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PHYLOGENETIC RELATIONSHIPS OF ORNAMENTAL CHAETODONTIDAE IN THE SOUTH COASTAL OF WEST JAVA, INDONESIA

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Abstract. *Marine ornamental trade has been developing for several years with Indonesia as one of the major exporter countries. Among the popular marine ornamental fish in the local and international markets belong to the family of Chaetodontidae. The existence of this family has been reported from several areas in Indonesia. However, no information is available in terms of their phylogenetic relationships of the fish from the south coast of West Java. The aim of this research was to asses the phylogenetic relationships among ornamental fish members of Chaetodontidae in the South Coast of West Java. Fish samples were collected from two trading sites Ujung Genteng and Taman Manalusu. Collected fish were identified using a previously published study. The evolutionary relationships among species were analyzed statistically through phylogenetic analysis based on maximum parsimony algorithm and Kimura 2- Parameter substitution model as implemented in PAUP 4.0 software. Tree branching pattern supported by 1000 bootstraps pseudo-replicates and out-group comparison. Daschyllus trimaculatus used as outgroup species. Based on the study, Chaetodontidae from the South Coast of West Java formed one monophyletic group compared to Dascylus trimaculatus with Chelmon rostratus was the basal species. All the remaining species were the derived species. There are CI and RI value gained. The consistency index (CI) value of this family is 0.5833 and the retention index (RI) is 0.5082.*

Keywords: *Actinopterygii, Chaetodontidae, diversity, phylogeny*

Citation
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INTRODUCTION

A high potential of the marine ornamental fish family was reported from the South Coast of Sukabumi precisely in its eastern part at Ujung Genteng (Wahyudin, 2011) and Taman Manalusu of Garut (Mayunar, 1996). The potency of marine ornamental fish in Ujung Genteng coastal areas was 4.2 million fishes/year. The potential of marine ornamental fish in Garut, including in Taman Manalusu, was 19.2 million fishes per year (Mayunar, 1996). However, no recent data was available because no recent study has been done in both areas. The latest study from Nuryanto et al. (2020) was only reported marine ornamental fish diversity collected from coastal waters of Pangandaran.

Sugianti & Mujiyanto (2013) reported that Chaetodontidae is a dominant family among marine ornamental fishes in coral ecosystems. According to Fessler & Westneat (2007), Chaetodontodae is a diverse family of marine percoids in all coral reef systems and all tropical seas. Radiation of this family was about 16 million years ago, resulting in 93 nominal species (Pyle & Kosaki, 2016). Froese & Pauly (2019) reported that 65 species of Chaetodontidae exist in Indonesia.

The high species diversity of Chaetodontidae attracts the interest of taxonomists and phylogeneticists. They are varied in subtle morphological differences (Allen & Erdmann, 2012). Morphometric measurement and meristic counts are vital characteristics of Chaetodontidae identification (Naeem et al., 2011). The previous study from Ali et al. (2017) had defined 22 morphometric characters and four meristic characters for species identification of Chaetodontidae.

Many studies had reported the diversity of Chaetodontidae at several localities in Indonesia (Wibowo et al., 2013; Hastuty et al., 2014; Yuliana et al., 2017; Fadli et al., 2018; Sahetapy et al., 2018;). Some other studies were working on the phylogeny analysis based on molecular data (Litlewood et al., 2004; Fessler & Westneat, 2007; Bellwood et al. 2010; Waldrop et al., 2016; Zhu et al., 2018) and morphological characters (Ferry-Graham et al., 2001; Smith et al., 2003, Nabila et a., 2019; Pambudi et al., 2019). However, no study has been reported on the phylogenetic relationships of Chaetodontidae from the south coast of West Java, Indonesia.

The objective of the present study was to understand the phylogeny of Chaetodontidae at Ujung Genteng and Taman Manalusu of the south coast of West Java, Indonesia and to asses their evolutionary relationships. The information obtained will be beneficial for a conservation program for Chaetodontidae on the South Coast of West Java.

