International Journal of Design & Nature and Ecodynamics
Vol. 20, No. 11, November, 2025, pp. 2633-2640
Journal homepage: http://iieta.org/journals/ijdne

DNA Barcoding Reveals Species Diversity and Cryptic Lineages of Commercially Important Carangidae in Aceh Waters, Indonesia

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https://doi.org/10.18280/ijdne.201114

Received: 6 September 2025
Revised: 16 October 2025
Accepted: 27 October 2025
Available online: 30 November 2025

Keywords:
COI, fisheries, genetics, Rambue, Western Indonesia

ABSTRACT

Trevally (family Carangidae), locally referred to as "Ikan Kuwe" or "Ikan Rambue," is one of the most commercially valuable marine fish groups in Aceh. Despite their high market demand and economic importance, scientific information on Carangidae species in this region remains limited. Comprehensive data, particularly molecular information, are essential for supporting sustainable fisheries management. In recent years, molecular approaches such as DNA barcoding have become increasingly important for accurate species identification and resource monitoring. This study aimed to identify commercially significant trevally species in Aceh through DNA barcoding using mitochondrial cytochrome c oxidase subunit I (COI) gene markers. Samples were collected from various fish landing sites across Aceh, including Banda Aceh, Lhokseumawe, Langsa, Meulaboh, Simeulue, and Aceh Singkil. DNA was extracted using a modified CTAB protocol, and COI gene sequences were analyzed using MEGA X software. In total, 20 Carangidae species were successfully identified, belonging to 11 genera, including *Alectis ciliaris*, *Atropus armatus*, *Atropus hedlandensis*, *Atropus mentalis*, *Carangichthys oblongus*, *Caranx heberi*, *Caranx ignobilis*, *Caranx melampygus*, *Caranx sexfasciatus*, *Caranx* sp., *Caranx papuensis*, *Caranx tille*, *Decapterus macarellus*, *Decapterus maruadsi*, *Ferdauia ferdau*, *Platycaranx malabaricus*, *Platycaranx talamparoides*, *Scyris indica*, *Selar crumenophthalmus*, and *Turrum coeruleopinnatum*, with a total of 140 sequences identified. Among these, *Caranx* was the most dominant genus, comprising approximately 35% of the total specimens, followed by *Atropus*, which accounted for 15%. This study provides a crucial molecular baseline for future conservation, fisheries management, and the detection of cryptic diversity in the region.

1. INTRODUCTION

The Carangidae family, commonly referred to in Indonesia as *Ikan Kuwe* or *Ikan Rambue*, includes a variety of pelagic fish species that hold substantial economic significance, particularly in regions such as Aceh. Based on data from the FAO (2020), Indonesia's total Carangidae catch amounted to approximately 1,034,529.384 tons. In Aceh Province alone, the record of the Ministry of Marine Affairs and Fisheries catch was 48,041.15 tons, generating a production value of IDR 1,120,702,238,000. Taxonomically, Carangidae consists of four subfamilies, 30 genera, and 147 identified species, and is widely distributed in tropical and subtropical marine environments [1]. While most species dwell in waters shallower than 20 meters, some can be found at depths reaching 100 meters [2]. Distinctive morphological traits of this family include the presence of two separate dorsal fins, a lateral line that curves near the head and runs straight toward the tail, and coarse, enlarged scales around the caudal peduncle [3]. Members of the Carangidae family exhibit a broad size range—from 16 cm up to 250 cm—and display diverse body forms, including elongated, fusiform (torpedo-like), and laterally compressed shapes [4]. Various species are known by common names such as jacks, pilotfish, trevallies, pompanos, amberjacks, kingfish, scads, rainbow runners, and queenfish [3, 5].

Identifying species within the Carangidae family presents significant challenges due to their highly similar morphometric and meristic traits, along with overlapping body shapes, sizes, and coloration patterns [3, 6]. Furthermore,

many Carangidae species undergo notable changes in morphology and pigmentation throughout different stages of their development, increasing the risk of taxonomic misidentification [5]. One prominent example is the giant trevally (*Caranx ignobilis*), which is often mistaken for other species due to its ontogenetic variations. Juvenile *C. ignobilis* typically displays a silvery yellow to silvery brown coloration, whereas adults exhibit a silvery white underside with a dorsal side ranging from silvery olive to blue-green. The coloration of this species may also vary—shifting to white or yellow—based on environmental factors [7, 8].

