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Research Article

A New Record of *Rochia maxima* (Koch, 1844) Through a Species Clarification of Lola Snail, Bangka Belitung Islands, Indonesia

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Abstract

The use of Lola snails (*Rochia maxima*) in the Bangka Belitung has continued to increase. However, research focused on Lola snails originating from the Bangka Belitung has not been thoroughly conducted. In previous study, the Lola snail sample found in the Bangka Belitung was *Trochus niloticus* (current name: *Rochia nilotica*). This study aimed to identify Lola snail species using the DNA barcoding as a way of clarifying Lola snail species that originated in the Bangka Belitung. Lola snail sampling was carried out at three locations which were Nasik Strait, Ketawai, and Rebo Waters. This study was conducted through five stages, including Lola snail tissue sampling, DNA extraction, amplification by PCR, sequencing, and data analysis. The results showed that the molecular identification of the Cytochrome Oxidase Subunit 1 (COI) gene in Lola snail samples were identified as *Rochia maxima* species (Koch, 1844). The results of the phylogenetic tree analysis showed that Lola snails found in the Bangka Belitung were close to *Tectus maximus* (or *Rochia maxima*) species. *R. maxima* has a lighter shell than *R. nilotica*, a clear conical shape, and a circle on the body that does not widen at the edges. Unlike zoologists who said that *R. maxima* is the primitive form of *R. nilotica*, the present study found that *they have the same morphology and are considered similar but genetically different*. The clarification of Lola snail species can be used to determine the conservation status and catching quota of Lola snails from the Bangka Belitung.

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1. Introduction

Lola (*Rochia* spp.) is a gastropod-class marine snail whose habitat in coral reefs (Seinor *et al*., 2020; Wahyudi *et al*., 2023). It has been found in Indo-Pacific waters, from Madagascar to Micronesia, Japan, Western Australia, New Caledonia, the Philippines, China, and Indonesia (Arifin *et al.,* 1998, Pakoa *et al.,* 2008; Jiang *et al*., 2019). In Indonesia, Lola snails have been found from eastern Indonesia in the Maluku Islands to western Indonesia in the Bangka Belitung Islands (Leimena *et al*., 2007: Tuhumury, 2013; Cappenberg and Wulandari, 2019; Akbar *et al*., 2019). In the Bangka Belitung Islands, they have been reportedly found in the Nasik Strait (Belitung Regency), Kelapan Island (South Bangka Regency), Perlang, and Ketawai Island (Central Bangka Regency) (Cappenberg and Wulandari, 2019; Akbar *et al*., 2019). The continued harvesting of Lola snails in the Bangka Belitung Islands could potentially exceed the national catch quota. The high economic value of Lola snails results in excessive exploitation as a source of community income (Purcell *et al*., 2019). The meat of Lola snails can be consumed as a source of protein and their shells can be used for various types of jewellery (Gillet *et al*., 2020; Purcell *et al*., 2020). The Lola are easy to collect, and shells can be stored in anticipation of sale or optimised sales as a result of their shallow and predictable habitat preference (Purcell and Ceccarelli, 2020). It is vulnerable to a high level of exploitation due to these characteristics. This assertion is further supported by evidence of archeological showing the long-term resilience of the population to occasional harvesting (Kinch *et al*., 2019; Ulm *et al*., 2019; Doyle *et al*., 2022).

Lola snail populations have declined due to unsustainable harvesting practices. The government, therefore, issued Regulation No. 7 of 1999 concerning "Preservation of Plant and Animal Species", which states that the Lola is considered a protected wild animal. The regulation were amended in KEPMEN LH No. 20 of 2018 concerning protected plants and animals, which were declassified as a protected animal. Moreover, according to the Decree of the Director General of Conservation of Natural Resources and Ecosystems Number SK.1/KSDAE/KKH/KSA.2/1/2021 regarding Quotas for Taking Natural Plants and Catching Wild Animals for the 2021 Period, the quota for catching Lola snails in Indonesia is set at 206.2 tons. However, in 2022, the quota for catching Lola snails increased to 336 tons/year. This increase was caused by the additional area of Lola snail-catching in several regions of Indonesia. Consequently, the quota for catching Lola snails in South Sumatra (Bangka Belitung) increased to 100 tons/year.

