

Phylogenetic of Marble Goby (*Oxyeleotris marmorata* Blkr.) in South Sumatra Based on Cytochrome C Oxidase Subunit I (COI) Gene

By Dade Jubaedah

Phylogenetic of Marble Goby (*Oxyeleotris marmorata* Blkr.) in South Sumatra Based on Cytochrome C Oxidase Subunit I (COI) Gene

Mochamad Syaifudin^{1,*} , Dade Jubaedah¹, Ferdinand Hukama Taqwa¹, Ria Octaviani¹

¹Universitas Sriwijaya, Faculty of Agriculture, Program Study of Aquaculture, Jl. Palembang-Prabumulih Km 32, Indralaya, Ogan Ilir 30862, South Sumatra, Indonesia.

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Corresponding Author

Tel.: +6282177933568

E-mail: msyaifudin@fp.unsri.ac.id

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Abstract

Marble goby (*Oxyeleotris marmorata*) in Indonesia, spread across Sumatra, Kalimantan and Papua. The purpose of this study was to utilize a sequence of mitochondrial DNA Cytochrome Oxidase Subunit I gene, to analyze the phylogenetic tree and genetic distance between cultured and captured populations. This research was conducted on March-August 2020. The methods used in barcoding species were DNA isolation, amplification using PCR (Polymerase Chain Reaction) and sequencing of the COI mtDNA gene. The domesticated samples (n=3) were collected from Gandus Fish Seed Center (GFSC), while the wild samples (n=3) were captured from the Musi River in Beruge Village, Babat Toman District, both in Musi Banyuasin Regency. The sequenced COI mtDNA gene fragments were obtained from the PCR method. Three samples performed good PCR results, while the other three didn't amplify properly. After the editing process, the COI gene sequencing produced a nucleotide length of 610 bp. Based on the BLAST (Basic Local Alignment Search Tool), domesticated marble goby (OMD2, OMD3) was in the same cluster with marble goby from the Musi River (OMS3). The genetic distance indicated that two specimens of domesticated marble goby were 100% identical, while the wild (OMS3) indicated a genetic distance of 0.0066 to domesticated species.

Introduction

The marble goby (*Oxyeleotris marmoratus*, Bleeker) also known as the sand goby is widely distributed in Southeast Asia, especially in Malaysia, Singapore, Thailand and Vietnam (Cheah, Senoo, Lam, & Ang, 1994; Mohsin & Ambak, 1983; Poh, Ving, & Shaliza, Ibrahim Vikineswary, 2015). It is also one of the indigenous species of freshwater fish in Indonesia. There are 17 species of marble goby, 11 of which are found globally and 8 species are found in Indonesia, which are *Oxyeleotris urophthalmoides*, *O. colasi*, *O. wisselensis*, *O. heterodon*, *O. paucipora*, *O. urophthalmus*, *O. marmorata* and *O. altipinna*. *Oxyeleotris marmorata*, commonly found in the Musi River (Kordi, 2013), is an

introduction species from China since 1927 (Food and Agriculture Organization (FAO) of United Nation, 2005; Wargasasmita, 2012), either for ornamental or consumption. It is an important commercial fish because of its good taste, rich nutrition, large size and potential in aquaculture (Zhao et al., 2017). In Indonesia, the species is spread across the water resources of Sumatra, Kalimantan and Papua (Fishbase, 2021). However, the presence of introduced species could threaten the loss of indigenous freshwater species in Sempor Reservoir, Kebumen (Lestari, Rukayah, & Jamilatun, 2019).

Domestication efforts of marble goby have been carried out at the Mariana Public Aquatic Fisheries Research Institute (BRPPU) and Gandus Fish Seed Center (GFSC), South Sumatra. There are 260 genetic data for

DNA Extraction

DNA was extracted from fin clips of all specimens. Total genomic DNA was extracted using the Realpure Genomic DNA Extraction Kit (Durviz S.L) following the manufacturer's manual. DNA extraction consists of 5 stages including, cell lysis, RNase treatment, DNA precipitation, washing and dissolution of DNA. Four μ l of RNase were added in the lysis step to minimise RNA contamination. Those samples that passed quality control (no observable RNA) based on DNA band visualization in the gel documentation were selected for used in PCR.

