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First morphological and molecular report of needledscaled queenfish (*Scomberoides tol*) from Cilacap Waters, Penyuu Bay, Indonesia

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Abstract

Fish misidentification often occurs in family Carangidae in Indonesia, especially genus *Scomberoides*, in Cilacap Waters. The condition can affect the fisheries management in the study area, because the management must be assessed to species level. The study aims to determine the physical characteristics and molecular information of the fish. Fish morphology was studied, tabulated, and documented according to its shape, colour, and general properties. Physical properties were measured and counted for morphometry and meristics study. DNA test was conducted to identify the species molecularly. DNA amplification method was polymerase chain reaction (PCR). The target gene used was the Cytochrome C Oxidase Subunit I (COI) gene. The primers used were FISH F1 and FISH R1. DNA sequencing used the Sanger dideoxy method. The fish was identified as *Scomberoides tol* physically with insignificant differences. There was no scutes and caudal peduncle groove in the fish. Its bases of anal and dorsal fin were equal in length. Finlets existed and semi-detached at posterior area to dorsal and anal fin. The type of scales and mouth was needle like and terminal, respectively. The fish shares 100% similarity of DNA with *S. tol* from previous studies across regions.

Keywords: Carangidae, DNA, fish, intraspecific variation, morphology

1. Introduction

Carangidae is one of the largest fish families from the Carangiformes order. Thus-far, 140 species and 32 genera of fish have been reported to belong to the Carangidae family (Abdussamad et al., 2013). The fish can be found in both tropical and subtropical waters (Yaseen et al., 2024). One of the most widely known genera by the public is *Scomberoides*. In Indonesia, the *Scomberoides* species that have been reported are *Scomberoides commersonianus*, *Scomberoides tol*, *Scomberoides tala*, and *Scomberoides lysan* (Arkham et al., 2021).

Most of the carangid fish have important economic and environmental value. The price is high due to their delicacy which produces high demand by the public (Feniola et al., 2024). Moreover, the fish also plays roles as both prey and predator in the food chain which enhance the sustainability of the aquatic ecosystem (Claeson et al., 2015).

Indonesian tends to overlook a species in genus *Scomberoides*, such as *S. commersonianus*, and identify the fish as talang queenfish or talang in local name. Uniquely, *S. tol*, *S. tala*, and *S. lysan* fish are also known as talang fish (Arkham et al., 2021). The public does not know the differences between those species.

There are still difficulties in identifying talang fish by naked eyes to the species level, particularly on *S. tol*, *S. tala*, and *S. lysan*. The morphological characteristics of the fish are mostly similar, both in body shape and number of fins (Abdussamad et al., 2013). Although there are many identification keys reported and available, the differentiation of the fish is

hard to notice. Moreover, morphological identification itself is highly dependent on the subjectivity of the observer or researcher where the experience and skills are clearly very influential (Santanumurti et al., 2024). In fact, misidentification of species in fish often occurs due to the similarity of body shape, color, and organs (Luo et al., 2021).

The fish have been found and reported in various regions in Indonesia such as Java Island (East Java, West Java) to Papua (Merauke) (Alipin et al., 2021; Mote and Indrayani, 2022; Yaseen et al., 2024). Nevertheless, information related to physical and molecular identification of the fish has never been reported, even carried out in Penyu Bay, Cilacap Waters, Central Java, Indonesia (Tjahjo and Riswanto, 2013; Munir, 2016).

The misidentification of the fish can affect the fisheries management in Indonesia. Generally, the management emphasizes quota-based regulation and considers the vulnerability status of fish in accordance with prevailing policies (Nurlaela, 2023). The quotas and assessments are applied to species level to help control exploitation and ensure the sustainability of fish stocks, accurately. The analysis possibly produces many errors when the species is misidentified. One proposed solution is to carry out physical and molecular identification of *Scomberoides* fish in Indonesia.

