
[biodiv] Submission Acknowledgement

1 message

Ahmad Dwi Setyawan <smujo.id@gmail.com>
To: Bayu Pranata <b.pranata@unipa.ac.id>

Wed, Nov 2, 2022 at 8:47 AM

Bayu Pranata:

Thank you for submitting the manuscript, "Phylogenetic of red snapper (Lutjanidae) in Yapen Island Waters" to Biodiversitas Journal of Biological Diversity. With the online journal management system that we are using, you will be able to track its progress through the editorial process by logging in to the journal web site:

Submission URL: <https://smujo.id/biodiv/authorDashboard/submission/12746>
Username: 050693

If you have any questions, please contact me. Thank you for considering this journal as a venue for your work.

Ahmad Dwi Setyawan

Biodiversitas Journal of Biological Diversity

[biodiv] Editor Decision

1 message

Ayu Astuti <smujo.id@gmail.com>
To: Bayu Pranata <b.pranata@unipa.ac.id>, Ridwan Sala <ridwansala@gmail.com>, Aradea Bujana Kusuma <aradea.bujana@gmail.com>


Fri, Nov 4, 2022 at 1:31 AM

Bayu Pranata, Ridwan Sala, Aradea Bujana Kusuma:

We have reached a decision regarding your submission to Biodiversitas Journal of Biological Diversity, "Phylogenetic of red snapper (Lutjanidae) in Yapen Island Waters".

Our decision is: Revisions Required

Biodiversitas Journal of Biological Diversity

 A-12746-Article Text-1065495-1-4-20221101 (wecompress.com).doc
1097K

[biodiv] Editor Decision

1 message

Smujo Editors <support@mail.smujo.id>

To: Bayu Pranata <b.pranata@unipa.ac.id>, Ridwan Sala <ridwansala@gmail.com>, Aradea Bujana Kusuma <aradea.bujana@gmail.com>

Sun, Dec 4, 2022 at 12:01 AM

Bayu Pranata, Ridwan Sala, Aradea Bujana Kusuma:

We have reached a decision regarding your submission to Biodiversitas Journal of Biological Diversity, "Phylogenetic of red snapper (Lutjanidae) in Yapen Island Waters".

Our decision is: Revisions Required

Reviewer A:

Dear Authors,

Thank you for submitting this paper that explores red snapper diversity in Yapen island waters, and more generally using the NCBI database. This is an interesting and useful study that provides some clear information on evolutionary relationships.

There are some revisions required in order to consider this manuscript for publication. I have included specific feedback on the word document version of the manuscript, please find attached. Make sure that any changes to the manuscript are shown using highlighted text or tracked changes. Additionally, please address the following key areas when making revisions:

1. Methods. Make sure the methods are clearly provided with regards to the number of samples that were collected, how maturity of fish was assessed, and where the samples were taken from. This is important from a repeatability standpoint.
2. Wording. Check through for several word choice and grammar errors. I have highlighted these where possible in the text.

With these revisions, the paper should be in a stronger position overall.

Recommendation: Revisions Required

[Biodiversitas Journal of Biological Diversity](#)



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Bayu Pranata <b.pranata@unipa.ac.id>

[biodiv] New notification from Biodiversitas Journal of Biological Diversity

2 messages

DEWI NUR PRATIWI <support@mail.smujo.id>
Reply-To: Ahmad Dwi Setyawan <editors@smujo.id>
To: Bayu Pranata <b.pranata@unipa.ac.id>

Mon, Dec 12, 2022 at 12:32 PM

You have a new notification from Biodiversitas Journal of Biological Diversity:

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Ahmad Dwi Setyawan

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Mon, Dec 12, 2022 at 12:35 PM

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[Quoted text hidden]



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1 message

DEWI NUR PRATIWI <support@mail.smujo.id>
Reply-To: Ahmad Dwi Setyawan <editors@smujo.id>
To: Bayu Pranata <b.pranata@unipa.ac.id>

Tue, Dec 20, 2022 at 8:34 AM

You have a new notification from Biodiversitas Journal of Biological Diversity:

There is new activity in the discussion titled "Proof Reading" regarding the submission "Phylogenetic of red snapper (Lutjanidae) in Yapen Island Waters".