Accurate species identification, particularly for fish recorded at fish landing sites (Tempat Pendaratan Ikan, TPI), is crucial for the sustainable management of capture fisheries [9]. In many leading fishing nations, including Indonesia, catch data are frequently recorded using vernacular or local names rather than standardized scientific nomenclature. For example, Carangidae species are often documented under various regional names such as *Cipa-Cipa*, *Kuwe Abu-Abu*, *Totol Kuning*, *Kuwe Bibir Tebal*, and *Kuwe Pectoral*, rather than by their taxonomic names (http://nelpin.kkp.go.id/). This practice complicates accurate stock assessments and biodiversity monitoring. Consequently, molecular identification techniques—such as DNA barcoding—have become indispensable for clarifying species-level classifications and addressing these inconsistencies.

DNA barcoding, first introduced by Hebert et al. [10], employs the mitochondrial cytochrome *c* oxidase subunit I (COI) gene as a universal marker for species identification across a broad range of organisms. This molecular technique has gained widespread acceptance for identifying marine fish species, including those belonging to the Carangidae family. Numerous studies have utilized DNA barcoding to delineate Carangidae species in various geographic regions. For example, Mat Jaafar [2] successfully barcoded 36 Carangidae species in the Indo-Malaya Archipelago. In the Philippines, Templonuevo et al. [11] applied the method to seven species found in Palawan. Along Vietnam's coastline, Thu et al. [12] identified 21 species spanning 16 genera within the Carangidae family. Similarly, Ahmed et al. [13] recorded 185 marine fish species in Bangladesh, including 12 Carangidae species. In Malaysia, Nur et al. [14] focused on 13 economically important Carangidae species. Despite these regional advancements, DNA barcoding studies specific to Indonesian Carangidae are still relatively scarce. One such effort by Andriyono et al. [5] involved the identification of five Carangidae species collected from traditional fish markets in Java and Bali.

In addition to aiding species identification, DNA barcoding has significantly contributed to the detection of cryptic species within the Carangidae family across various regions. For instance, Mat Jaafar et al. [6] uncovered cryptic diversity among species such as *Atule mate*, *Selar crumenophthalmus*, and *Seriola nigrofasciata* in the Indo-Malaya Islands. Similarly, a study by Nur et al. [14] demonstrated substantial intraspecific genetic divergence in *Carangoides coeruleopinnatus* and *C. gymnostethus* from Malaysian waters, suggesting the possible existence of cryptic species within these taxa.

To date, comprehensive research on Carangidae species in the Aceh region remains limited. For instance, Batubara et al. [15] documented three Carangidae species from Simeulue Island, while Dekar et al. [16] reported the presence of *Carangoides malabaricus*, *Caranx sexfasciatus*, and *Caranx crysos* in the Aceh River, Aceh Besar. In another study, Zulfahmi et al. [17] identified six species belonging to the Carangidae family in the coastal waters of Sabang, Aceh. However, none of these investigations utilized DNA barcoding techniques for species identification, and the lack of such reliable molecular tools has limited accurate stock assessment and biodiversity monitoring in this economically important region. Instead, they relied solely on morphological traits, which may lead to misidentification due to the high degree of similarity among Carangidae species.

Therefore, the present study aims to develop the first comprehensive COI sequence reference library for Carangidae species in Aceh and to identify potential cryptic species diversity within the collected specimens. This molecular database will serve as a foundational resource for improving species identification accuracy and will support more effective fisheries management strategies, both regionally in Aceh and nationally across Indonesia.

2. MATERIALS AND METHODS

2.1 Sample collection

Fish samples were collected from multiple fish landing sites across the Aceh region, including Banda Aceh, Lhokseumawe, Langsa, Meulaboh, Simeulue, and Aceh Singkil (Figure 1). Specimens were identified to the species level as accurately as possible based on available taxonomic references [3]. Following field collection, the samples were transported to the Genetics and Aquatic Biodiversity Laboratory at the Faculty of Marine and Fisheries, Universitas Syiah Kuala, Banda Aceh, for further analysis. In line with the sampling guidelines proposed by Keyse et al. [18], a minimum of five specimens per species were collected for molecular analysis.