Unfortunately, many publications related to *Scomberoides* fish from Indonesia did not use molecular identification methods such as DNA barcoding (Asni et al., 2022; Mote and Indrayani, 2022). Whereas the technology has high identification accuracy and efficiency without requiring whole fish samples (Santanumurti et al., 2024). Considering these challenges, related research is needed, especially to examine *Scomberoides* species found in Penyu Bay, Cilacap, Central Java. The study aims to determine the physical characteristics and molecular information of the fish. The results are valuable toward the biodiversity and richness of Indonesia's marine life. Furthermore, its findings are expected to support improved conservation efforts for fish species across the country.

2. Materials and Methods

2.1. Time and Place

Present study was conducted between 10th and 28th February 2025. It was started by collecting the samples and followed by studying the physical characteristics and DNA test. Samples collection was conducted once in Cilacap Waters (**Figure 1**). Meanwhile the rest of study were conducted simultaneously in Research and Community Service Laboratory of Faculty of Fisheries and Marine Sciences, Jenderal Soedirman University, and Bionesia Laboratory, Bali, Indonesia.

2.2. Samples and Data Collection

Samples were collected to the laboratory using cooler box to be measured, dissected, and analysed. The sample used in this study was one sample for morphological and molecular. Fish dimension was measured to collect length (cm) and weight (g) measurement board with 1 mm precision and digital scale with 0.1 g precision. Moreover, samples were observed to determine its physical characteristics according to fish morphology, morphometry, and meristic. Some tissues of fish organs were preserved in the container with ethanol 95% for molecular study (Santanumurti et al., 2024).

2.3. Morphological Characteristics Study

Fish morphology was studied, tabulated, and documented according to its shape, colour, and general properties. Furthermore, some part of physical properties was measured and counted for morphometry and meristic study (Yedier et al., 2023). The results were guided and confirmed by using fish identification book with title "The Living Marine Resources of the Western Central Pacific. FAO Species Identification Field Guide for Fishery Purposes," (Carpenter and Niem, 1999).

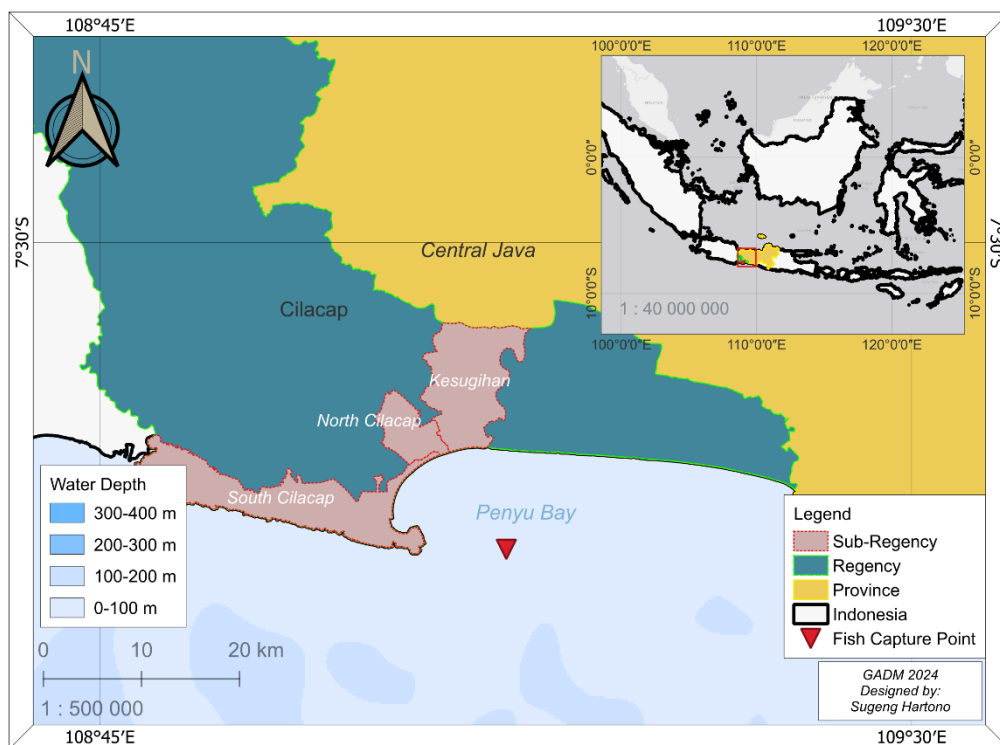


Figure 1. Map of Research Location in this study. The sample was collected from Penyus Bay, Cilacap Waters, Central Java, Indonesia.