In relation to previous research, the presence of Lola snails in the Bangka Belitung Islands has been found one species and identified as a species of *Trochus niloticus* (Accepted name: *Rochia nilotica*) (Akbar *et al*., 2019; Cappenberg and Wulandari, 2019). One of the first efforts to conserve organisms is to provide taxonomic and genetic information. Taxonomic and genetic information on Lola snails is very much needed to determine the right species for conservation methods and catching quotas, especially in the Bangka Belitung Islands.

The purpose of this study is to identify the Lola snail species present in the Bangka Belitung Islands using the DNA Barcoding method to clarify their identity.

2. Materials and Methods

2.1 Materials

This study was conducted from April to November 2021. The sampling of Lola snails was carried out at three locations in the Bangka Belitung Islands, including Nasik Strait (Belitung Regency: Yellow box on Figure 1), Ketawai Island (Central Bangka Regency: Red box on Figure 1), and Rebo Waters (Bangka Regency: Green box on Figure 1). The locations were chosen based on the distribution of Lola snails in the Bangka Belitung Islands, according to a literature study. The sampling locations are shown in Figure 1. Before sampling, sterile plastic bottles were thoroughly disinfected with 96% alcohol. DNA extraction were performed using micropipettes from Eppendorf (Germany), vortex, and mini centrifuge. Polymerase Chain Reaction (PCR) was used T100 PCR Thermal Cycler BioRad (USA). The sequence analysis was conducted in PT Genetika Science Indonesia.

2.2.1 Ethical approval

This study does not require approval because it does not use experimental animals.

2.2 Methods

The sampling of the Lola snail was done by cutting a bit of the Lola snail tissue or meat (±1 cm) with surgical scissors. The tissue samples obtained were put in a sample tube and treated with a 96% alcohol preservative (Marquina *et al*., 2021).

2.2.1 DNA isolation and extraction

Before isolation and extraction, Lola snail samples were washed with Low TE (Tris-EDTA buf-

fer) to remove any alcohol solution as a preservative. Furthermore, Lola snail samples were isolated and extracted using a silica column through four stages of lysis, binding, washing, and elution, following the DNeasy Blood and Tissue Kit Qiagen commercial kit procedure.

The positive results of PCR amplification were sent to the sequencing service company for sequencing. The DNA sequencing process was done using an Abi 1377 sequencer machine by sequencing facility 1st Base in Malaysia. The analysis was performed using MEGA X (Molecular Evolutionary Genetics Analysis)