2.2 Extraction, PCR, and DNA sequencing

Genomic DNA was extracted using a modified Cetyl Trimethylammonium Bromide (CTAB) protocol [19]. Amplification of the partial cytochrome *c* oxidase subunit I (COI) gene—commonly used as a DNA barcode—was carried out using the primer pair FishF1 (5'-TCA ACC AAC CAC AAA GAC ATT GGG AC-3') and FishR1 (5'-TAG ACT TCT GGG TGG CCA AAG AAT CA-3'), as outlined by Ward et al. [20]. Polymerase Chain Reaction (PCR) was conducted in a 25 µL reaction mixture, which included 12.5 µL of MyTaq Red Mix, 2.0 µL of genomic DNA template, 1 µL of each primer, and 8.5 µL of nuclease-free water. Amplification was performed using a SensoQuest Gradient Thermal Cycler (https://www.sensoquest.de/). The PCR cycling conditions comprised an initial denaturation at 95°C for 2 minutes; 30 cycles of denaturation at 94°C for 45 seconds, annealing at 60°C for 45 seconds, and extension at 72°C for 1 minute; followed by a final elongation step at 72°C for 10 minutes, and a hold at 4°C [21-23]. Successfully amplified PCR products were submitted to First BASE Laboratories (Malaysia) for sequencing, which was performed using the BigDye Terminator v3.1 Cycle Sequencing Kit and the ABI PRISM 3730xl DNA Analyzer (Applied Biosystems, Foster City, CA), in accordance with the manufacturer's protocol.

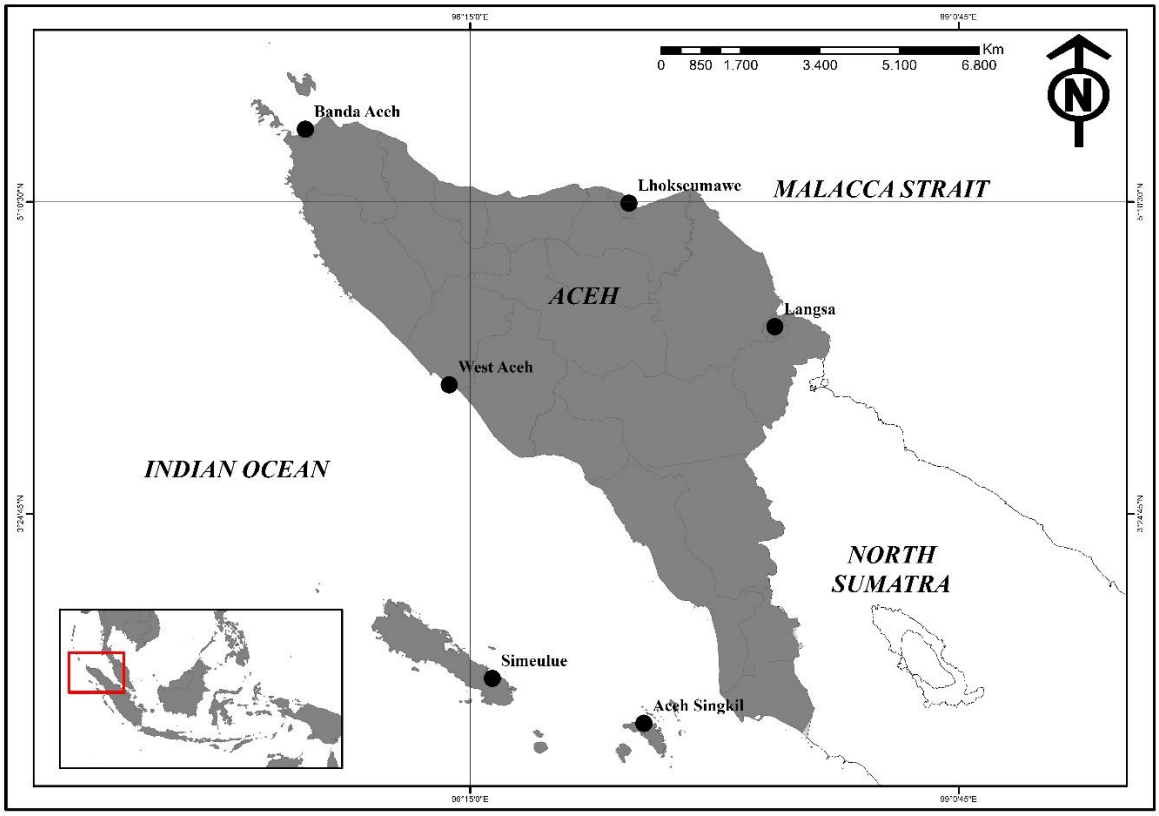

Figure 1. Map of Aceh Province showing the sampling locations of Carangidae species along the coastline, indicated by black dots