MATERIALS AND METHODS

Sampling Sites and Time

Samples were collected from a middleman fish trader at Ujung Genteng (7°361927’00” S - 7°3614413’00” S and 106°3841607’5329” E - 106°4019733’00”) in Sukabumi and at Taman Manalusu (7.5884374 S - 7.5899312 S and 107.6054907 E - 107.6241195 E) in Garut (Figure 1) from February to April 2018

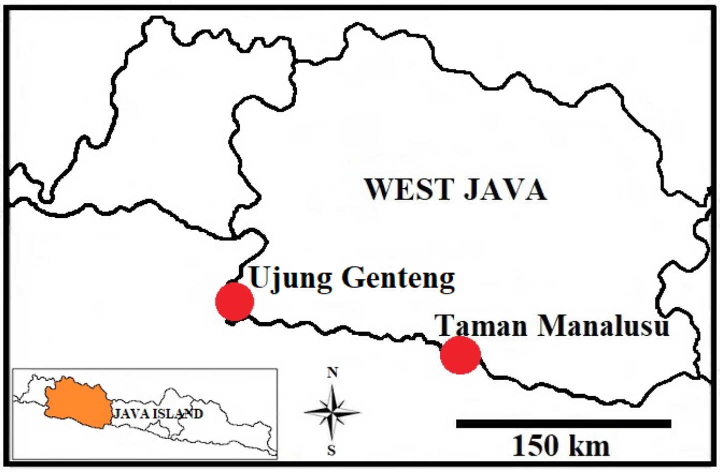

Figure 1. Sampling sites in Ujung Genteng and Taman Manalusu

Specimen Handling and Identification

All specimens were photographed using a 16-megapixel camera. Samples were preserved using standard wet preservation methods with final preservation in ethanol 70%. Specimens were then identified based on color type and pattern, meristics and morphometric characters. Identification was guided by Allan & Erdmann (2012). The acceptability (validity) of the species names resulted from identification were then checked to the data available in FishBase (Froese & Pauly, 2019).

Phylogenetic Analysis

The phylogenetic tree was reconstructed based on meristic and morphometric characters. The schematic figure of the morphometric characters is illustrated (Figure 2). A total of 24 morphology characters had used during the study. The meristic and morphometric are listed (Table 1).

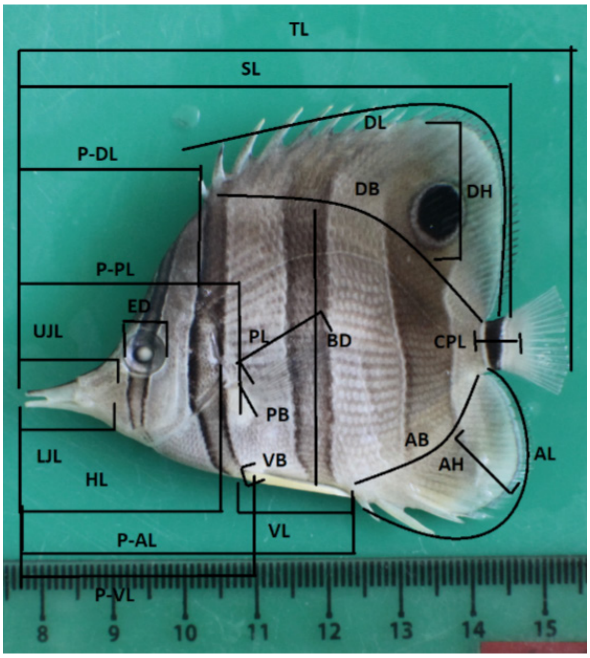

Figure 2. Schematic illustration of the morphometric measurement

Table 1. Morphology characters for phylogenetic tree reconstruction

Characters	Annotation
TL	Total length
SL	Standard length
HL	Head length
ED	Eye diameter
DFH	Dorsal fin height
VFL	Ventral fin length
AFB	Anal fin base
Afh	Anal fin height
P-AL	Pre-anal length
P-VL	Pre-ventral length
CPL	Caudal peduncle length
HL:ED	Ratio head length to eye diameter
SL:HL	Ratio standard length to head length
LJ:AB	Ratio lower jaw length to anal-fin base
DFL:DFB	Ratio Dorsal fin length to dorsal-fin base
AFL:AFB	Ratio Anal fin length to anal-fin base
VFL:VFB	Ratio ventral fin length to ventral fin base
DR	Dorsal rays
PR	Pectoral rays
BSDF	Black spot on the dorsal fin
OBB	Orange bar on the body
BBB	Black bar on the body
BBCP	Black bar on caudal peduncle
SB	Silvery body

The characters in Table 1 were transformed into multistate characters with three different states and symbolized as 0, 1 and 2. The symbol 0 represents primitive characters in outgroup species. The symbols 1 and 2 represent of derived characters present in Chaetodontidae. The meaning of each symbol is available in Table 2.