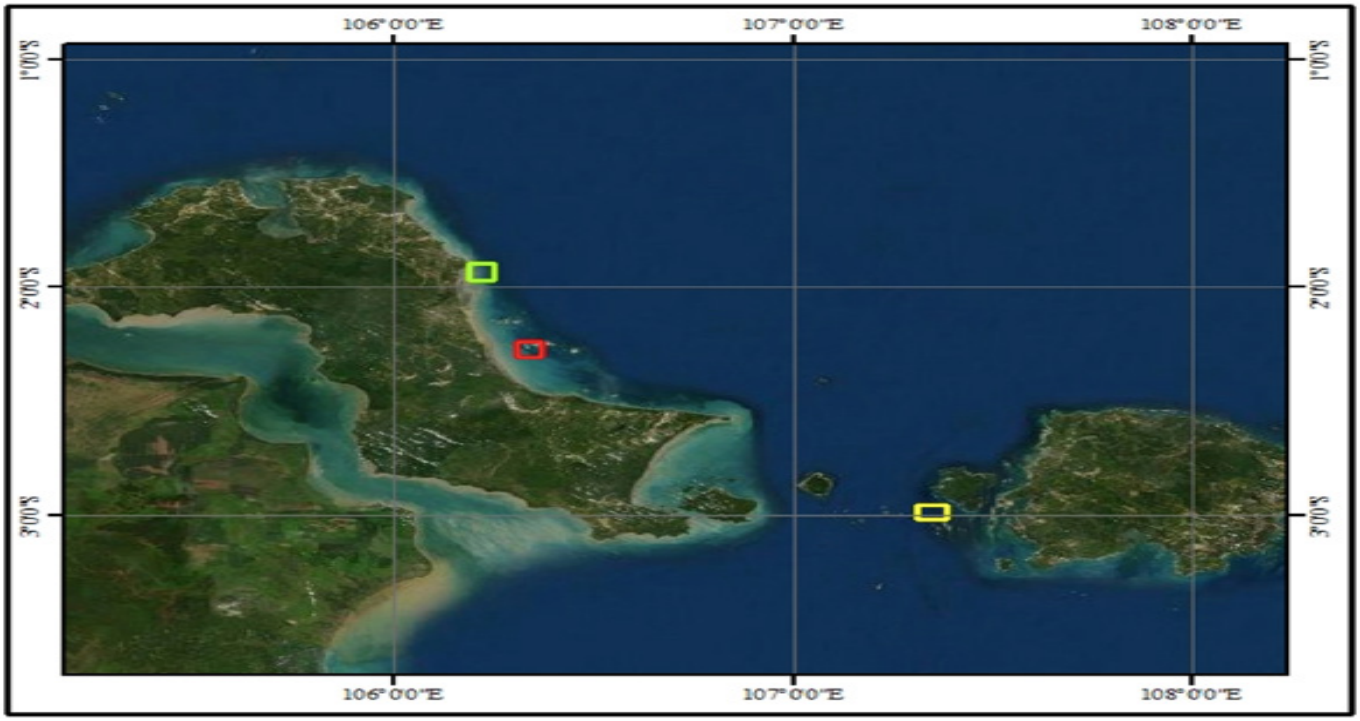

Figure 1. Location of sampling in the Bangka Belitung Islands, Indonesia (Selat Nasik (Belitung Regency): Yellow box, Ketawai Island (Central Bangka Regency): Red box, and Rebo Waters (Bangka Regency): Green box)

2.2.2 Amplification by PCR

The target gene segments were amplified using a PCR (Polymerase Chain Reaction) machine. The primers used in this study were universal primers for mollusks; LCO1490:5'-GGTCAACAAATCATAAAGATATTGG-3' and HCO2198:5'-TAAACTTCAGGGTGACCAAAAAATCA-3' (Folmer *et al*., 1994). The mixture of materials used was GoTaq®Green Master Mix (25-50 µl), LCO1490 primer (0.5-5 µl), HCO2198 primer (0.5-5 µl), DNA template (1-5 µl), and Nuclease-Free Water (25-50 µl). Amplification was carried out using a PCR machine with pre-denaturation conditions of 94°C for five minutes, followed by 35 cycles consisting of denaturation at 94°C for 30 seconds, annealing at 43°C for 90 seconds, extension at 72°C for one minute, and final extension at 72°C for five minutes (Barco *et al*., 2015). The results of PCR amplification were then tested for quality using agarose gel 1.5% with GelRed dye and the results were visualized using a Gel Doc machine.

2.2.3 DNA Fragment Sequencing and Phylogenetic Analysis

software for nucleotide sequence reading and alignment to obtain more accurate results. The nucleotide alignment data acquired were then matched with the data available on GenBank at NCBI (National Center for Biotechnology Information) using BLAST (Basic Local Alignment Search Tool). The phylogenetic construction analysis in this study used MEGA X software with the neighbour-joining tree method of the 3-parameter Tamura evolution model with distributed gamma intervals and 1000x replication bootstraps (Tamura *et al*., 2013).