2.3 Data analysis

COI gene sequences were aligned and edited using MEGA X software [24]. To confirm species identity, the edited sequences were compared against reference databases, including BLAST (http://www.ncbi.nlm.nih.gov/BLAST) and the Barcode of Life Data System (BOLD) (www.boldsystems.org). Genetic distances were estimated using the Kimura 2-Parameter (K2P) model in MEGA version X [24]. A barcoding gap analysis was also performed to evaluate nearest-neighbor distances and assess the presence of distinct inter- and intraspecific divergence. Furthermore, a Neighbor-Joining (NJ) phylogenetic tree of COI haplotypes was constructed using MEGA X, with 1,000 bootstrap replicates to evaluate the reliability and robustness of the resulting tree topology. The phylogenetic tree was rooted using *Anyperodon leucogrammicus* as the outgroup, with the reference sequence obtained from GenBank (Accession No. OK284518).

3. RESULTS AND DISCUSSION

Through molecular identification, this study successfully identified 20 distinct Carangidae species in the region. These included *Alectis ciliaris*, *Atropus armatus*, *Atropus hedlandensis*, *Atropus mentalis*, *Carangichthys oblongus*, *Caranx heberi*, *Caranx ignobilis*, *Caranx melampygus*, *Caranx sexfasciatus*, *Caranx* sp., *Caranx papuensis*, *Caranx tille*, *Decapterus macarellus*, *Decapterus maruadsi*, *Ferdauia ferdau*, *Platycaranx malabaricus*, *Platycaranx talamparoides*, *Scyris indica*, *Selar crumenophthalmus*, and *Turrum coeruleopinnatum*. The relative distribution of each genus is detailed in Table 1.

Table 1. List of commercially important Carangidae species identified in this study, their sampling locations, sample sizes, and GenBank accession numbers from Aceh, Indonesia

No.	Genus	Species	Sampling Location						Total	Accession No.
			BNA	LA	LH	MBO	SML	SGK		
1	*Alectis*	*Alectis ciliaris*			4				4	PX468956-PX468959
2	*Atropus*	*Atropus armatus*		1		1			2	PX468960-PX468961
3		*Atropus hedlandensis*	1			2	5	1	9	PX468962-PX468970
4		*Atropus mentalis*		4					4	PX468971-PX468974
5	*Carangichthys*	*Carangichthys oblongus*					1	5	6	PX468975-PX468980
6	*Caranx*	*Caranx heberi*						1	1	PX468981
7		*Caranx ignobilis*	2					5	7	PX468982-PX468988
8		*Caranx melampygus*	1				4	5	10	PX468989-PX468998
9		*Caranx sexfasciatus*	8	5		1	3	5	22	PX468999-PX469002
10		*Caranx sp.*						2	2	PX469003-PX469024
11		*Caranx papuensis*						4	4	PX469025-PX469026

12		*Caranx tille*				4			4	PX469027-PX469030
13	*Decapterus*	*Decapterus macarellus*					5		5	PX469031-PX469035
14		*Decapterus maruadsi*		3					3	PX469036-PX469038
15	*Ferdauia*	*Ferdauia ferdau*		6	3				9	PX469039-PX469047
16	*Platycaranx*	*Platycaranx malabaricus*				3			3	PX469048-PX469050
17		*Platycaranx talamparoides*	2			12			14	PX469051-PX469064
18	*Scyris*	*Scyris indica*	3					2	5	PX469065-PX469069
19	*Selar*	*Selar crumenophthalmus*		3			5		8	PX469070-PX469077
20	*Turrum*	*Turrum coeruleopinnatum*	6	9	1	2			18	PX469078-PX469095
		Total	**23**	**31**	**8**	**25**	**23**	**30**	**140**	