2.4. Molecular Study

Tissue preservation was initiated as a preliminary step for molecular study (Yuan et al., 2014). The specimen was then sent to the BIONESIA Laboratory (Bali, Indonesia) for DNA testing. It was labelled with the specimen code BIOSUB312.001 and tested once.

DNA testing was conducted through several sequential steps, including (1) preparation of tissue samples, (2) DNA extraction using the 10% Chelex protocol, (3) DNA amplification using the Polymerase Chain Reaction (PCR) technique, (4) visualization of PCR results, and (5) DNA sequencing. Tissue sample preparation involved collecting approximately 10 grams of tissue from the fish specimen. The DNA extraction process was carried out to isolate the DNA, which involved preparing a 10% Chelex solution, adding the tissue sample into a microtube containing the Chelex solution, heating the mixture at 95°C for 45 minutes, mixing the solution and tissue, centrifuging the mixture to separate contents, and collecting the supernatant containing DNA for amplification (Yuanawati et al., 2022).

DNA amplification via PCR followed the BIONESIA laboratory protocol. The target gene used in the study was the Cytochrome C Oxidase Subunit I (COI) gene. The primers used were FISH F1 (5'-TCA ACC AAC CAC AAA GAC ATT GGC AC-3') and FISH R1 (5'-TAG ACT TCT GGG TGG CCA AAG AAT CA-3') as described by (Ward et al., 2005).

The total PCR reaction volume was 26 µL, consisting of 2 µL of extracted DNA template, 1.25 µL of each primer at a concentration of 10 mM, 9 µL of double-distilled water (ddH₂O), and 12.5 µL of ReadyMix. The PCR mixture was then amplified using an Applied Biosystems™ 2720 Thermal Cycler. The thermal profile used in the PCR protocol consisted of pre-denaturation at 94°C for 3 minutes, denaturation at 94°C for 30 seconds, annealing at 50°C for 30 seconds, and extension at 72°C for 60 seconds. The denaturation to extension cycle was repeated 38 times, followed by a final extension step at 72°C for 2 minutes. PCR product visualization was performed using 1% agarose gel electrophoresis stained with GelRed® Nucleic Acid Gel Stain. Positive samples showed visible DNA bands under UV light.

DNA sequencing was carried out using the Sanger dideoxy method at Genetika Science Company, Jakarta. The sequencing output was in the form of sequence files (Ab1 format),

which were further analysed computationally. The sequence data were edited and aligned using the ClustalW method in MEGA XI software. Each base arrangement was manually checked to ensure the quality of the data used (Megarani et al., 2020).

Further analysis was conducted by matching the sequences with genetic information available in the NCBI GenBank database using the Basic Local Alignment Search Tool (BLAST) on the NCBI website (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). The degree of similarity and data accuracy were recorded for each sequence.

Genetic data was analysed to produce phylogenetic tree. The aim was to review its genetic relationship with other samples and to confirm the BLAST identification results at the species level. A phylogenetic tree was constructed using the Neighbor-Joining (NJ) method with 1000 bootstrap replications in MEGA XI software.

3. Results and Discussion

3.1. Morphology of *S. tol* in Cilacap Waters

Fish samples from Cilacap Waters were identified as *S. tol* in family Carangidae. The observation results (see **Table 1**) showed that the fish matched the characteristics of the species morphologically. The genus was confirmed due to some existing characteristics according to (Smith-Vaniz, 1999). The fish had no scutes and caudal peduncle groove. Bases of anal and dorsal fin were equal in length. Moreover, finlets existed and semi-detached at posterior area to dorsal and anal fin. Meanwhile, the species level was confirmed due to the similarity on the type of scales and mouth.

Table 1. The results of morphology observation on fish samples of *S. tol* found in Cilacap Waters. The *S. tol* collected in Cilacap Waters has 6 vertically oval blackspots, no cutes developed along posterior part of lateral line; no caudal peduncle groove, fusiform body shape, body strongly compressed, large eyes, slightly concave dorsal head, terminal mouth, small scales, and forked caudal shaped.

