

Phylogenetic of red snapper (*Lutjanidae*) in Yapen Island Waters, Papua, Indonesia

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Manuscript received: 1 November 2022. Revision accepted: 1 February 2023.

Abstract. *Sala R, Kusuma AB, Pranata B. 2023. Phylogenetic of red snapper (Lutjanidae) in Yapen Island Waters, Papua, Indonesia. Biodiversitas 24: 716-723.* Red snappers are an economically valuable fishery resource. Most of these snapper species are inhabitants of coral reef ecosystems. A variety of red snapper species can be found in the northern waters of Papua, particularly in the Yapen Regency. However, information regarding the biological and ecological aspects of these fish is virtually unavailable. On the other hand, the utilization intensity of red snapper as a source of community income continues to increase. By using DNA barcode sequences, this study attempted to examine species diversity and relationships among Lutjanidae family species. The study was carried out from June to August 2022 in the waters of Yapen Regency by taking fish samples from the fish caught by local hand-lining fishers. Red snapper samples were identified morphologically and molecularly. According to molecular analyses, it was identified nine red snapper species from the genera of *Lutjanus*, *Aphareus* and *Pristipomoides*. The morphological characteristics of the species from the genus of *Aphareus* are similar to those from the genus of *Pristipomoides* yet different from those of the species from the genus of *Lutjanus*. The phylogenetic tree consisted of four clades with significant bootstrap values ranging from 98 to 99%. Clades 1, 2 and 3 comprise the species from the genus of *Lutjanus*, while clade 4 contains species from the genera of *Aphareus* and *Pristipomoides*. The greatest genetic distance was found between *Lutjanus fulvus* and *Pristipomoides multidentis*, while the smallest genetic distance was found between *Lutjanus vitta* and *Lutjanus ehrenbergii*. Based on the study results, some management implications are discussed. For example, information on species biodiversity maps is needed to determine the target stock of a managed species so that management objectives are more focused on the species level and not on the genus or family level.

Keywords: Biodiversity, molecular, Papua waters, phylogenetic

INTRODUCTION

Red Snappers are demersal fish belonging to the Lutjanidae family and the *Lutjanus* genus. Red Snappers inhabit coral reef environments and are dispersed over the East and Indo-West Pacific, East and West Atlantic (Souza et al. 2019), the home to forty-three species of snappers from the Lutjanidae family (Allen et al. 2013).

Snappers belonging to the genus *Lutjanus* have small to large body sizes, oval bodies, and triangular-shaped heads. Snappers vary in coloring, typically having a reddish, yellow, gray, or brown background with a darker pattern of stripes or stems and frequently having a huge black spot on the upper side under the dorsal soft front fin (Allen 1985). The species from the genus *Lutjanus* have remarkably similar morphologies, including one with a recently altered yellow stripe (Iwatsuki et al. 2015). High morphological similarity across species and genera might make identification more difficult. The morphological similarity has the potential to lead to identification mistakes.

Reef fish, including groupers and snappers, are economically significant. This condition can lead to the intense exploitation of reef fish resources in diverse Indonesian sea regions. Through Decree No. 19/2022 issued by the Indonesian Minister of Marine Affairs, the

Indonesian government has concluded that reef fish in fisheries management areas (FMA), such as FMA 717, which encompasses the northern portion of West Papua, are overexploited with utilization rates exceeding one.

The waters of the northern part of Papua, including the waters of the Yapen Regency, are the State Fisheries Management Area of the Republic of Indonesia (WPPNRI). According to Decree Number, 50/KEPMEN-KP/2017 of the Minister of Maritime Affairs and Fisheries of the Republic of Indonesia, the red coral fish resources in these and nearby waters have been fully exploited. The lack of proper catch identification hinders the management of red snapper fisheries. In general, red snappers include *L. malabaricus*, *L. timoriensis*, and *L. erythropterus*, but the Indo-West Pacific contains forty-three species of red snappers. Sadly, there is currently no information regarding the quantity of Red Snapper species in the area. Red snapper species may have varying susceptibilities to fishing activities. Therefore, distinct management methods are needed to maintain sustainable fishing. Developing conservation plans and long-term management methods requires knowledge of the species and subpopulations involved (Bakar et al. 2018).