Note: BNA=Banda Aceh; LA=Langsa; LH=Lhokseumawe; MBO= Meulaboh; SML= Simeulue; SGK= Aceh Singkil

3.1 Nucleotide diversity

The obtained COI sequences were 624 base pairs (bp) in length, with an average nucleotide composition of A = 24.63%, T = 28.04%, C = 27.49%, and G = 17.89%. Among these sequences, 395 sites were conserved, while 229 sites were variable. Of the variable sites, 209 were parsimony-informative, and 20 were singleton sites. The nucleotide composition revealed a higher AT content (54.62%) compared to GC content (45.38%), indicating a slight AT bias. These results are summarized in Table 2.

Table 2. Summary statistics of nucleotide frequency distribution in the COI gene sequences of Carangidae species collected from Aceh

	Min.	Mean	Max.	SE
G %	16.83	17.89	19.07	0.04
C %	25.80	27.49	30.13	0.10
A %	22.60	24.63	25.80	0.06
T %	29.99	28.04	32.37	0.07
AT %	50.96	54.62	56.89	0.11
GC %	43.11	45.38	49.04	0.11
GC % Codon Pos 1	54.81	56.61	59.13	0.08
GC % Codon Pos 2	40.87	41.83	42.31	0.01
GC % Codon Pos 3	31.25	37.72	48.08	0.30

3.2 Species delimitation

The BLAST and BOLD analyses revealed sequence similarities ranging from 98.90% to 100.00% with reference entries in the databases, confirming the accurate identification of the 20 Carangidae species. Moreover, a distinct barcoding gap was observed, with maximum intraspecific divergences remaining below 2%, while the nearest neighbor distances ranged from 2.05% to 15.86% (Table 3, Figure 2). The Neighbor-Joining (NJ) phylogenetic tree further demonstrated that all analyzed species formed well-supported monophyletic clades, with no indication of overlap among them (Figure 3). These results underscore the reliability of the COI gene as an effective marker for species-level identification within the Carangidae family.

Additionally, genetic distance and phylogenetic analyses indicated a close relationship between *Caranx melampygus* and *Caranx papuensis*, which exhibited the lowest interspecific genetic distance (2.05%). The second closest relationship was observed between *Platycaranx malabaricus* and *Platycaranx talamparoides* (2.18%) (Table 3). In contrast, the highest genetic distance was recorded between *Caranx heberi* and *Turrum coeruleopinnatum* (21.87%), followed by *Caranx heberi* and *Atropus armatus* (21.51%) (Table 4).

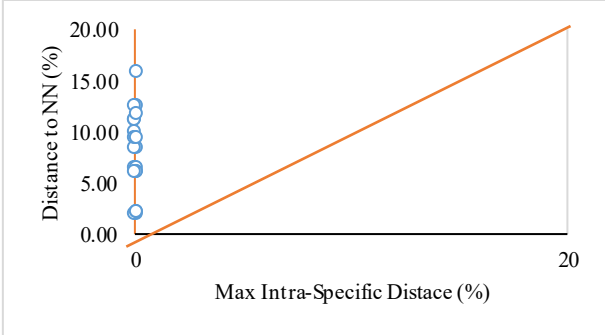

Figure 2. Maximum intraspecific divergence (K2P%) plotted against nearest-neighbor distance (K2P%) for the 20 Carangidae species identified in Aceh
The presence of a barcode gap is indicated by datapoints located above the red line, where interspecific divergence exceeds intraspecific variation