Details	Observation results
Body characteristics	No scutes developed along posterior part of lateral line; no caudal peduncle groove; finlets existed and semi-detached at posterior area to dorsal and anal fin; black pigmented at outer dorsal fin; dorsally bluish, ventrally silver or white, with 6 vertically oval blackspots, the first 4 intersect the lateral line; bases of anal and second dorsal fin about equal in length; II detached spines in front of anal fin; pelvic fins shorter than pectoral fins in length; anal fin lobe immaculate and white.
Body shape lateral	Fusiform or normal.
Cross section	Body strongly compressed; dorsal and ventral profiles equally convex.
Type of eyes	Large, round, and positioned laterally.
Dorsal head and nape profile	Slightly concave.
Type of mouth/snout	Terminal and moderately pointed; upper jaw extends to posterior margin of pupil.
Position of mouth	Slightly oblique, located at the end of the snout, but angled slightly upward.
Type of scales	Very small, cycloid-type scales, needle-like, and difficult to see with the naked eye.
Caudal shape	Forked.

3.2. Morphometry and meristic of *S. tol* in Cilacap Waters

The present study measured approximately 32 external shapes of *S. tol* collected from Cilacap Waters to analyse its morphometry (see **Table 2**). Some parts of the fish were compared to previous studies to see the difference among samples from various regions. Total length of the fish from present study (37.73 cm) was longer than any fish from previous studies.

However, the snout length (24.32%) and the body depth (22%) were shorter by 4–5% and around 2% respectively than any others.

Table 2. The results of morphometry observation on fish samples of *S. tol* found in Cilacap Waters compared with previous studies. This study showed complete morphometric characteristics of *S. tol*, with lower snout length compared with others.

Characteristics	Present study (n=1)	Smith-Vaniz and Staiger (1973)♣ (n=148)	Guun (1990) (n=23)	Yokogawa and Takemori (2001) (n=1)	Kim et al. (2018) (n=2)	
					PKU5 2395	PKU6 0285
Weight (g)	261	-	-	-	-	-
Total length (cm)	37.73	-	8.7–27	16.38	12.45	9.9
Fork length (cm)	33.81	-	-	-	11.18	8.84
Standard length (cm)	31.93	2.0–46.8	-	13.58	10.7	8.5
Pre dorsal length (cm)	16.23	-	-	-	-	-
Pre pectoral length (cm)	6.27	-	-	-	-	-
Pre pelvic length (cm)	6.74	-	-	-	-	-
Pre anal length (cm)	15.88	-	-	-	-	-
Head length (cm)	6.25	-	-	-	-	-
Snout length (in % HL)	24.32	29.1–32.8	-	-	29.1	28.3
Head width (cm)	1.9	-	-	-	-	-
Head depth (cm)	3.22	-	-	-	-	-
Eye diameter (cm)	1.5	-	-	-	-	-
Distance between eyes (cm)	1.8	-	-	-	-	-
Body depth (in % FL)	22	20–24.7	22.1–24	-	24	24.6
Body width (cm)	2.3	-	-	-	-	-
Dorsal fin spine base length (cm)	3.33	-	-	-	-	-
Longest dorsal fin length (cm)	2.81	-	-	-	-	-
Dorsal finlets base length (cm)	11.52	-	-	-	-	-
Pectoral fin length (cm)	4.14	-	-	-	-	-
Pelvic fin base length (cm)	0.99	-	-	-	-	-
Longest pelvic fin length (cm)	3.56	-	-	-	-	-
Two detached spine base length (cm)	0.8	-	-	-	-	-
Two detached spine length (cm)	1.29	-	-	-	-	-
Anal fin base length (cm)	3.48	-	-	-	-	-
Longest anal fin length (cm)	1.91	-	-	-	-	-
Anal finlets base length (cm)	11.22	-	-	-	-	-
Caudal height (cm)	7.95	-	-	-	-	-
Caudal peduncle (cm)	1.57	-	-	-	-	-
Top caudal fin length (cm)	7.54	-	-	-	-	-
Middle caudal fin length (cm)	1.9	-	-	-	-	-
Bottom caudal fin length (cm)	7.17	-	-	-	-	-

Note: ♣—Includes holotype specimen.