3. Results and Discussion

3.1 Result

The analysis based on the monthly data of Aqua-Modis satellite in April 2021 found that the sea surface temperature analysis of the Bangka Belitung Seas shows a range between 30.5 and 31.3°C (Figure 2). Temperature tolerance for Lola snails of 0,1-11 m deep ranges from 28-34°C. Temperature is one of the factors that support Lola's life; specifically, the optimal temperature for consumption oxygen is at 31°C

(Helsinga, 1981).

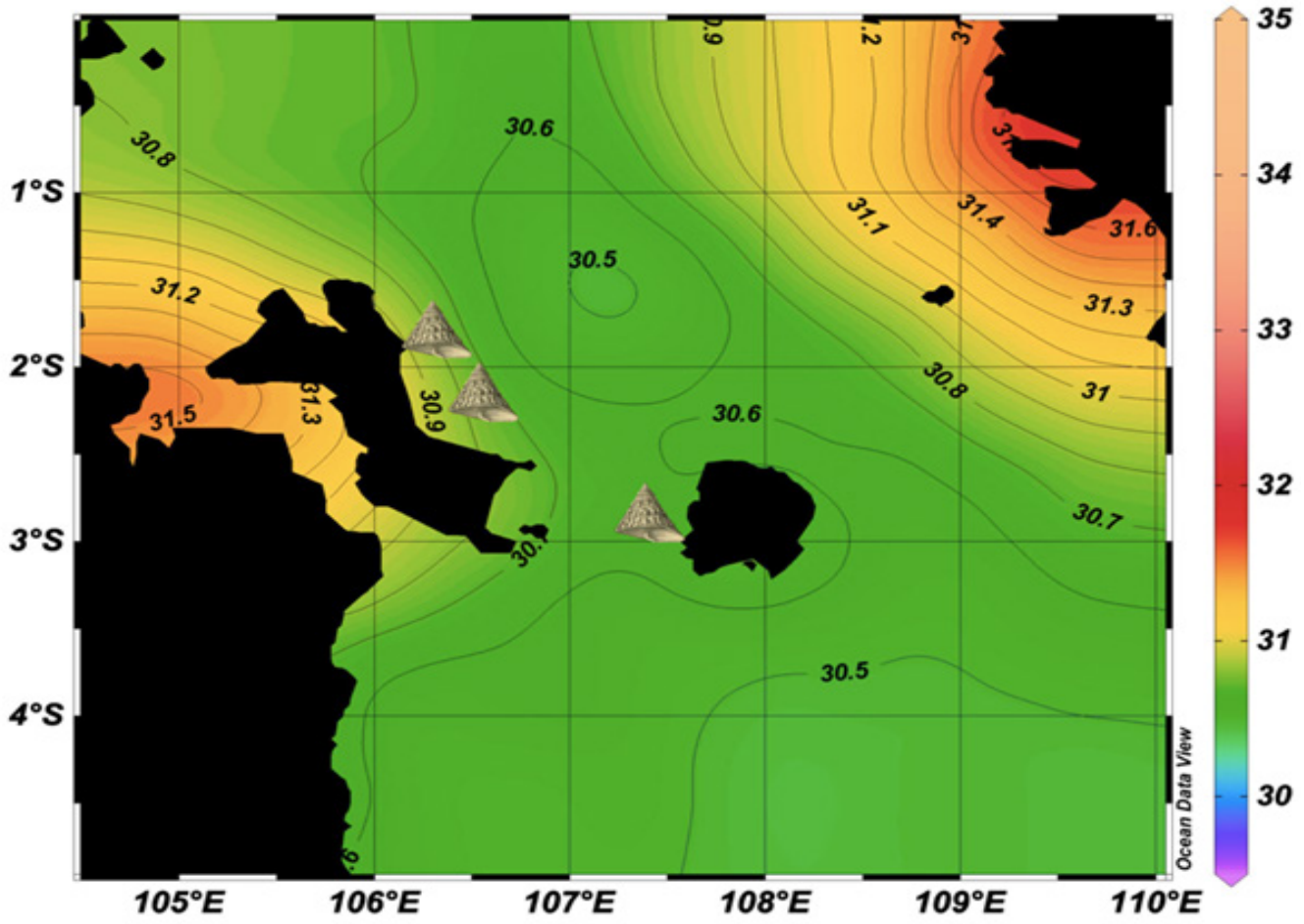

Figure 2. The Monthly Aqua-Modis data on Sea Surface Temperature of Bangka Belitung in April 2021.