Link: <https://smujo.id/biodiv/authorDashboard/submission/12746>

Ahmad Dwi Setyawan

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Bayu Pranata <b.pranata@unipa.ac.id>

[biodiv] Editor Decision

1 message

Ayu Astuti <support@mail.smujo.id>

Wed, Dec 21, 2022 at 10:35 PM

To: RIDWAN SALA <ridwansala@gmail.com>, ARADEA BUJANA KUSUMA <aradea.bujana@gmail.com>, BAYU PRANATA <b.pranata@unipa.ac.id>

RIDWAN SALA, ARADEA BUJANA KUSUMA, BAYU PRANATA:

We have reached a decision regarding your submission to Biodiversitas Journal of Biological Diversity, "Phylogenetic of red snapper (Lutjanidae) in Yapen Island Waters, Papua, Indonesia".

Our decision is to: Accept Submission

Biodiversitas Journal of Biological Diversity

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

Abstract. Red Snapper are an economically valuable fishery resource. Most of these snapper species are inhabitants of coral reef ecosystems. The 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 relationship 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 contained 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.

Keywords: Molecular, Papua waters, Phylogenetic, Biodiversity (9 pt)

Abbreviations (if any): All important abbreviations must be defined at their first mention there. Ensure consistency of abbreviations throughout the article.

Running title: Diversity of Red Snapper Species

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.

Comment [A1]: Discuss these implications in a bit more detail.

Comment [A2]: Remove this statement

Comment [A3]: Italicise the genus name

Comment [A4]: italics

Comment [A5]: There is no comma required after the first author as per the Biodiversitas citation style. Please check the author guidelines and revise citations accordingly

47 In general, red snappers include *L. malabaricus*, *L. timoriensis*, and *L. erythropterus*, but the Indo-West Pacific contains
48 forty-three species of red snappers. Sadly, there is currently no information regarding the quantity of Red Snapper species
49 in the area. Red snapper species may have varying susceptibilities to fishing activities. Therefore, distinct management
50 methods are needed to maintain sustainable fishing. Developing conservation plans and long-term management methods
51 requires knowledge of the species and subpopulations involved (Bakar et al. 2018).

52 The search for species identity based on morphology does not provide full confidence compared to using a molecular
53 approach due to the “evolution convergent” (Zou and Zhang, 2016). The morphological traits of organisms inhabiting
54 distinct environments can vary (Heino, 2014; Shuai et al. 2018). Using genetic markers, species identity can be accurately
55 determined. Molecular studies have relied significantly on genetic markers (Chan et al. 2021). Genetic markers are
56 genomic DNA segments that provide information about taxonomic differentiation (Patwardhan et al. 2014; Grover et al.
57 2016). DNA sequences have been employed as genetic markers for species identification and the discovery of novel
58 species (Allen et al. 2013; Iwatsuki et al. 2015). Mitochondrial DNA (mtDNA) is one of the genomic DNA segments
59 frequently employed in molecular studies.

60 Mitochondrial DNA has been utilized extensively to answer questions concerning genetic diversity, population
61 evolution, and cellular structure (Gupta et al. 2015). The cytochrome oxidase c subunit I (COI) gene was employed in this
62 study for molecular identification and phylogenetic construction. The COI gene is a “DNA barcode” (Pentinsaari et al.,
63 2016). It is a dependable tool for monitoring biodiversity and reconstructing phylogenetic data (Pei et al. 2017). The
64 purpose of phylogenetic studies is to recreate the evolutionary history of a species or taxon (Jarvis et al., 2017), which is
65 represented by a tree-like diagram (Ramos et al. 2021).

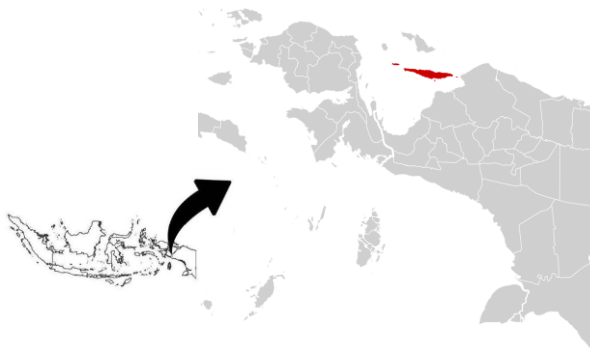
66 Earlier research on the family Lutjanidae employed the COI gene for genetic analysis (Gold et al. 2015; Bakar et al.
67 2018; Fadli et al. 2020; Shan et al. 2021; Halim et al. 2022). Researchers also used the COI gene to identify a new species
68 of red snapper (*L. papuensis*) in the Cendrawasih Bay of Papua New Guinea (Allen et al. 2013). In this study, we gathered
69 Lutjanidae specimens from fish landing places in Yapen. We identified the species based on their morphological and
70 molecular characteristics. The current study aimed to ascertain the number of species within the family Lutjanidae and to
71 reconstruct a phylogenetic tree to establish the evolutionary link between species.