The results of meristic observation on countable parts of fish fin are displayed on **Table 3**. Seven parts showed similar results from previous studies. A slight difference was only noticed on pectoral fin, where (Smith-Vaniz and Staiger, 1973) found one spine on the pectoral fin of *S. toI* collected from the Malay Archipelago and Indian Ocean. The spine was not found from any others, especially from samples at least the last decade.

Table 3. The results of meristic observation on fish samples of *S. toI* found in Cilacap Waters compared with previous studies. *S. toI* found in this study had almost the same meristic characteristics with Smith-Vaniz and Staiger (1973) and Guun (1990).

Characteristics	Present study (n=1)	Smith-Vaniz and Staiger (1973) (n=148)	Guun (1990) (n=23)	Yokogawa and Takemori (2001) (n=1)	Kim et al. (2018) (n=2)	
					PKU52395	PKU60285
Dorsal fin spines	VII+I	VI–VII+I	VI–VII+I	VI+I	VI+I	VII+I
Dorsal fin rays	19	19–21	19–21	19	21	21
Pectoral fin rays	15	I+15–18	-	18	18	18
Pelvic fin spines	I	-	-	I	I	I
Pelvic fin rays	6	-	-	5	5	5
Anal fin spines	II+I	II+I	II+I	II+I	II+I	II+I
Anal fin rays	18	18–20	17–20	17	19	19

3.3. Molecular Identification

The study was successfully amplified COI gene of *Scomberoides* from Cilacap Waters, Penyus Bay, Central Java, Indonesia. **Figure 2** showed the gel electrophoresis results where DNA fragments separated and visualized based on their molecule size (Cermakova et al., 2023). The results showed that the size of the samples taken was between the 600-700 bp marker and was in accordance with the size of the COI gene. Sajjad et al. (2023) stated that the COI gene is a genetic marker to identify living things with a size of 650 bp. Thus, the gene successfully obtained in the study is the COI gene.

The results of the molecular analysis showed that the fish in the study were *S. toI*. It was confirmed by the similarity reaching 100% with *S. toI* with accession numbers DQ885123.1 and KU535574 (see **Table 4**) (Jaafar, 2014; Kim et al., 2018). The results of current study are the first report of molecular data of *S. toI* from Cilacap Waters, Central Java, Indonesia.

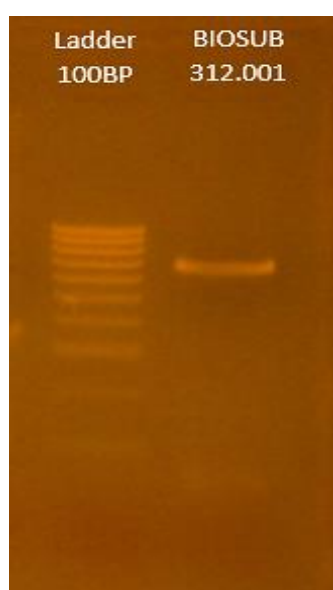


Figure 2. The electrophoresis of COI gene from *Scomberoides* in the present study. The DNA fragment was separated and visualized clearly with the size molecule of the COI gene (600-700 bp).

There are only six records of *S. tol* in Indonesia itself that have been entered into NCBI: HM392323.1 (West Java), JN312861.1 (West Nusa Tenggara), MN257526.1 (Aceh), GU673882.1 (Bali), GU674249.1 (East Java), and West Papua (ON888875.1). The results of the study contribute to the data of *S. tol* from various provinces of Indonesia.

Table 4. Similarity results of *Scomberoides* from this study compared with NCBI. *Scomberoides* collected in this study had 100% similarity with *Scomberoides tol* with accession number of DQ885123.1 and KU535574.