DNA Amplification

DNA of the four marble goby were used in PCR with primer pairs of FishF2-5'TCGACTAATCATAAAGATATCGGCAC3' and FishR2-5'ACTTCAGGGTGACCGAAGAATCAGAA3' to amplify 650 bp fragment (Ward et al., 2005). PCR was performed in a final volume of 50 μ l using MyTaq™ Red Mix (Bioline). Each reaction contained 1 μ l of 10 μ M each primer (F2 and R2 primers) (Ward et al., 2005), 20 μ l of nuclease-free water, 25 μ l *myTaq polymerase red mix* and 3 μ l of DNA template. The thermal cycling protocol was as follows: initial denaturation at 95°C for 1 min (1 cycle) followed by 35 cycles of 95°C for 15 sec, annealing at 50°C for 30 sec, extension or elongation at 72°C for 15 sec and a final extension at 72°C for 4 min. Furthermore, PCR products were run in electrophoresis 1% agarose gel at 75V for 35 minutes and visualized to determine the DNA bands using Gel Documentation. The size of PCR product was measured using 1 kb marker. DNA samples that were successfully amplified using PCR were then sequenced in the target area of the COI gene. PCR products were commercially sequenced (Sanger sequencing, GATC Biotech Ltd.) at 1st Base DNA Sequencing Service.

Data Analysis

Six sequences of COI gene (OMS3, OMD2 and OMD3) from forward2 and reverse2 were saved in Fasta format (OMS1, OMS2 and OMD1 were discarded from the analysis due to low quality of PCR product and

sequencing result). The sequences were analyzed their identity using BLAST (Basic Local Alignment Search Tool) in NCBI (National Center for Biotechnology Information). For sequence comparisons, pairwise genetic distances were quantified based on the Kimura 2-parameter (K2P) distance model (Kimura, 1980). Voucher sequences from GenBank, and consensus sequences of each samples generated from this study were used to construct phylogenetic tree. The phylogenetic tree of marble goby was constructed using the Neighbor-Joining (NJ) method on MEGA software X Version (Sudhir Kumar, Stecher, Li, Knyaz, & Tamura, 2018; Stecher, Knyaz, Tamura, & Kumar, 2020). Bootstrapping value was carried out in 1000 replications. In the phylogenetic construction, *Oreochromis niloticus* (KM438538.1) (Syarifudin, Bekaert, et al., 2017) was also added as species outgroup.

Results and Discussion

Molecular Identification

The resultant fragments of sequences were approximately 680 - 698 base pairs (bp). After trimming process with MEGA (Molecular Evolutionary Genetics Analysis) version 7 (S. Kumar, Stecher, & Tamura, 2016), the length of sequences were 610 bp and no gaps within sequences. The BLASTn analysis showed that COI sequences of marble goby in this study accordance with those in the GenBank database. The identity percentage was exhibited in Table 1.

The result of BLASTn analyses in Table 1 denoted that nucleotide sequences of the domesticated fish, OMD2 and OMD3 were identical, showing 99.51% matched to *Oxyeleotris marmorata* from Malaysia (KT022088.1) and USA (AY722177.1), meanwhile the wild marble goby (OMS3) indicated highest similarity (100%) to *Oxyeleotris marmorata* from Cambodia (EF609424.1), West Java Indonesia (KU692726.1) and Vietnam (MH721190.1). Sequence similarity higher than 97% was the criterion for authentication at the species level (Wong & Hanner, 2008) and a similarity lower than that was used for recognition at the genus level. This result denoted that distinguishing species using DNA barcoding is very accurate. The COI is effectively used as species authentication method because intraspecific

Table 1. Identity percentage of nucleotide of marble goby.