Table 2. The meaning of symbols of characters used during the study

Symbol	Annotation
0	Short or less or none
1	Vague or medium
2	Long or plenty or pronounced

The evolutionary relationship among the members of Chaetodontidae was estimated through phylogenetic tree reconstruction based on the maximum parsimony algorithm. The tree reconstruction conducted in PAUP 4.0. Software (Swofford, 2002). The branching polarity of the tree was estimated by comparing the ingroup samples (Chaetodontidae) with the out-group species. This study used *Dascyllus trimaculatus* as the outgroup species. The reliability of the tree branching pattern improved by applying 1000 bootstraps pseudo-replicates.

Data Analysis

The consistency and retention indexes were analyzed mathematically by the software PAUP 4.0 (Swoford, 2002). Evolutionary relationships and character alteration among species of Chaetodontidae were analyzed descriptively based on the branching pattern and character changes present on the phylogenetic tree.

RESULTS AND DISCUSSION

Evolutionary Relationships

The evolutionary relationship among species within Chaetodontidae is illustrated in Figure 3. The phylogenetic tree (Figure 3) had a consistency index (CI) of 0.5833 and retency index (RI) of 0.5082.

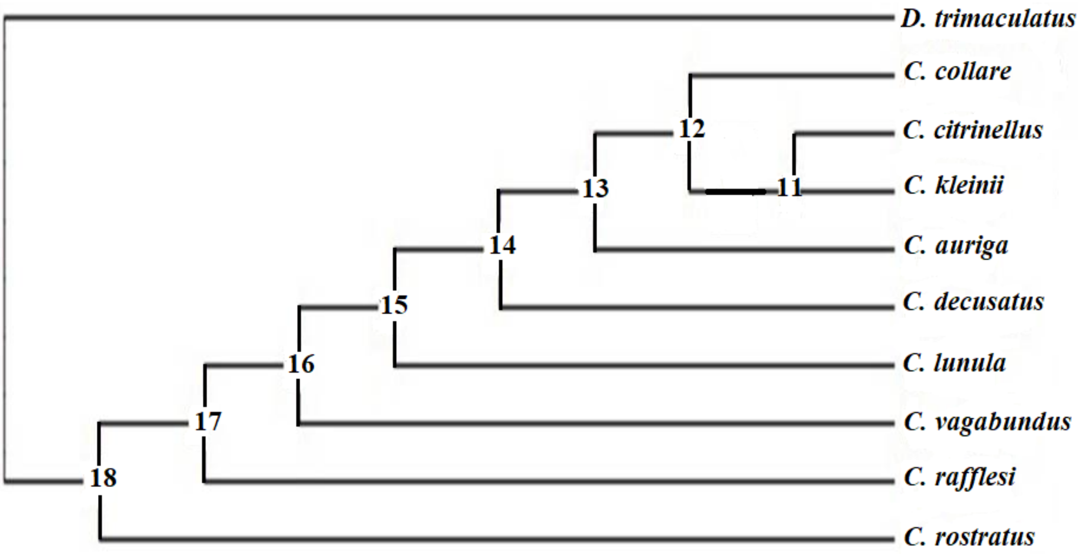

Figure 3. The Phylogenetic tree showing evolutionary relationship of Chaetodontiae

It can be seen (Figure 3) that Chaetodottidae formed a monophyletic clade compared to *D. trimaculatus* as an outgroup. The tree also showed that *Chelmon rostratus* referred to basal species since it has diverged first, while all Chaetodon species are derived species. The result proved that phylogenetic classification and relationship (Figure 3), support the traditional Linnaean classification on the monophyly of Chaetodontidae, which based on morphological similarity (phenetic). That result of our study, similar to the study from Littlewood et al. (2004), proved that a phylogenetic study on *Chaetodon* (Chaetodontidae) supports the morphological classification of that genus. It also proved that careful and precise selection morphological characters might lead to a similar result of traditional Linnaean (phenetic) and phylogenetic classification.

The phylogenetic tree (Figure 3) shows that *Daschyllus trimaculatus* separated from all Chaetodontidae. The position of *D. trimaculatus* on the tree indicates that the choice of *D. trimaculatus* as outgroup species was appropriate. The position also indicates that *D. trimaculatus* owned primitive characters that reliable to be a comparison to the ingroup species members of Chaetodontidae. It means that the obtained tree had reliable branching topology. It was due to *D. maculatus* shared more primitive characters and have closed relationships with all members of Chaetodontidae since they belong to a single order Perciformes. Springer et al. (2003) and Rohland et al. (2007) had noted that the use of closed related taxa as outgroup species in phylogenetic analysis increased the reliability of tree branching patterns and relationships among ingroup specimen.