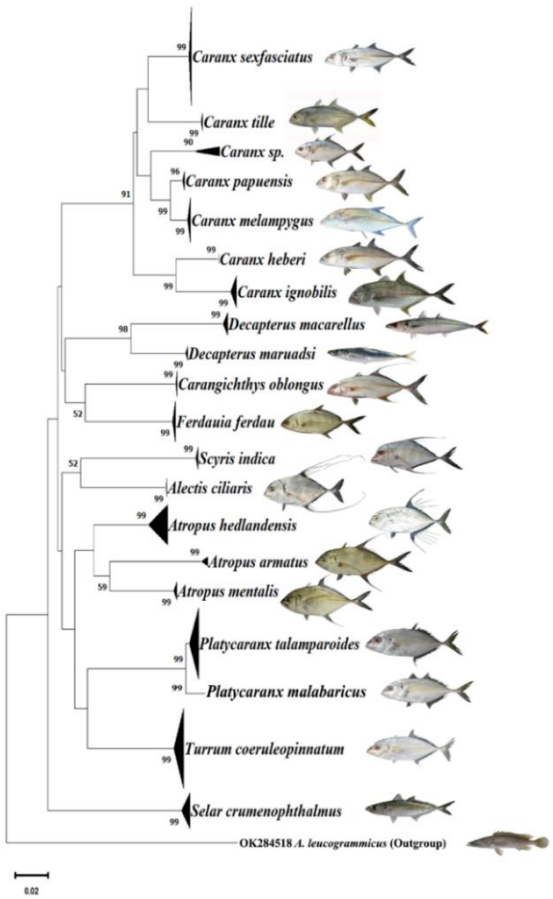

Figure 3. Neighbor-Joining (NJ) tree of COI barcodes for all Carangidae samples
Bootstrap values (> 70%) are shown at the nodes. *Anyperodon leucogrammicus* was used as the outgroup to root the tree.

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 Neighbour	Distance to Nearest Neighbour (K2P%)
1	*Alectis ciliaris*	0.00	0.006	*Scyris indica*	12.57
2	*Atropus armatus*	0.00	0.005	*Atropus mentalis*	10.00
3	*Atropus hedlandensis*	0.01	0.030	*Atropus mentalis*	8.57
4	*Atropus mentalis*	0.00	0.002	*Atropus hedlandensis*	8.57
5	*Carangichthys oblongus*	0.00	0.002	*Ferdauia ferdau*	11.29
6	*Caranx heberi*	N/A	0.000	*Caranx ignobilis*	6.48
7	*Caranx ignobilis*	0.00	0.006	*Caranx heberi*	6.48
8	*Caranx melampygus*	0.00	0.008	*Caranx papuensis*	2.05
9	*Caranx papuensis*	0.00	0.003	*Caranx melampygus*	2.05
10	*Caranx sexfasciatus*	0.00	0.013	*Caranx tille*	6.18
11	*Caranx* sp.	0.02	0.025	*Caranx melampygus*	6.17
12	*Caranx tille*	0.00	0.002	*Caranx sexfasciatus*	6.18
13	*Decapterus macarellus*	0.00	0.005	*Decapterus maruadsi*	9.45
14	*Decapterus maruadsi*	0.01	0.010	*Decapterus macarellus*	9.45
15	*Ferdauia ferdau*	0.00	0.005	*Carangichthys oblongus*	11.29
16	*Platycaranx malabaricus*	0.02	0.021	*Platycaranx talamparoides*	2.18
17	*Platycaranx talamparoides*	0.00	0.010	*Platycaranx malabaricus*	2.18
18	*Scyris indica*	0.00	0.003	*Alectis ciliaris*	12.57
19	*Selar crumenophthalmus*	0.00	0.011	*Atropus armatus*	15.86
20	*Turrum coeruleopinnatum*	0.01	0.043	*Atropus mentalis*	11.85

N/A = represented by a single specimen.

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

No.	Species	1	2	3	4	5	6	7	8	9	10
1	*Alectis ciliaris*	**0.00**									
2	*Atropus armatus*	14.67	**0.00**								
3	*Atropus hedlandensis*	15.03	11.07	**0.01**							
4	*Atropus mentalis*	12.65	10.00	8.57	**0.00**						
5	*Carangichthys oblongus*	16.56	13.45	15.42	14.63	**0.00**					
6	*Caranx heberi*	17.49	21.51	17.22	18.94	18.90	**N/A**				
7	*Caranx ignobilis*	18.45	20.53	17.21	19.93	18.80	6.48	**0.00**			
8	*Caranx melampygus*	15.10	16.97	15.96	15.94	16.88	9.77	10.70	**0.00**		
9	*Caranx papuensis*	15.61	17.18	15.51	16.36	16.70	9.81	10.27	2.05	**0.00**	
10	*Caranx sexfasciatus*	15.27	19.50	16.22	16.21	14.81	8.86	10.34	6.67	6.26	**0.00**
11	*Caranx* sp.	15.38	14.26	9.34	13.31	15.52	9.85	9.56	6.17	6.28	8.43
12	*Caranx tille*	15.87	16.76	17.04	15.84	14.30	8.95	8.70	8.39	9.02	6.18
13	*Decapterus macarellus*	18.54	16.77	18.17	17.01	16.07	20.48	20.27	19.30	19.03	18.61
14	*Decapterus maruadsi*	15.26	15.65	18.49	16.93	16.45	18.98	19.18	16.44	17.11	15.85
15	*Ferdauia ferdau*	14.99	15.63	16.09	13.37	11.29	17.78	16.82	17.13	16.18	14.80
16	*Platycaranx malabaricus*	16.18	13.82	15.65	14.58	15.12	21.49	20.78	18.20	17.77	17.47
17	*Platycaranx talamparoides*	16.74	13.32	15.49	14.11	16.01	21.19	20.95	18.39	18.56	17.46
18	*Scyris indica*	12.57	13.95	16.67	16.02	15.24	18.18	18.55	17.04	17.49	17.66
19	*Selar crumenophthalmus*	15.98	15.86	18.33	16.08	16.06	18.09	19.15	18.46	18.46	17.43
20	*Turrum coeruleopinnatum*	13.29	12.22	12.78	11.85	13.18	21.87	20.10	17.28	17.21	16.78