Comment [A6]: Do you mean globally or locally?

72 MATERIALS AND METHODS

73 Study sites

74 We conducted this study in Yapen Regency, Papua, between June and August of 2022 (Figure 1). Extraction,
75 electrophoresis, and amplification were conducted at the Genetic Laboratory of *Universitas Bengkulu*. Additionally, we
76 collected data for 16 Lutjanidae nucleotide sequences from the National Center for Biotechnology Information (NCBI
77 (<https://www.ncbi.nlm.nih.gov>) (Table 1).
78



79 **Figure 1.** Sampling locations in the Yapen Regency
80
81

82
83

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 multidentis</i>	Australia: West Coast	MK092068
<i>Aphareus rutilans</i>	China	NC063973
<i>Aphareus rutilans</i>	China	ON152703

84 **Sampling method**

85 Samples were selected using purposive random sampling. Snappers were obtained from Fish Landing Places (TPI),
86 fish markets, and fishing spots. Early morphological identification referred to the identification book of Moore & Colas
87 (2016); White et al. (2013). One centimeter of red snapper dorsal fin tissue was removed and placed in a tube containing
88 ethanol 80%.

Comment [A7]: When did this take place?

Comment [A8]: In what locations?

Comment [A9]: 80% ethanol

89 **Morphological identification**

90 The identification of red snapper samples was based on their morphometric and meristic characteristics. We measured
91 and photographed the weight, total length, standard length, number of pectoral fin spines, number of dorsal fin spines, and
92 number of anal fin spines of each specimen.

Comment [A10]: What equipment was used to do this?

93 **Extraction, amplification, and sequencing**

94 DNA extraction followed the instructions from the Geneaid gSYNCTM DNA extraction kit. Amplification of the
95 cytochrome oxidase subunit I (COI) gene used a set of COI primers developed by A. Ward et al. (2005): F1 5'-TCA ACC
96 AAC CAC AAA GAC ATT GGC AC-3' dan R1 5'-TAG ACT TCT GGG TGG CCA AAG AAT CA-3'. PCR mix Go Taq
97 Green Master Mix consisted of Go Taq Green 25 µL, 1.5 µL DNA template, 19.5 µL nuclease free water, and 5 µL
98 primer. The thermal cycle setting was 95°C for 4 minutes during initial denaturation, followed by 35 cycles of denaturation
99 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.
100 The amplification results were electrophoresed to visualize the presence of DNA in the PCR product. The purified PCR
101 results were then sent to 1st BASE Sequencing Service Sdn. Bhd. (Malaysia) for sorting purposes.

Comment [A11]: Include the full term on the first mention

102 **Data analysis**

103 The DNA sequencing results were aligned and edited using MEGA X software. The sequence data were then matched
104 with the database available online at the NCBI (National Center for Biotechnological Information) genbank
105 (www.ncbi.nlm.nih.gov). The BLAST (Basic Local Alignment Searc Tool) method was used to assess the homology
106 between the sequences from the study sample and the genetic data sequences stored in the genbank (Toha et al. 2020).
107 BLAST results were tabulated to show the identity of the study sample. Genetic distance analysis and phylogenetic tree
108 reconstruction were carried out using the Neighbor Joining Method, Kimura-2 parameter model and bootstrap value of
109 1000× with the help of MEGA X software.

110 **RESULTS AND DISCUSSION**

111 **Result**

Comment [A12]: Results

112 *Morphological character analysis*

113 The morphometric and meristic characteristics of the Lutjanidae red snappers found in this study are described in
114 Table 2. The morphological identification results showed that nine species belonged to the genera *Lutjanus*, *Aphareus* and
115 *Pristipomoides*. *L. vitta*, *L. decussatus*, *L. rufolineatus*, *L. malabaricus*, *L. erythropterus*, *L. ehrenbergii* and *L. fulvus*

Comment [A13]: Provide some general details on the number of individuals that were identified and sampled

116 belong to the genus *Lutjanus*; *A. rutilans* comes from the genus *Aphareus*; and *P. multidentis* belongs to the genus
 117 *Pristipomoides*. The three species with maximum and minimum length and weight are *L. erythropterus* (Max. 49.5 cm –
 118 Min. 45 cm), *P. multidentis* (Max. 48.8 cm – Min. 42 cm) and *L. malabaricus* (Max. 29 cm – Min. 52 cm). Other species
 119 include *L. erythropterus* (Max. 1986 gr – Min. 1560 gr), *P. multidentis* (Max. 1380 gr – Min. 804 gr) and *L. malabaricus*
 120 (Max. 2611 gr – Min. 378 gr).