The search for species identity based on morphology does not provide full confidence compared to using a

molecular approach due to the “evolution convergent” (Zou and Zhang 2016). The morphological traits of organisms inhabiting distinct environments can vary (Heino 2014; Shuai et al. 2018). Using genetic markers, species identity can be accurately determined. Molecular studies have relied significantly on genetic markers (Chan et al. 2021). Genetic markers are genomic DNA segments that provide information about taxonomic differentiation (Patwardhan et al. 2014; Grover et al. 2016). DNA sequences have been employed as genetic markers for species identification and the discovery of novel species (Allen et al. 2013; Iwatsuki et al. 2015). Mitochondrial DNA (mtDNA) is one of the genomic DNA segments frequently employed in molecular studies.

Mitochondrial DNA has been utilized extensively to answer questions concerning genetic diversity, population evolution, and cellular structure (Gupta et al. 2015). The cytochrome oxidase c subunit I (COI) gene was employed in this study for molecular identification and phylogenetic construction. The COI gene is a “DNA barcode” (Pentinsaari et al. 2016). It is a dependable tool for monitoring biodiversity and reconstructing phylogenetic data (Pei et al. 2017). The purpose of phylogenetic studies is to recreate the evolutionary history of a species or taxon (Jarvis et al. 2017), which is represented by a tree-like diagram (Ramos et al. 2021).

Earlier research on the family Lutjanidae employed the COI gene for genetic analysis (Gold et al. 2015; Bakar et al. 2018; Fadli et al. 2020; Shan et al. 2021; Halim et al. 2022). Researchers also used the COI gene to identify a new species of red snapper (*L. papuensis*) in the Cendrawasih Bay of Papua New Guinea (Allen et al. 2013). In this study, we gathered Lutjanidae specimens from fish landing places in Yapen. We identified the species based on their morphological and molecular characteristics. The current study aimed to ascertain the number of species within the family Lutjanidae in Yapen

Island waters and to reconstruct a phylogenetic tree to establish the evolutionary link between species.

MATERIALS AND METHODS

Study sites

We conducted this study in Yapen Regency, Papua, Indonesia, between June and August of 2022 (Figure 1). Extraction, electrophoresis, and amplification were conducted at the Genetic Laboratory of Universitas Bengkulu. Additionally, we collected data for 16 Lutjanidae nucleotide sequences from the National Center for Biotechnology Information (NCBI (<https://www.ncbi.nlm.nih.gov>) (Table 1).

Sampling method

Samples were selected using purposive random sampling. Snappers were obtained from Fish Landing Port. Snappers were obtained from Fish Landing Places (TPI). Every morning, fishermen bring their catch of fish to the fish landing port. We also collect snapper at fish markets. Fish markets and fishing spots. Early morphological identification referred to the identification book of White et al. (2013); Moore and Colas (2016). One centimeter of red snapper dorsal fin tissue was removed and placed in a tube containing 80% ethanol.

Morphological identification

The identification of red snapper samples was based on their morphometric and meristic characteristics. We measured and photographed the weight, total length, standard length, number of pectoral fin spines, number of dorsal fin spines, and number of anal fin spines of each specimen. Measurement of morphometric characters using LCD Digital Calipers Taffware.