Sample	Query Cover (%)	Similarity (%)	Accession Number
<i>Scomberoides tol</i>	100	100	DQ885123.1
<i>Scomberoides tol</i>	100	100	KU535574
<i>Scomberoides commersonnianus</i>	100	94.5	KJ013058.1
<i>Scomberoides commersonnianus</i>	100	94.35	OQ386602.1
<i>Scomberoides commersonnianus</i>	100	93.87	PP090605.1
<i>Scomberoides tala</i>	100	92.37	OQ386069.1
<i>Scomberoides tala</i>	100	92.37	OQ387737.1
<i>Scomberoides lysan</i>	100	92.21	OQ385640.1
<i>Scomberoides lysan</i>	100	91.76	OQ386295.1

3.4. Phylogenetic Tree

Phylogenetic tree is a branching diagram used to describe the evolutionary relationships between species, populations, or genes based on the similarities and differences in their genetic or morphological characteristics (Dornburg and Near, 2021). The results of current study indicated that the sample certainly included the fish sample in Clade 1 of phylogenetic tree meaning the results of current study identified the fish as *S. tol* (see **Figure 3**).

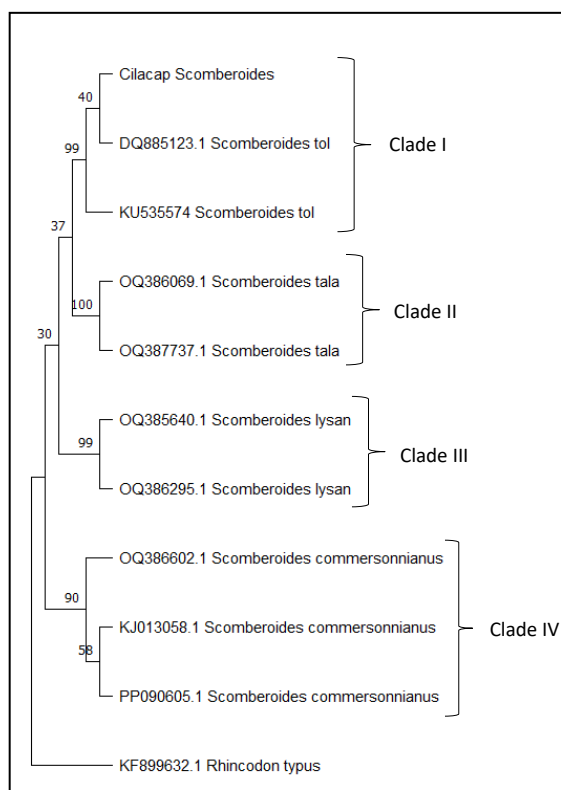


Figure 3. Phylogenetic tree of *S. tol* from current study and its relationship with other *Scomberoides* using Neighbor-Joining (NJ) method with 1000 bootstrap replications in MEGA XI software. *S. tol* found in this study had evolutionary relatives with *S. tol* since they were from the same ancestral branch (clade I).

3.5. Discussion

Morphologically, *S. tol* has a round black blotches while *S. tala* has vertically elongated stripe of black blotches (Abdussamad et al., 2022). Compared to *S. lysan*, *S. tol* has a black body mark that is more round and visible (Abdussamad et al., 2022). In terms of body characteristics, *S. tol* has a oblong elongate and compressed body shape, while *S. commersonianus* and *S. pelagicus* has a deeper and more robust body shape (Abdussamad et al., 2022). According to this comparison, morphologically, the *Scomberoides* sample obtained from Cilacap in this study was *S. tol*. The comparison of *Scomberoides* found in this study with others showed in **Figure 4**.