Comment [A14]: Wording isn't clear here. What do you mean? Surely this would be based on the age of the specimens

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

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

122 **Molecular identification**

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

126 **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

127 **Genetic distance analysis**

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

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

	1	2	3	4	5	6	7	8
1 <i>BKS29_L. vitta</i>								
2 <i>BKS23_L. rufolineatus</i>	0.115							
3 <i>BKS47_L. fulvus</i>	0.122	0.090						
4 <i>BKS07_L. erythropterus</i>	0.192	0.161	0.167					
5 <i>BKS36_L. ehrenbergii</i>	0.086	0.121	0.129	0.179				
6 <i>BKS06_L. malabaricus</i>	0.178	0.166	0.172	0.113	0.149			
7 <i>BKS17_L. decussatus</i>	0.082	0.125	0.125	0.165	0.097	0.176		
8 <i>BKS18_A. rutilans</i>	0.174	0.172	0.173	0.160	0.171	0.170	0.175	
9 <i>BKS21_P. multidentis</i>	0.182	0.193	0.205	0.187	0.193	0.201	0.180	0.129

Comment [A15]: Explain clearly what numbers 1-8 are

134 **Phylogenetic analysis**

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

141 **Discussion**

142 *Morphological characteristics*

143 This study discovered members of the genus *Lutjanus* with small to large bodies. Species in the genus *Lutjanus* have
144 an oval and deep body. They are also slender and fusiform in shape (Allen, 1985). Species belonging to the genus *Lutjanus*
145 have a continuous dorsal fin with a tiny incision between the thorny and soft parts. The red snappers vary in appearance,
146 typically having a reddish, yellow, gray, or brown background with a darker pattern of stripes or stems and are frequently
147 distinguished by a huge blackish spot on the upper side beneath the dorsal fin. Some species, including *L. vitta*, *L.*
148 *decussatus*, *L. ehrenbergii*, and *L. rufolineatus*, have black spots and stripes on their bodies. *L. vitta* is defined
149 morphologically by diagonal lines above and horizontal lines below the lateral line. From the eye to the tail fin, a
150 brownish-yellow stripe is present on this species. Moreover, *L. decussatus* is defined morphologically by the presence of
151 eight bands and a big black patch at the base of the caudal fin. *L. ehrenbergii* is distinguished morphologically by the
152 presence of three to four horizontal lines of variable width on the underside of the scales and a prominent black spot under
153 the dorsal fin. *L. rufolineatus* is distinguished by the presence of 7-8 yellow horizontal stripes. In this study, we did not see
154 any black spots and horizontal and vertical stripes in *L. fulvus*, *L. malabaricus* or *L. erythropterus*. The number of pectoral
155 fin soft spines in the *Lutjanus* genus varies between 14-17, while the number of dorsal fin spines ranges between IX-XI
156 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.
157 Each member of the genus *Lutjanus* has a truncated and emarginate tail.

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

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

168 The above description demonstrates that distinct morphological traits identify species from the genera *Lutjanus*,
169 *Aphareus*, and *Protipomoides*, as well as species within the same genus. Nevertheless, the species of the three genera share
170 similar meristic traits. Molecular analysis can clarify the species-level differentiation of these fish groups.

171 *Morphology molecular agreement in genetic distance*

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

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

Comment [A16]: Include citation here

Comment [A17]: Cite here



Figure 2. Comparison of morphological characters of some Lutjanidae species

Comment [A18]: Why were these specific species selected? Remove the red underline from the images.

187
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189 *Phylogenetic tree*

190 The phylogenetic analysis in this study resulted in four main clades, these clades have bootstrap values ranging from
191 96 – 99% (Figure 3). The first, second, and third clades are members of the genus *Lutjanus*, whilst the fourth clade is
192 composed of members from the genera *Pristipomoides* and *Aphareus*. Each clade consists of descendants of a common
193 ancestor. In our investigation, *L. vitta*, *L. decussatus*, and *L. ehrenbergii* formed the first clade. All three species are
194 descended from a common ancestor. The three species share the same physical characteristics, which include an oval body
195 shape and a slim build. These species have similar canines and body spots. The second clade is composed of the species *L.*
196 *fulvus* and *L. rufolineatus*. Both share a common ancestor. The two species possess an oval body shape; nevertheless, their
197 body depth is greater than that of species in the first group. *L. malabaricus* and *L. erythropterus* constitute the third clade.
198 Both species have the same lineage and have comparable morphologies. The discovered individuals can be differentiated
199 by the shape of their snouts.

