporting the precision and monophyly of each morphologically identified specimen. This result was consistent with previous snapper's DNA barcoding studies, such as the commercial red snappers (*Lutjanidae* sp.) from three marine regions in Malaysia, which showed genetic distance ranging from 0.1% − 0.7% [30]. Furthermore, numerous snapper species exhibited a lack of COI genetic variation, including *L. bengalensis, L. decussatus, L. fulviflamma, L. fulvus, L. gibbus, L. johnii, L. kasmira, L. lunulatus,* and *L. russelli.* These results could be attributed to several factors. Firstly, the fish were from the same population and shared identical genetic material. Secondly, a low genetic diversity value indicated overexploitation of these species in Aceh. Overfishing often led to reduced genetic variation in fish populations [31]. Snappers, along with groupers, are among the fishes with the highest prices in Aceh. The fish are targeted and exploited to supply local and regional markets. This study was limited to identifying species using COI genes and looking at the genetic diversity of species in a population. There is a possibility of bias in sampling due to a lack of knowledge in snapper morphological data in Aceh waters. It is hoped that in future, research on snapper morphology and genetics, especially in Aceh, can explore more species and also investigate the relationship between weight length and population dynamics of snapper in a population to ascertain whether the populations are indeed overexploited.

Declines in snapper populations have been reported in several parts of the world. For example, Guardia et al. [32], found that the population of Mutton (*L. analis*) and Cubera snappers (*L. cyanopterus*.) in the southwest shelf of Cuba had experienced overfishing. A similar situation also occurred in some parts of Indonesia. Halim et al. [33] in a study conducted in the Coral Triangle, eastern Indonesia, found that Humpback red (*L. gibbus*) and Moluccan snappers (*L. boutton*) were heavily exploited. Without good management efforts, the snapper fishery in Aceh could face similar challenges. However, at the beginning of 2023, the Governor of Aceh issued regulation No. 3 of 2023 about Sustainable Fisheries Management Action Plan in Aceh Waters (2023-2027). This regulation includes provisions for the management of commercially important reef fish fisheries in Aceh, including for snappers and groupers.

The genetic distance and phylogenetic analysis showed that *L. decussatus* with *L. lemniscatus* had a close relationship (genetic distance: 4.90%). This was consistent with the result of Bakar et al. [15] for snappers in Malaysia. The second close relationship was observed between *L. decussatus* with *L. lunulatus* (5.10%). Another closely related pair was *L. kasmira* and *L. bengalensis* with a genetic distance of 5.37%. Direct observation showed that both fish shared a similar color pattern with four horizontal blue stripes on a bright yellow body [8]. Moreover, study by Barman et al. [34] and Rahayu et al. [35] also noticed the same observation.

The genetic data produced in this study holds significant importance for future snapper fisheries management, specifically in the Aceh region. This study has successfully established a reliable DNA barcode reference library of important significant snappers from Aceh. This database can be used as a reference for many genetic-related studies in the future. In addition, the obtained data can also be used to combat fraud in fisheries due to intentional substitutions. Also, this molecular approach that improves species identification addresses taxonomic uncertainties and facilitates a nuanced understanding of biodiversity.

Snappers are one of the most "mislabeled" commodities in fisheries products across various countries [36-38]. According to several studies, snapper-processed fish products are sometimes substituted with less valuable species for higher-valued ones. For example, Marko et al. [36], based on the genetic technique found that 77% of the red snappers (*L. campechanus*) sold in the US belonged to a different species. Willette et al. [39], reported that the frequency of mislabeling in sushi restaurants in Los Angeles was consistently high (77%) for halibut, red snappers, yellowfin tuna, and yellowtail. In another study, Veneza et al. [40] found that 22% of the red snappers (*L. purpureus*) fillets were replaced by vermilion snappers (*Rhomboplites aurorubens*), having a lower price in Brazil. Furthermore, Isaacs and Hellberg [41] utilized DNA barcodes to detect mislabeled red snappers (*Lutjanus campechanus*) fillets in Orange County, CA, USA.

4. CONCLUSIONS

In conclusion, the study showed substantial contributions to the molecular taxonomy of snappers from Aceh and is a significant addition to the DNA barcode library of marine fishes from Indonesia and worldwide. It provided genetically based data by successfully barcoding 15 species of commercially important snappers. The results offered a reliable DNA barcode reference library of Aceh snappers, serving as the initial dataset for future fisheries management in Aceh.

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