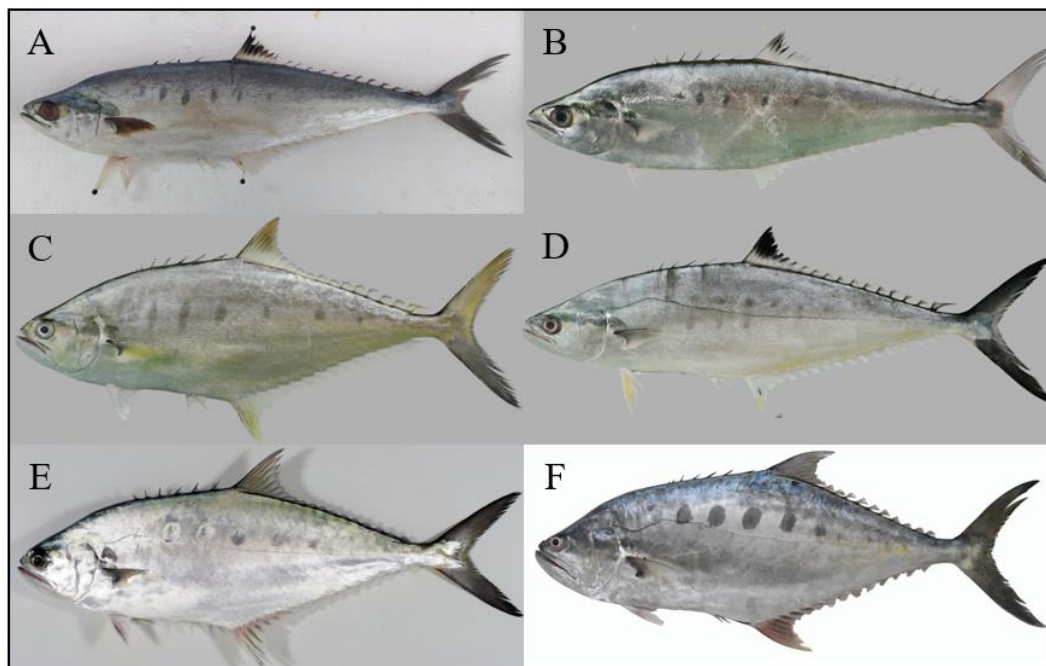


Figure 4. The morphology comparison of *Scomberoides*. (A) *S. tol* from this study; (B) *S. tol*; (C) *S. tala*; (D) *S. lysan*; (E) *S. commersonianus*; (F) *S. pelagicus* (Matsunuma et al., 2019; Abdussamad et al., 2022; Su et al., 2025).

The species *S. tol* is widely distributed in the surface waters of coastal regions across many countries (Smith-Vaniz, 1999). It has been reported from the South China Sea (Kyushin et al., 1982), the Red Sea (Dor, 1984), Australian Waters (Allen and Swainston, 1988), and throughout the Indo-Pacific region (Kimura et al., 1998).

Several authors have conducted morphological studies on *S. tol* from various localities, and their findings are consistent with those of the present study. The earliest known work was by (Cuvier and Valenciennes, 1832), who described the species as *Chorinemus tol* from Malabar, India. Subsequent studies include Smith-Vaniz and Staiger (1973) in the Malay Archipelago and Indian Ocean, (Gunn, 1990) in Australia, Carpenter et al. (1997) in Kuwait, Lin and Shao (1999) in Taiwan, Yokogawa and Takemori (2001) in Japan, Nakabo (2002) also in Japan, Psomadakis et al., (2015) in Pakistan, Kim et al. (2018) in South Korea, and Low and Jaafar (2021) in Singapore.

The finding from Kim et al. (2018) claimed that the species has caudal peduncle groove. The claim obviously created a contradiction in the diagnosis of *S. tol* morphology. Only some closely related species in Carangidae (*S. lysan*, *S. tala*, and *S. commersonianus*) have caudal peduncle groove (Smith-Vaniz, 1999; Abdussamad et al., 2013).

Environmental factors may have influenced the development of the caudal peduncle groove observed in the study by (Kim et al., 2018). The groove is a key adaptation that enhances swimming efficiency and speed in Carangidae, supporting their predatory lifestyle (Burhanuddin and Erviani, 2016). Therefore, it is probable that factors related to swimming and predation—such as water currents and feeding competition in South Korean Waters—contributed to the development of the feature in *S. tol*. Alternatively, the presence of the

groove could also be attributed to ontogenetic variation, a concept in fish taxonomy where morphological features change as a fish matures from juvenile to adult (Hilton and David, 2007).

The slight differences in morphometry of *S. tol* in Cilacap Waters can be explained by its relationship to growth rate. According to Von Bertalanffy, (1957); Kinne, 1960; Brett (1979), the rate depends on many factors such as abiotic and biotic factors separately or in mixed manner, which affect fish metabolism and growth. Generally, the value decreases greatly at the onset of maturity. There are fish that grow quickly at a young age and reach maturity earlier eventually being outgrown by slower-growing individuals, indicating that early growth advantages do not always continue throughout the fish's lifespan. The total length of the fish clearly showed the fish was older compared to fish from previous studies. Hence, the value of the snout length and body depth were lower insignificantly than other comparative samples.