The arguments are that the proper selection of outgroup specimens and morphological characters support a high value of consistency index (CI) and retention index (RI) of the phylogenetic tree. In this study, we obtained the CI and RI values of the tree were 0.5833 and 0.5082, respectively. Both values indicate that the used characters had low homoplasy. According to Ucu (2016), a high CI value indicates that the tree has a low homoplasy, and the obtained tree has reliable branching topology. A comparison to previous studies from Nabila et al. (2019) on the Acathuridae and Pambudi et al. (2019) on the Labridae indicated that our study got the same result as those both studies. The reason could be due to that the present study, and the studies by Nabila et al. (2019) and Pambudi et al. (2019) used similar morphology characters that were morphometric measurements.

Characters Changes

As explained in the previous section above, Chaetodontidae formed a monophyletic clade compared to the outgroup species from Pomacentridae, *D. trimaculatus*. In this case, *D. trimaculatus* is more primitive species than all the members of Chaetodontidae. The characters of *D. trimaculatus* were plesiomorphic, while those of Chaetodontidae were apomorphic or derived. Characters alteration among nodes is summarized (Figure 4).

It can be seen (Figure 4) that autapomorphic characters separate among nodes and species, respectively. Synapomorphic characters combine them. For example, Chaetodontidae separated from *Daschyllys trimaculatus* by three apomorphic characters (blue box in Figure 4). Those characters were character number 2 (standard length), character 4 (eye diameter) and character number 7 (anal fin base). *Chelmon rostratus* was separated from the remaining chaetodontids by synapomorphy characters. The characters are character 13 (ratio standard length to head length), character 14 (ratio lower jaw length to upper jaw length), character 16 (ratio anal fin length to anal-fin base), character 18 (dorsal rays) and character 19 (pectoral soft rays). It explained by Szucsich & Pass (2008) that several different species might form a clade by their shared derived characters (synapomorphic character). Moreover, Mueller et al. (2004) stated that two or more taxa might be monophyly. It is due to shared advance characters derived from their most common ancestor (synapomorphic characters).

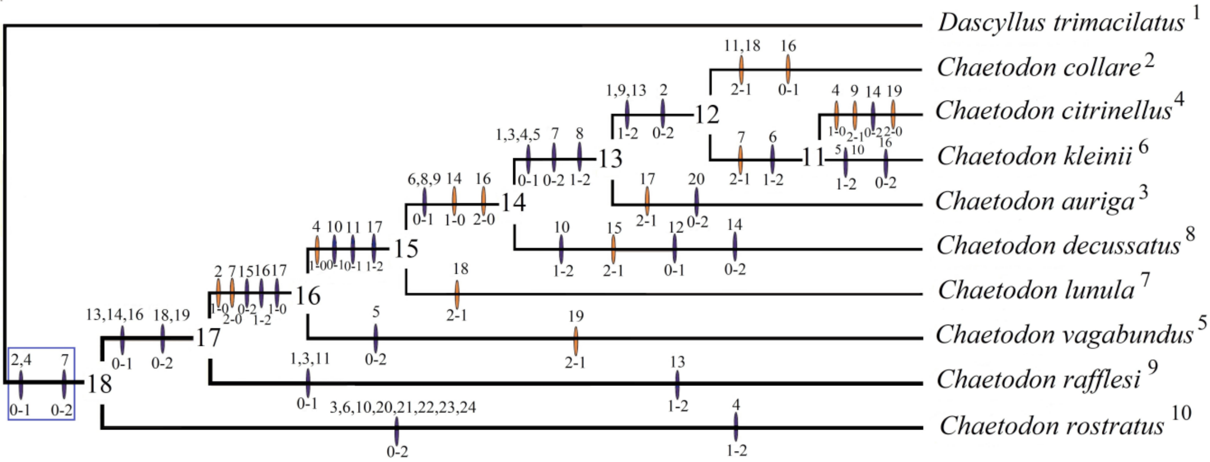

Figure 4. Phylogenetic tree of Chaetodontidae showing characters changes among nodes
(▮ = reversal character; ▮ = derived character)

Taken together, it can be concluded that Chaetodontidae from Ujung Genteng and Taman Manalusus formed a monophyletic clade. The evolutionary relationship of Chaetodontidae supported by high consistency and retency indexes. *Chelmon rostratus* is the basal species, while all *Chaetodon* were the derived species.

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