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

205 *Implications of molecular analysis for fisheries resource management*

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

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

219 *L. rufolineatus* individuals caught in this study had reached the second stage of gonadal maturity. Some *L. ehrenbergii*
220 individuals had reached the first stage of gonadal maturity, whereas others had not. In the meantime, the size of captured *L.*
221 *vitta*, *L. fulvus*, and *A. rutilans* had not yet reached the size of the fish to attain gonadal maturity. This finding cannot be
222 inferred with certainty, however, because the size of the fish that initially experienced gonadal maturation is affected by
223 changes in environmental factors. Excessive and indiscriminate fishing can reduce the size of fish in the wild.
224

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

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

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

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Another impact of overfishing is the loss of biodiversity, both at the species and molecular level. 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.

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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 a 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.

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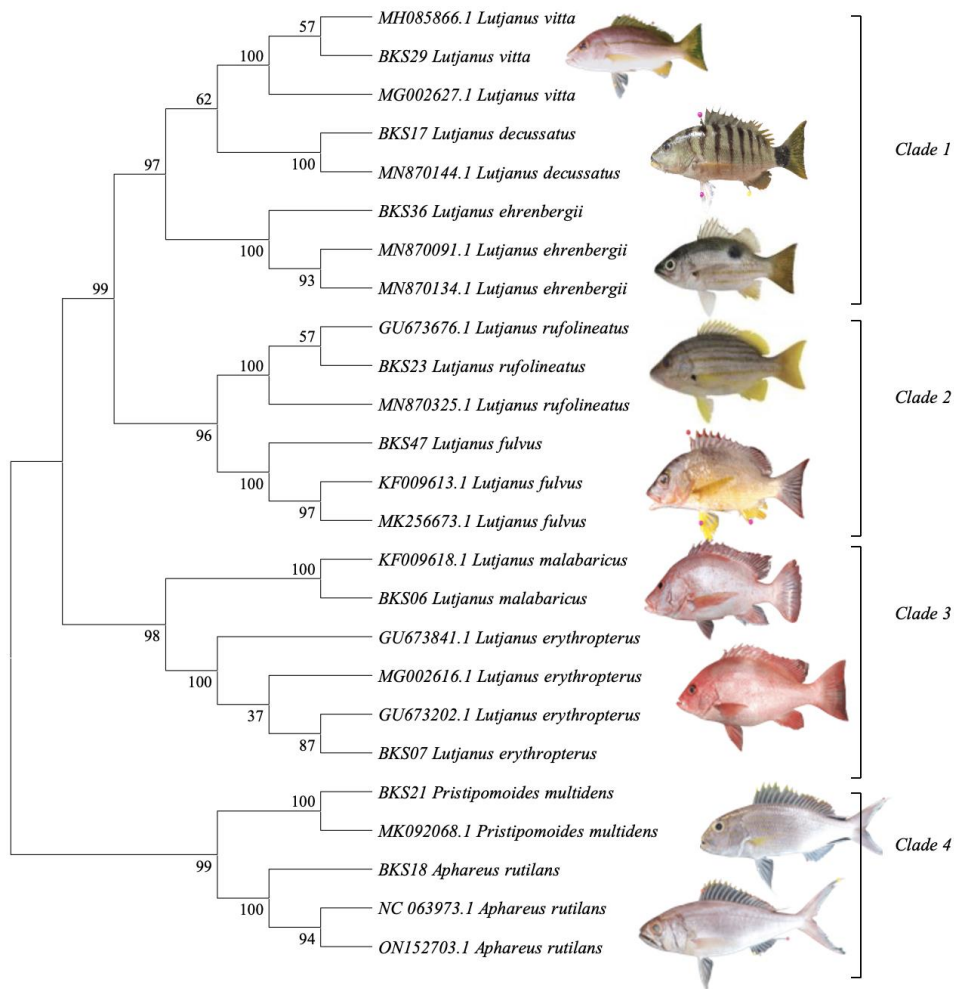
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Comment [A19]: How was maturation identified? Discuss clearly in methods



244
245 **Figure 3.** Evolutionary relationships of taxa Lutjanidae in Yapen Regency
246

Comment [A20]: Useful content here but provide a legend for evolutionary distance and highlight which of these are your own findings.

247 **ACKNOWLEDGEMENTS**

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251 235/E5/PG.02.00.PT/2022. Research contract number No. 235/E5/PG/02.00.PT/2022 (dated May 30, 2022) and derivative
252 contract No. 190.c/UN42.15/PG/2022 (June 7, 2022).

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Comment [A21]: Are the author initials available?

Comment [A22]: No need for caps here

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Comment [A23]: Italicise scientific name here

Comment [A24]: No need for caps here