The existence of a fin pectoral spine found in Smith-Vaniz and Staiger's samples (1973) made the diverse results to current study. The difference was called as intraspecific differences or intraspecific variation, which is normally found in many animals. It occurs due to genetic variation within a population or different ecological pressures that cause populations to specialize in different ways (Gregory, 2011). In fish, the case can be found in some species from Aegean Sea (Koutsidi et al., 2024) or Nile River and Lake Nasser (Jawad et al., 2021).

The sample of needlescaled queenfish from Cilacap Waters was still confirmed as *S. tol* according to its morphometric and meristic traits. Even though there were slight differences with other samples from previous studies. The present study found no significant difference on measurable and countable parts of the fish. However, it is recommended that the stakeholders of fisheries in Indonesia to maintain the environmental quality of the waters, as the pollution and overfishing may lead to mutations and affect the physical development of the fish.

Molecular data accurately identify the species which is essential for conservation efforts and biodiversity assessments. The information also helps resolving taxonomic ambiguities and supporting the discovery of new species. Since there are many challenges in identifying *S. tol* in Indonesia, the results of current study facilitated to distinguish the species among genus *Scomberoides* which existed in the region.

The record was registered with NCBI with accession number PV563873.1. As NCBI is the Global Molecular Data Centre, it allows scientists around the world to access and utilise the data (Sayers et al., 2025). Scientists and the public can find, compare, and analyse biological data from around the world, including *S. tol* from Cilacap Waters (Central Java, Indonesia). NCBI has standard formats and validation so that the molecular data entered has high accuracy and consistency (Sayers et al., 2025).

The phylogenetic tree also shows groups of closely related species (Rice et al., 2022). If the DNA sequence of the target fish is grouped (clade) with a known species, it is certain that the specimen belongs to that species. In the case of genus *Scomberoides*, it currently has five reported species, *S. tol*, *S. tala*, *S. lysan*, *S. commersonianus*, and *S. pelagicus* (Abdussamad et al., 2022). However, the phylogenetic tree data presented in current study did not display *S. pelagicus* as its own clade. It is because the fish was only reported in a publication from India in 2021 and the molecular data has not been recorded in NCBI, yet (Abdussamad et al., 2022).

Unfortunately, the number of fish samples is the limitation in this study. Only one sample was identified morphologically and molecularly. This was due to the difficulty in obtaining *S. tol* sampel. On the island of Java, especially Central Java, the presence of *S. commersonianus* is more frequently reported (Dwi et al., 2019). Furthermore, small pelagic fish like *Scomberoides* were already fully exploited according to Ministerial Decree No. 19 of 2022 (Nurlaela, 2023). Furthermore, data from the Cilacap Ocean Fisheries Port (2024) indicates that needlescaled queenfish (*S. tol*) were not landed in Cilacap waters (Cilacap Ocean Fisheries Port, 2024). This may be the reason why *S. tol* was difficult to find during fish collection activities in Cilacap Waters, Penyus Bay, and was the first discovery in this study. Further research needs to be conducted by adding more samples so that the data will be more detailed.

4. Conclusions

The study concluded the identification of a fish sample collected from Cilacap Waters, Central Java, Indonesia which was confirmed as *S. tol* according to its physical traits and molecular information. The morphology was aligned with the relevant identification guidebook, while the morphometric and meristic traits were not significantly different compared to previous studies from various waters. On the other hand, DNA test proved that the fish sample from study area shares 100% similarity of DNA with the samples from previous studies across regions. As the first record of *S. tol* in Cilacap Waters, the finding can be used to analyse the fish population and stock accurately in the future while maintaining the quality of its habitat. Thus, the sustainability and biodiversity of aquatic life can be achieved in the area.

Conflicts of Interest

There are no conflicts to declare.

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AI Writing Statement

The authors did not employ any artificial intelligence-assisted technology during the writing process.

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