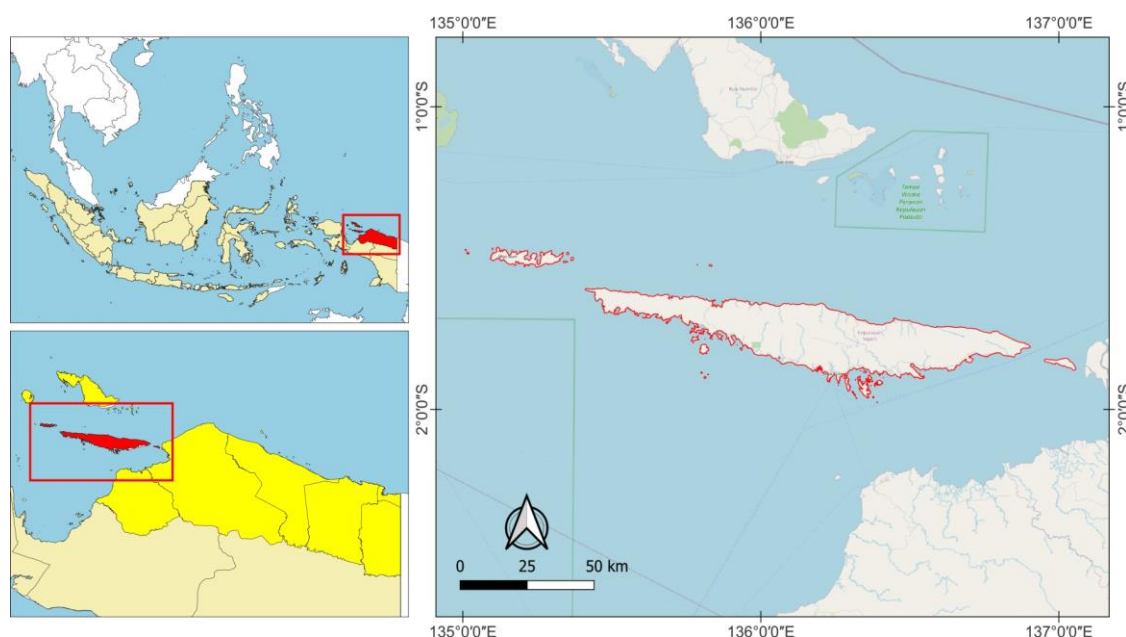


Figure 1. Sampling locations in the Yapen Regency, Papua, Indonesia

Table 1. Lutjanidae sequence from NCBI

Species	Location	Access code
<i>Lutjanus vitta</i>	Indonesia: Java	MH085866
<i>Lutjanus vitta</i>	Malaysia	MG002627
<i>Lutjanus decussatus</i>	Indonesia: Maluku, Ambon Island, Ambon	MN870144
<i>Lutjanus ehrenbergii</i>	Indonesia: Maluku, Ambon Island, Ambon	MN870091
<i>Lutjanus ehrenbergii</i>	Indonesia: Maluku, Ambon Island, Ambon	MN870134
<i>Lutjanus rufolineatus</i>	Indonesia	GU673676
<i>Lutjanus rufolineatus</i>	Indonesia: Maluku, Ambon Island, Ambon	MN870325
<i>Lutjanus fulvus</i>	Philippines: Aurora, Region 3	KF009613
<i>Lutjanus fulvus</i>	Indonesia	MK256673
<i>Lutjanus malabaricus</i>	Philippines: Aurora, Region 3	KF009618
<i>Lutjanus erythropterus</i>	Indonesia	GU673841
<i>Lutjanus erythropterus</i>	Australia	GU673202
<i>Lutjanus erythropterus</i>	Malaysia	MG002616
<i>Pristipomoides multidens</i>	Australia: West Coast	MK092068
<i>Aphareus rutilans</i>	China	NC063973
<i>Aphareus rutilans</i>	China	ON152703

Extraction, amplification, and sequencing

DNA extraction followed the instructions from the Geneaid gSYNCTM DNA extraction kit. Amplification of the cytochrome oxidase subunit I (COI) gene used a set of COI primers developed by Ward et al. (2005): F1 5'-TCA ACC AAC CAC AAA GAC ATT GGC AC-3' dan R1 5'-TAG ACT TCT GGG TGG CCA AAG AAT CA-3'. Polymerase Chain Reaction (PCR) mix Go Taq Green Master Mix consisted of Go Taq Green 25 µL, 1.5 µL DNA template, 19.5 µL nuclease-free water, and 5 µL primer. The thermal cycle setting was 95°C for 4 minutes during initial denaturation, followed by 35 cycles of denaturation at 95°C for 30 seconds, annealing at 54°C for 45 seconds, elongation at 72°C for 1 minute, post PCR at 72°C for 7 minutes. The amplification results were electrophoresed to visualize the presence of DNA in the PCR product. The purified PCR results were then sent to 1st BASE Sequencing Service Sdn. Bhd. (Malaysia) for sorting purposes.

Data analysis

The DNA sequencing results were aligned and edited using MEGA X software. The sequence data were then matched with the database available online at the NCBI (National Center for Biotechnological Information) GenBank (www.ncbi.nlm.nih.gov). The BLAST (Basic Local Alignment Search Tool) method was used to assess the homology between the sequences from the study sample and the genetic data sequences stored in the GenBank (Toha et al. 2020). BLAST results were tabulated to show the identity of the study sample. Genetic distance analysis and phylogenetic tree reconstruction were carried out using the Neighbor-Joining Method, Kimura-2 parameter model and bootstrap value of 1000× with the help of MEGA X software.