No.	Species	11	12	13	14	15	16	17	18	19	20
1	*Alectis ciliaris*										
2	*Atropus armatus*										
3	*Atropus hedlandensis*										
4	*Atropus mentalis*										
5	*Carangichthys oblongus*										
6	*Caranx heberi*										
7	*Caranx ignobilis*										
8	*Caranx melampygus*										
9	*Caranx papuensis*										
10	*Caranx sexfasciatus*										
11	*Caranx* sp.	**0.02**									
12	*Caranx tille*	9.62	**0.00**								
13	*Decapterus macarellus*	17.90	17.60	**0.00**							
14	*Decapterus maruadsi*	16.48	16.00	9.45	**0.01**						
15	*Ferdauia ferdau*	15.44	14.35	15.15	14.86	**0.00**					
16	*Platycaranx malabaricus*	16.87	17.84	14.58	15.81	13.10	**0.02**				
17	*Platycaranx talamparoides*	16.42	17.90	14.49	15.46	13.38	2.18	**0.00**			
18	*Scyris indica*	16.89	16.48	17.49	17.44	16.72	17.24	17.72	**0.00**		
19	*Selar crumenophthalmus*	18.34	17.44	20.71	18.34	18.59	18.67	19.12	18.04	**0.00**	
20	*Turrum coeruleopinnatum*	16.81	16.41	15.67	15.40	15.16	13.60	13.60	13.19	17.55	**0.01**

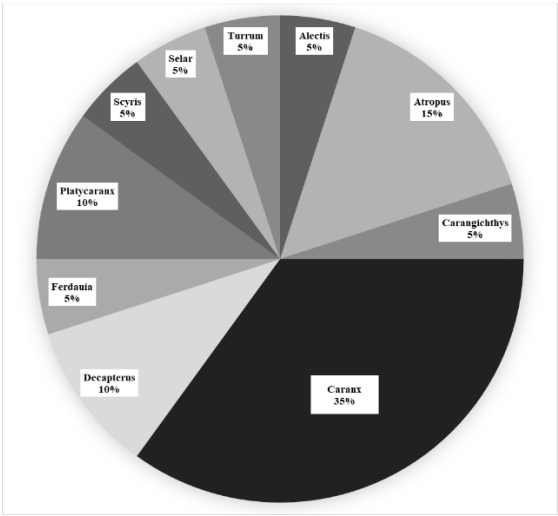

Figure 4. Genus composition of Carangidae collected from Aceh waters

This study represents the first comprehensive molecular identification of Carangidae species in the Aceh region, utilizing DNA barcoding based on the mitochondrial cytochrome c oxidase subunit I (COI) gene. A total of 20 species were successfully identified from multiple fish landing sites across Aceh. The genus *Caranx* was the most frequently represented, accounting for approximately 35% of the identified specimens, followed by *Atropus*, which comprised 15% of the total Carangidae samples (Figure 4). The number of species reported in this study is comparable with the study by Andriyono et al. [5], who barcoded 20 Carangidae species from traditional fish markets in Java and Bali, Indonesia. In addition, the number of species reported in this study is higher than in the study by Templonuevo et al. [11], who barcoded seven species 7 species of carangids from Cuyo, Palawan, Philippines, and Ramadhaniaty et al. [25], who barcoded three Carangidae species from Nias Islands, Indonesia. However, the number of reported species is lower compared to studies by Mat Jaafar et al. [6] and Thu et al. [12], who barcoded 36 and 21 species of Carangidae from Malaysia and Vietnam, respectively.