No.	Species	Origin	Accession no.	Identity (%)
Samples code: OMD3 and OMD2				
1	<i>Oxyeleotris marmorata</i>	Malaysia	KT022088.1	99,51
2	<i>Oxyeleotris marmorata</i>	USA	AY722177.1	99,51
3	<i>Oxyeleotris marmorata</i>	Indonesia	KU692726.1	99,35
Sample code: OMS3				
1	<i>Oxyeleotris marmorata</i>	Indonesia	KU692726.1	100
2	<i>Oxyeleotris marmorata</i>	Cambodia	EF609424.1	100
3	<i>Oxyeleotris marmorata</i>	Vietnam	MH721190.1	99

4 variation is low, but has high interspecific variation values especially in adjacent taxa (Ward et al., 2005). DNA barcoding validates to recognize species for international trading, either certifying fisheries products consumption or ornamental fish trade (Dahrudin et al., 2016). It has been successfully authorize species larval stages of marble goby in Thailand for sustainable fishery resource management (Panprommin et al., 2020).

Genetic Distance and Phylogenetic

Genetic distance at this study was also used to determine the genetic relationship between domesticated (OMD2 and OMD3) and wild stock (OMS3) marble goby in South Sumatra (Table 2). It indicated that two specimens of domesticated marble goby were 100% identical, while the wild (OMS3) showed a genetic distance of 0.0066 to domesticated species. The domesticated marble goby were also identic to the same species from Malaysia (KT001058.1), while OMS3 was identic to marble of goby from Cambodia (EF609424.1), Thailand (MK448189.1) and W15 Java, Indonesia (KU692718.1 and KU692726.1). Hebert et al. (2003) stated that a genetic distance difference of less or equal to 3% indicates molecularly identical species. The smaller the genetic distance between individuals in a population, the more uniform the population is. Conversely, the greater the genetic distance of an individual in a population, the more diverse the population will be. The largest genetic distance (0.2082) was found between *O. marmorata* and species outgroup *Oreochromis niloticus* from Stirling (KM438538.1), followed to *Palatogobius paradoxus* (0.1557) from America (MF049134.1). It is clearly denoted that within *O. marmorata* barcode variation was low in compare to the sequence variation between species in genus *Oxyeleotris*. Genetic distance indicates the ratio of a genetic distinction between species or populations (Dogan, Dogan, & Nurhan, 2016). Therefore, a smaller genetic distance value creates a more indistinguishable appearance partial sequence of CO1 gene compared between the two species (Basith, Abinawanto, Kusri, & Yasman, 2021).

The phylogenetic tree of marble goby was presented in Figure 2. This study determined the level of evolution and kinship of a species, where the cluster *O. marmorata* was separated from *O. selheimi* (AY722166.1, AY722179.1) and *O. lineolata* (KJ669574.1, AY722165.1) (bootstrap value/bv of 97%). Within species, *O. marmorata* was separated into two sub-clusters (bv of 68%). The first sub-cluster consisted of *O. marmorata* from Thailand (MK448189.1, MK448069.1), Malaysia (KT001058.1), Cambodia (EF609424.1), Indonesia (KU692718.1, KU692726.1), Vietnam (MH721190.1) including samples of *O. marmorata* from the Musi River (OMS2, OMS3) and domesticated fish (OMD2, OMD3). The second sub-cluster consists of *O. marmorata* from Thailand (MK628379.1, KF410694.1) and Malaysia (KT022088.1). Meanwhile, *O. marmorata* from USA (AY722176.1 and AY722177.1 and AY722177.1) made distant subcluster to the same species afore mention.