RESULTS AND DISCUSSION

Morphological character analysis

The morphometric and meristic characteristics of the Lutjanidae red snappers found in this study are described in Table 2. The morphological identification results showed that nine species belonged to the genera *Lutjanus*, *Aphareus* and *Pristipomoides*. *Lutjanus vitta*, *L. decussatus*, *L. rufolineatus*, *L. malabaricus*, *L. erythropterus*, *L. ehrenbergii* and *L. fulvus* belong to the genus *Lutjanus*; *A. rutilans* come from the genus *Aphareus*; and *P. multidens* belongs to the genus *Pristipomoides*. The three species with maximum and minimum length and weight are *L. erythropterus* (Max. 49.5 cm - Min. 45 cm), *P. multidens* (Max. 48.8 cm - Min. 42 cm) and *L. malabaricus* (Max. 29 cm - Min. 52 cm). Other species include *L. erythropterus* (Max. 1986 g - Min. 1560 g), *P. multidens* (Max. 1380 g - Min. 804 g) and *L. malabaricus* (Max. 2611 g - Min. 378 g).

Molecular identification

Molecular identification was conducted using the Basic Local Alignment Search Tool at the National Center for Biotechnology Information. Table 3 displays the results of molecular identification. The identification results indicate that the DNA sequences of the nine species share a high degree of similarity (99.68% to 100%) with the NCBI database.

Genetic distance analysis

Genetic distance analysis was conducted using the Kimura-2 parameter method and resulted in variations in genetic distance between nine species of red snappers. The largest genetic distance was found between *L. fulvus* and *P. multidens*. Meanwhile, *L. vitta* and *L. ehrenbergii* were discovered to have the smallest genetic distance. A small genetic distance number indicates a high level of morphological similarity of the observed species (the smaller the distance, the higher the morphological similarity of the observed species and vice versa).

Table 2. The measurement of the morphometric and meristic characteristics of the Lutjanidae family

Species	Number of individuals	Min. length (cm)	Max. length (cm)	Min. weight (g)	Max. weight (g)	Pectoral fin	Dorsal fin	Dorsal rays	Anal spines	Anal rays	Caudal fin
<i>L. vitta</i>	3	22.6	27.3	137	300	14-16	IX-X	13-14	III	8-9	Emarginate
<i>L. rufolineatus</i>	3	22.7	25.9	252	312	16-17	XI	13	III	9	Emarginate
<i>L. malabaricus</i>	4	29	52	378	2611	16-17	XI	14-15	III	9-10	Truncate
<i>L. erythropterus</i>	6	45	49.5	1560	1986	16	XI	15-16	III	10	Truncate
<i>L. ehrenbergii</i>	8	17.7	22.3	89	200	14-15	IX-X	14	III	9	Truncate
<i>L. fulvus</i>	2	19	21.1	133	174	16	X	15	III	9	Emarginate
<i>L. decussatus</i>	2	17.8	17.9	96	102	16	X	14	III	9	Emarginate
<i>A. rutilans</i>	2	31	32.7	276	283	15-16	XII-XI	9-10	III	8	Forked
<i>P. multidentis</i>	2	42	49.8	804	1380	16	IX-X	11	III	8	Forked

Table 3. The BLAST species data at GenBank National Center for Biotechnology Information (NCBI)

Specimen code	Species	Query cover	Similarity	Accession
BKS06	<i>Lutjanus malabaricus</i>	99%	99.53%	KF009618
BKS36	<i>Lutjanus ehrenbergii</i>	97%	99.54%	KP194151
BKS47	<i>Lutjanus fulvus</i>	99%	99.68%	KF009613
BKS29	<i>Lutjanus vitta</i>	99%	99.84%	NC042930
BKS07	<i>Lutjanus erythropterus</i>	97%	100%	GU673202
BKS12	<i>Lutjanus rufolineatus</i>	97%	100%	MN870075
BKS17	<i>Lutjanus decussatus</i>	96%	99.84%	MN870144
BKS18	<i>Aphareus rutilans</i>	100%	99.53%	KF009564
BKS21	<i>Pristipomoides multidentis</i>	99%	99.84%	KF430626

Table 4. Genetic distance among collected red snappers of the Lutjanidae family

	<i>L. vitta</i>	<i>L. rufolineatus</i>	<i>L. fulvus</i>	<i>L. erythropterus</i>	<i>L. ehrenbergii</i>	<i>L. malabaricus</i>	<i>L. decussatus</i>	<i>A. rutilans</i>
BKS29_ <i>L. vitta</i>								
BKS23_ <i>L. rufolineatus</i>	0.115							
BKS47_ <i>L. fulvus</i>	0.122	0.090						
BKS07_ <i>L. erythropterus</i>	0.192	0.161	0.167					
BKS36_ <i>L. ehrenbergii</i>	0.086	0.121	0.129	0.179				
BKS06_ <i>L. malabaricus</i>	0.178	0.166	0.172	0.113	0.149			
BKS17_ <i>L. decussatus</i>	0.082	0.125	0.125	0.165	0.097	0.176		
BKS18_ <i>A. rutilans</i>	0.174	0.172	0.173	0.160	0.171	0.170	0.175	
BKS21_ <i>P. multidentis</i>	0.182	0.193	0.205	0.187	0.193	0.201	0.180	0.129