The genetic distance patterns and barcode gap observed in this study are consistent with previous barcoding efforts in the Indo-Malay region. Mat Jaafar et al. [6] and Nur et al. [14] reported similar divergence thresholds for Carangidae in Malaysia, while Thu et al. [12] recorded comparable inter- and intraspecific divergences along the Vietnamese coast. This concordance underscores the robustness of COI-based barcoding as a standardized method for species discrimination across geographic boundaries. In addition, the findings of the genetic distance and phylogenetic analyses suggest a close evolutionary relationship between *Caranx melampygus* and *Caranx papuensis*, as indicated by their low genetic divergence (2.05%). A similarly close relationship was observed between *Platycaranx malabaricus* and *Platycaranx talamparoides* (2.18%), supporting their close taxonomic grouping. Both *Caranx papuensis* and *Caranx melampygus* exhibited a similar spotted body, but *Caranx melampygus* has bright blue second dorsal, anal, and caudal fins [3].

Interestingly, the study also identified a *Caranx* specimen that could not be assigned to a known species, suggesting the potential presence of a cryptic or unrecorded species in Aceh waters. This aligns with earlier reports of cryptic diversity within the Carangidae, such as those reported by Mat Jaafar et al. [6], who uncovered hidden lineages within *Atule mate* and *Selar crumenophthalmus* in the Indo-Malaya region. Such findings highlight the limitations of relying solely on morphology for species identification, especially in taxonomically complex groups like Carangidae, which often exhibit overlapping phenotypic traits and ontogenetic shifts in coloration and morphology.

The establishment of a COI sequence reference library for Carangidae in Aceh holds significant implications for fisheries management. Accurate species identification is critical for monitoring fishery resources, especially in regions like Indonesia, where catch records are often reported under local or generic names (e.g., "Ikan Kuwe"). Misidentification can result in flawed stock assessments, inappropriate management strategies, and potential overexploitation of commercially valuable species. By providing molecular-level species resolution, this study offers a foundation for improving the accuracy of fish landing data and supporting evidence-based conservation policies.

Despite its contributions, this study has some limitations. The number of specimens per species was constrained by availability at landing sites, and sampling was limited to a single collection period. Future research should involve broader temporal and spatial sampling to capture seasonal variation and potential population structure. Moreover, while the COI gene is highly effective for initial species identification, integrating nuclear markers or genome-wide approaches such as RAD-seq or eDNA could provide deeper insights into population connectivity, hybridization events, and phylogeographic patterns.

In conclusion, this study demonstrates the power of DNA barcoding in revealing species diversity and resolving taxonomic ambiguities in Aceh's Carangidae. The genetic baseline provided here not only enhances our understanding of local marine biodiversity but also serves as a critical tool for sustainable fisheries management and biodiversity conservation in Indonesia's coastal ecosystems.

4. CONCLUSIONS

This study successfully established the first COI-based DNA barcode reference library for Carangidae species in Aceh, Indonesia. Through molecular analysis of samples collected from multiple fish landing sites, 20 Carangidae species were identified, with *Caranx* and *Atropus* emerging as the most dominant genera. The presence of a distinct barcode gap and monophyletic clustering in the NJ tree confirmed the reliability of COI sequences for accurate species identification. The molecular data generated in this study provide essential baseline information that can enhance fisheries monitoring, inform management decisions, and support the conservation of marine biodiversity in Aceh and beyond. Future research should build on this work by incorporating additional molecular markers and expanding sampling efforts to assess population structure and genetic diversity across broader temporal and geographic scales. This COI-based barcode reference can support national fisheries monitoring programs and contribute to the implementation of species-specific catch regulations in Indonesia.

ACKNOWLEDGMENT

This study was funded by Universitas Syiah Kuala (H-Index

Scheme, contract number: 127/UN11.2.1/PT.01.03/PNBP/2023).

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