The second cluster is occupied by species that are still in the same genus of marble goby. There were two species found in the second cluster, i.e. *O. selheimi* from Los Angeles (America) and *O. lineolata* (Los Angeles, USA) and *O. lineolata* (Australia). The third cluster was *P. paradoxus* (America), while, the fourth cluster was consisted of *O. niloticus* (Stirling), as an outgroup species. The *Oxyeleotris* was belong to Butidae family, while *Palatogobius* w3 belong to Gobiidae family. A previous study using sequence data of five molecular markers (two6 mitochondrial and three nuclear) indicated that Butidae being sister group to the Gobiidae clade, 3 the exclusion of Eleotrididae (Agorreta et al., 2013). A bootstrap value greater than 70% indicates that the data is relatively stable (Lemey, Selemi, & Vandamme, 2009). The phylogenetic tree construction resulted in 3 scale bar of 0.02. According to Wardani et al. (2017), a phylogenetic tree with a 0.01 scale bar shows a genetic distance with a change in nucleotides 1 time every 100 bp. So that the phylogenetic constructs obtained indicate a genetic distance with nucleotide changes 2 times in every 100 bp. DNA barcoding technology has been utilized and validated for many aquatic species with detected more variation among

Table 2. Genetic distance between species marble goby based on COI gene.

No.	Species	Genetic Distance																						
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	
1.	<i>O. marmorata</i> _OMD2_(Indonesia)*																							
2.	<i>O. marmorata</i> _OMD3_Gandus_(Indonesia)*	0.000																						
3.	<i>O. marmorata</i> _OMS2_Musi River_(Indonesia)*	0.000	0.000																					
4.	<i>O. marmorata</i> _OMS3_Musi River_(Indonesia)*	0.000	0.000	0.000																				
5.	<i>O. marmorata</i> _Malaysia_KT001058.1	0.002	0.002	0.002	0.002																			
6.	<i>O. marmorata</i> _Cambodia_EF609424.1	0.002	0.002	0.002	0.002	0.000																		
7.	<i>O. marmorata</i> _Indonesia_KU692718.1	0.002	0.002	0.002	0.002	0.000	0.000																	
8.	<i>O. marmorata</i> _Thailand_MK448189.1	0.002	0.002	0.002	0.002	0.000	0.000	0.000																
9.	<i>O. marmorata</i> _Indonesia_KU692726.1	0.002	0.002	0.002	0.002	0.000	0.000	0.000	0.000															
10.	<i>O. marmorata</i> _Malaysia_KT001057.1	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004														
11.	<i>O. marmorata</i> _Thailand_MK448069.1	0.004	0.004	0.004	0.004	0.002	0.002	0.002	0.002	0.002	0.002													
12.	<i>O. marmorata</i> _Vietnam_MH721190.1	0.004	0.004	0.004	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.004												
13.	<i>O. marmorata</i> _Los Angeles_AY722176.1	0.008	0.008	0.008	0.008	0.006	0.006	0.006	0.006	0.006	0.006	0.008	0.008											
14.	<i>O. marmorata</i> _USA_AY722177.1	0.008	0.008	0.008	0.008	0.006	0.006	0.006	0.006	0.006	0.006	0.008	0.008	0.000										
15.	<i>O. marmorata</i> _Malaysia_KT022088.1	0.008	0.008	0.008	0.008	0.006	0.006	0.006	0.006	0.006	0.006	0.008	0.008	0.000	0.000									
16.	<i>O. marmorata</i> _Thailand_MK628379.1	0.008	0.008	0.008	0.008	0.006	0.006	0.006	0.006	0.006	0.006	0.008	0.008	0.000	0.000	0.000								
17.	<i>O. marmorata</i> _Thailand_KF410694.1	0.012	0.012	0.012	0.012	0.010	0.010	0.010	0.010	0.010	0.010	0.012	0.012	0.004	0.004	0.004	0.004							
18.	<i>O. selheimi</i> _Los Angeles_AY722166.1	0.122	0.122	0.122	0.122	0.122	0.122	0.122	0.122	0.122	0.122	0.124	0.124	0.120	0.124	0.124	0.124	0.124	0.128					
19.	<i>O. selheimi</i> _Los Angeles_AY722179.1	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.136	0.136	0.132	0.136	0.136	0.136	0.136	0.140	0.072				
20.	<i>O. lineolata</i> _Los Angeles_AY722165.1	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.134	0.136	0.136	0.132	0.136	0.136	0.136	0.136	0.140	0.072	0.000			
21.	<i>O. lineolata</i> _Australia_KJ669574.1	0.136	0.136	0.136	0.136	0.136	0.136	0.136	0.136	0.136	0.136	0.138	0.138	0.134	0.138	0.138	0.138	0.138	0.142	0.074	0.006	0.006		
22.	<i>Palatogobius paradoxus</i> _USA_MF049134.1	0.167	0.167	0.167	0.167	0.167	0.167	0.167	0.167	0.167	0.167	0.163	0.167	0.165	0.165	0.165	0.165	0.165	0.169	0.181	0.196	0.196	0.196	
23.	<i>Oreochromis niloticus</i> _Stirling	0.217	0.217	0.217	0.217	0.217	0.217	0.217	0.217	0.217	0.217	0.216	0.217	0.216	0.214	0.214	0.214	0.214	0.217	0.192	0.206	0.204	0.183	