Phylogenetic analysis

Reconstruction of the phylogenetic tree was conducted using the Neighbor-Joining Method, Kimura-2 parameter model and bootstrap value of 1000× with the help of MEGA X software. The phylogenetic tree shows the genetic relationships and evolutionary history between species or taxa based on current molecular data (Jarvis et al. 2017). The phylogeny tree was constructed from the nine individual sequences obtained from this study and sixteen individual sequences from the GenBank (Table 1). We added sixteen individual DNA sequences from various countries to strengthen the position of the sequences obtained in this study.

Discussion

Morphological characteristics

This study discovered members of the genus *Lutjanus* with small to large bodies. Species in the genus *Lutjanus*

have an oval and deep bodies (Allen 1985). They are also slender and fusiform in shape (Allen 1985). Species belonging to the genus *Lutjanus* have a continuous dorsal fin with a tiny incision between the thorny and soft parts (Allen 1985). The red snappers vary in appearance, typically having a reddish, yellow, gray, or brown background with a darker pattern of stripes or stems and are frequently distinguished by a huge blackish spot on the upper side beneath the dorsal fin. Some species, including *L. vitta*, *L. decussatus*, *L. ehrenbergii*, and *L. rufolineatus*, have black spots and stripes on their bodies. *Lutjanus vitta* is defined morphologically by diagonal lines above and horizontal lines below the lateral line. From the eye to the tail fin, a brownish-yellow stripe is present on this species. Moreover, *L. decussatus* is defined morphologically by the presence of eight bands and a big black patch at the base of the caudal fin. *Lutjanus ehrenbergii* is distinguished morphologically by the presence of three to four horizontal

lines of variable width on the underside of the scales and a prominent black spot under the dorsal fin. *Lutjanus rufolineatus* is distinguished by the presence of 7-8 yellow horizontal stripes. In this study, we did not see any black spots and horizontal and vertical stripes in *L. fulvus*, *L. malabaricus* or *L. erythropterus*. The number of pectoral fin soft spines in the *Lutjanus* genus varies between 14-17, while the number of dorsal fin spines ranges between IX-XI and 13-14 soft spines. All species had the same number of hard spines on the anal fin, namely III, and 8-10 soft spines. Each member of the genus *Lutjanus* has a truncated and emarginate tail.

Those of the genus *Lutjanus* have a distinct body form than members of the genus *Aphareus*. Red snappers belonging to the genus *Aphareus* have an elongated and fusiform body (Allen 1985). *Aphareus rutilans* is one of the *Aphareus* species identified in this research. In addition to its body shape, *A. rutilans* lacks canines and vomerine teeth, unlike members of the genus *Lutjanus*. *Aphareus rutilans* has little teeth in its jaws. The *Aphareus* genus has a forked tail, in contrast to the *Lutjanus* genus, which has a tail that is between emarginate and truncate. *Aphareus rutilans* has a continuous dorsal fin with no grooves between the hard and soft spiny sections. The final dorsal and anal fins are stretched out.

The body of *Pristipomoides* species is comparable to that of *Aphareus* species. This study recognized *P. multidentis* as one of the species from the genus *Pristipomoides*. *Pristipomoides multidentis* and *A. rutilans* have continuous dorsal fins with no grooves between the hard and soft spines. Both species possess prolonged dorsal and anal fin rays in addition to a tail fork. *Pristipomoides multidentis* possesses canines and vomerine teeth on the front of its jaw.

The above description demonstrates that distinct morphological traits identify species from the genera *Lutjanus*, *Aphareus*, and *Protipomoides*, as well as species within the same genus. Nevertheless, the species of the

three genera share similar meristic traits. Molecular analysis can clarify the species-level differentiation of these fish groups.

Morphology molecular agreement in genetic distance

Our current findings show that the two species of red snappers, *L. ehrenbergii* and *L. vitta*, have the smallest genetic distance value (0.086). A small genetic distance value suggests that two species share a close genetic kinship. Our findings indicate that the two species share a similar ancestor. There is a horizontal line on the body of both species, with a huge black spot on the body of *L. ehrenbergii* and a large yellow spot on the underside of the soft dorsal fin of *L. vitta*. Indentations exist between the hard and soft spiny portions of each species. The shape and number of spines on the anal fins of both species are likewise similar (Figure 2).

The farthest genetic distance (0.205) was found between *L. fulvus* and *P. multidentis*. In this study, a high genetic distance score suggests a significant difference between physical traits. This is demonstrated by the morphological differences between *L. fulvus* and *P. multidentis*. *Pristipomoides multidentis* has a moderately extended body shape, whereas *L. fulvus* has an oval body that ranges from relatively deep to thin and fusiform in shape. *Pristipomoides multidentis* possesses a continuous dorsal fin with no grooves separating the hard and soft spines. Both the dorsal and anal fins are stretched out. In contrast, *L. fulvus* has a small incision between the thorny and soft parts of the dorsal fin. In addition, *L. fulvus* has an emarginate tail, while *P. multidentis* has a forked tail. *Lutjanus fulvus* has a reddish-yellow body color and yellow spots on the tops of its eyes, but *P. multidentis* has a yellowish to pale pink body color. There are five or six golden dashed lines found on the body of *P. multidentis*. The species also has a pair of gold and blue stripes on its snout and cheeks.

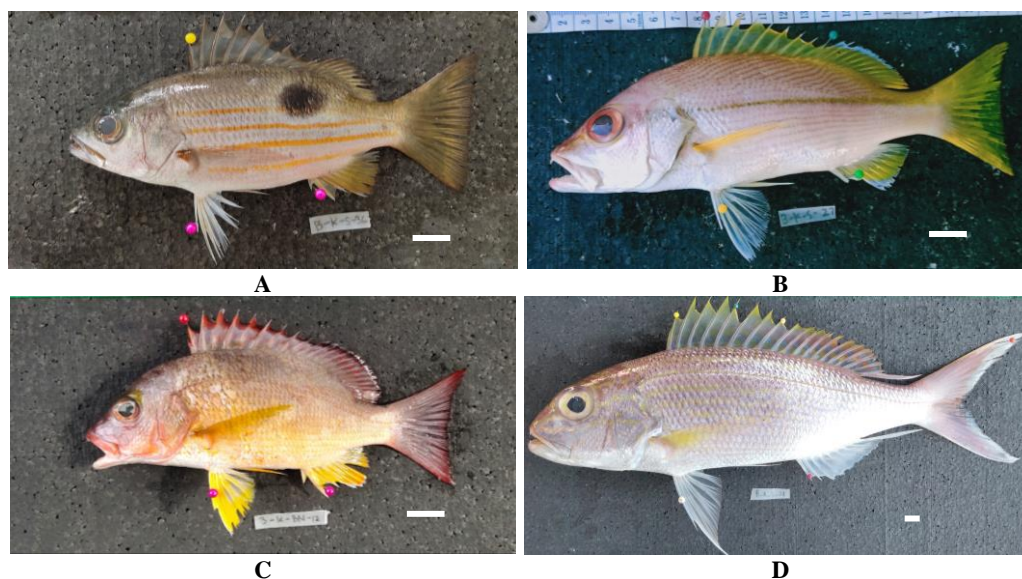
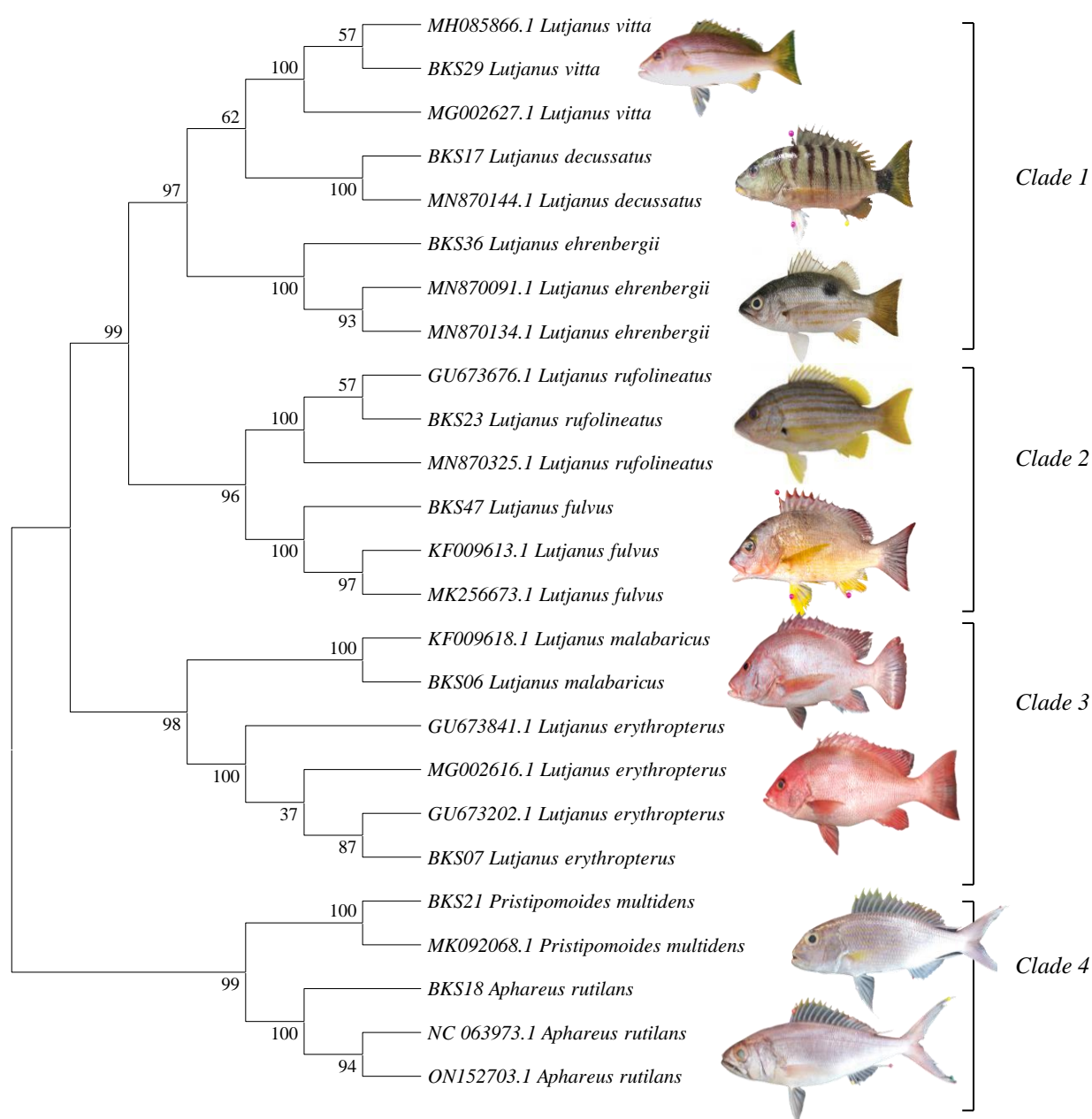