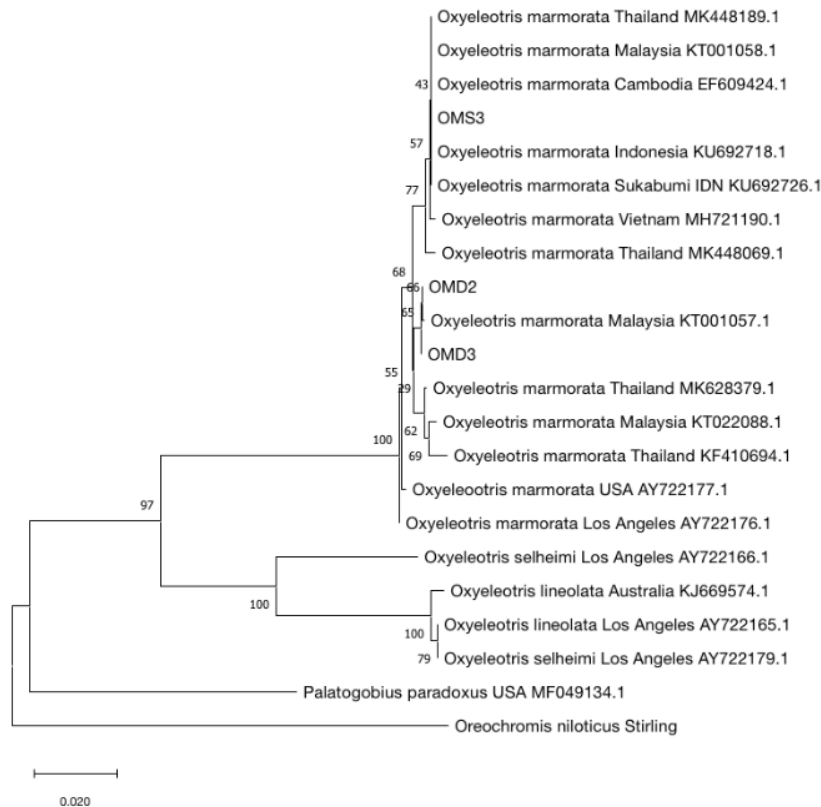


Figure 2. Phylogenetic tree of marble goby from South Sumatra

congeneric species than among conspecific individual (Ward et al., 2005). Therefore it can effectively used to distinguish a complex of morphologically distinct species in the Indo-Pacific (Last, Manjaji, & Yearsley, 2005).

Conclusions

In summary, DNA barcoding have been developed for species authentication for pivotal aquaculture and wild species of marble goby. Thus, the DNA barcodes will support fish products inspection and regulation requirements by establishing correct labeling of domesticated and wild marble goby in the market.

Ethical Statement

All listed co-authors declare that the present study was conducted in an ethical, professional and responsible manner.

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Author Contribution

The conception and design of the study: MSF; the acquisition of data, or the analysis and interpretation: RO, FHT; Funding Acquisition: MSF, writing-original draft: RO, DJ; writing-review and editing: MSF, FHT, DJ.

Conflict of Interest

The author(s) declare that they have no known competing financial or non-financial, professional, or personal conflicts that could have appeared to influence the work reported in this paper.

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