Figure 2. Comparison of morphological characters of some Lutjanidae species. A. *Lutjanus ehrenbergii*, B. *Lutjanus vitta*, C. *Lutjanus fulvus*, D. *Pristipomoides multidentis*. Bar = 2 cm.

Table 5. Maximum size, optimal harvest size and first gonadal maturity of the Lutjanidae family

Species	Lmax	Lopt	Lmat	Wmat	Reference
<i>Lutjanus malabaricus</i>	54	39	29	1822	Mous et al. (2021)
<i>Lutjanus erythropterus</i>	70	50	37	773	
<i>Lutjanus vitta</i>	43	31	23	174	
<i>Aphareus rutilans</i>	120	85	64	2129	
<i>Pristipomoides multidens</i>	92	66	49	1356	
<i>Lutjanus fulvus</i>	40	-	21.45	-	Hassana et al. (2022)
	-	-	22.5 (FL)	-	Shimose and Nanami (2014)
<i>Lutjanus rufolineatus</i>	-	-	14.6-18.1 (FL)	-	Taylor et al. (2018)
<i>Lutjanus ehrenbergii</i>	35	-	20.1	-	Allen (1985)
<i>Lutjanus decussatus</i>	35	-	-	-	

Note: Lmax: maximum attainable total length at Indonesian latitudes; Lmat: Length at maturation (cm); Lopt: Optimum Harvest Size (cm); Wmat: Weight at maturation (gram); FL: Fork Length

**Figure 3.** Evolutionary relationships of taxa Lutjanidae in Yapen Regency (Research Sample Code namely: BKS29, BKS17, BKS36, BKS23, BKS47, BKS06, BKS07, BKS21 and BKS18)

Phylogenetic tree

The phylogenetic analysis in this study resulted in four main clades, these clades have bootstrap values ranging from 96-99% (Figure 3). The first, second, and third clades are members of the genus *Lutjanus*, whilst the fourth clade is composed of members from the genera *Pristipomoides* and *Aphareus*. Each clade consists of descendants of a common ancestor. In our investigation, *L. vitta*, *L. decussatus*, and *L. ehrenbergii* formed the first clade. All three species are descended from a common ancestor. The three species share the same physical characteristics, which include an oval body shape and a slim build. These species have similar canines and body spots. The second clade is composed of the species *L. fulvus* and *L. rufolineatus*. Both share a common ancestor. The two species possess an oval body shape; nevertheless, their body depth is greater than that of the species in the first group. *Lutjanus malabaricus* and *L. erythropterus* constitute the third clade. Both species have the same lineage and comparable morphologies. The discovered individuals can be differentiated by the shape of their snouts.

The Neighbor-Joining method for constructing the phylogenetic tree can boost the results of the genetic distance analysis. *Lutjanus ehrenbergii* and *L. vitta* have the smallest genetic distance value, forming a paraphyletic clade with a bootstrap value of 97%. *Lutjanus fulvus* and *P. multidentis*, which generated polyphyletic tree branches, were discovered to have the highest genetic distance value. We did not find any new variation after several sequences from GenBank were combined in the phylogenetic analysis.

Implications of molecular analysis for fisheries resource management

The paradigm shifts in fisheries resource management, from traditional species-based management to the Approach to Fisheries Management Ecosystem (AFME) (Staples et al. 2014; Hutubessy and Mosse 2015), do not eliminate the importance of understanding the characteristics of the managed resource species. It is believed that disregard for species-level resource characteristics has slowed the application of AFME in fisheries resource management (Howell et al. 2021). The significance of species-level characteristics in fish management lies in the fact that each fish species responds differently to the applied management intervention. For instance, the reaction to fishing efforts influences catches size variations.

Reef fish, especially Red Snappers, are the dominant species of fish captured by fishers in Yapen waters. Red snappers, particularly *L. malabaricus*, *L. erythropterus*, and *P. multidentis*, have substantial economic value. To satisfy local market demand, intense fishing is conducted. The information on the size structure of each individual fish is vital for fish management in Yapen seas, among other places. Table 5 indicates the optimal size for capturing *L. malabaricus* and *L. erythropterus*. In the meantime, the size of the captured *P. multidentis* individuals did not meet the optimal harvest size, possibly due to their immature gonads.

Lutjanus rufolineatus individuals caught in this study had reached the second stage of gonadal maturity. Some *L. ehrenbergii* individuals had reached the first stage of gonadal maturity, whereas others had not. In the meantime, the size of captured *L. vitta*, *L. fulvus*, and *A. rutilans* had not yet reached the size of the fish to attain gonadal maturity. This finding cannot be inferred with certainty, however, because the size of the fish that initially experienced gonadal maturation is affected by changes in environmental factors. Excessive and indiscriminate fishing can reduce the size of fish in the wild.

Another impact of overfishing is the loss of biodiversity, both at the species and molecular levels. Our research provides basic information about the types of red snappers traded in the local market. This information can be used as a database for the presence of red snapper species in Yapen waters. We identified red snappers using morphological and molecular analysis approaches, so the results were perfectly accurate. Combining morphological and molecular approaches can reduce taxonomic ambiguity in observed species (Dwifajri et al. 2022). The combination of the two approaches is very much needed because of the high morphological similarity between red snapper species within one genus and between genera.

Data on taxonomic certainty can be used to create maps of species biodiversity, identify species with the potential for aquaculture development and high economic value, and formulate legislative protection strategies for endangered species. Currently, the central government has established a fully exploited status for Red Snapper fishing in the waters of Cenderawasih Bay, including Yapen Island and its surroundings. This status is solely granted to red snappers in general, but the Indo-West Pacific is home to forty-three species of red snappers. Alternatively, distinct species may have varying susceptibilities to capture. Consequently, conservation must occur not only at the family or genus level but also at the species level. According to the above description, the success of fishery resource management depends on information on the target species. To accurately determine the characteristics of a species, phylogenetic studies using a molecular method are necessary to trace species.

ACKNOWLEDGEMENTS

We would like to thank the Ministry of Education, Culture, Research and Technology for funding this study through a research scheme with DIPA Directorate of Research, Technology and Community Service Directorate General of Higher Education, Research and Technology Ministry of Education, Culture, Research and Technology. Research contract No. 235/E5/PG/02.00.PT/2022 (May 30, 2022) and derivative contract No. 190.c/UN42.15/PG/2022 (June 7, 2022).

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