Table 1. Genetic distance between Rochia maxima from Bangka Belitung, Trochus niloticus and Tectus maximus.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	MSPUBB_A_*Rochia maxima*																
2	MSPUBB_B_*Rochia maxima*	0.003															
3	MSPUBB_C_*Rochia maxima*	0.003	0														
4	MSPUBB_D_*Rochia maxima*	0.003	0	0													
5	MSPUBB_E_*Rochia maxima*	0.003	0	0	0												
6	MSPUBB_F_*Rochia maxima*	0.003	0	0	0	0											
7	MSPUBB_I_*Rochia maxima*	0.003	0	0	0	0	0										
8	MSPUBB_J_*Rochia maxima*	0.003	0	0	0	0	0	0									
9	MSPUBB_K_*Rochia maxima*	0.003	0	0	0	0	0	0	0								
10	MSPUBB_L_*Rochia maxima*	0.003	0	0	0	0	0	0	0	0							
11	MSPUBB_M_*Rochia maxima*	0.003	0	0	0	0	0	0	0	0	0						
12	MSPUBB_N_*Rochia maxima*	0.003	0	0	0	0	0	0	0	0	0	0					
13	MSPUBB_O_*Rochia maxima*	0.003	0	0	0	0	0	0	0	0	0	0	0				
14	MSPUBB_P_*Rochia maxima*	0.003	0	0	0	0	0	0	0	0	0	0	0	0			
15	AY923938.1_*Trochus niloticus*	0.386	0.379	0.379	0.379	0.379	0.379	0.379	0.379	0.379	0.379	0.379	0.379	0.379	0.379		
16	EU530150.1_*Tectus maximus*	0.066	0.062	0.062	0.062	0.062	0.062	0.062	0.062	0.062	0.062	0.062	0.062	0.062	0.062	0.333	

3.1.1 Molecular Identification

Table 2. Species of Lola snails from Bangka Belitung Islands.

Sample Id	Sample	Species	Query Cover %	Per Ident %	Accession Id
MSPUBB_A	Ketawai Island	*Rochia maxima*	96	96.69	EU530150.1
MSPUBB_B	Ketawai Island	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_C	Ketawai Island	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_D	Rebo Waters	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_E	Rebo Waters	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_F	Rebo Waters	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_I	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_J	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_K	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_L	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_M	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_N	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_O	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1
MSPUBB_P	Nasik Strait	*Rochia maxima*	96	96.85	EU530150.1

Molecular identification using mtDNA COI gene is an alternative way to identify biota to avoid and minimize accidental morphological misidentification, considering that morphological identification is also influenced by abiotic factors such as environmental changes that affect body shape, skin color, and other external characteristics. The results of COI barcode identification obtained sequences for the Lola snail samples, with base sequence lengths ranging from 600 to 700 bp (Table 3). All samples were successfully amplified, and most of the barcodes yielded clear matches to the sequences in the National Center for Biotechnology Information Basic Local Alignment Search Tool database with >96% similarity.

3.1.2 Phylogenetic analysis

The phylogenetic tree analysis using the neighbor joiningneighbour-joining tree method showed that the Lola snails found in the Bangka Belitung Islands are closely related to *Tectus maximus* (Accepted name: *Rochia maxima*) type (Figure 4). It showed that the BLAST analysis results were consistent with the characteristics of the phylogenetic tree's branches. The higher the similarity between the nucleotide sequences, the higher the similarity value, which results in proximity on the branches of the phylogenetic tree (Pearson, 2013; Bajusz *et al*., 2021). In addition, the phylogenetic tree construction of the Lola snail

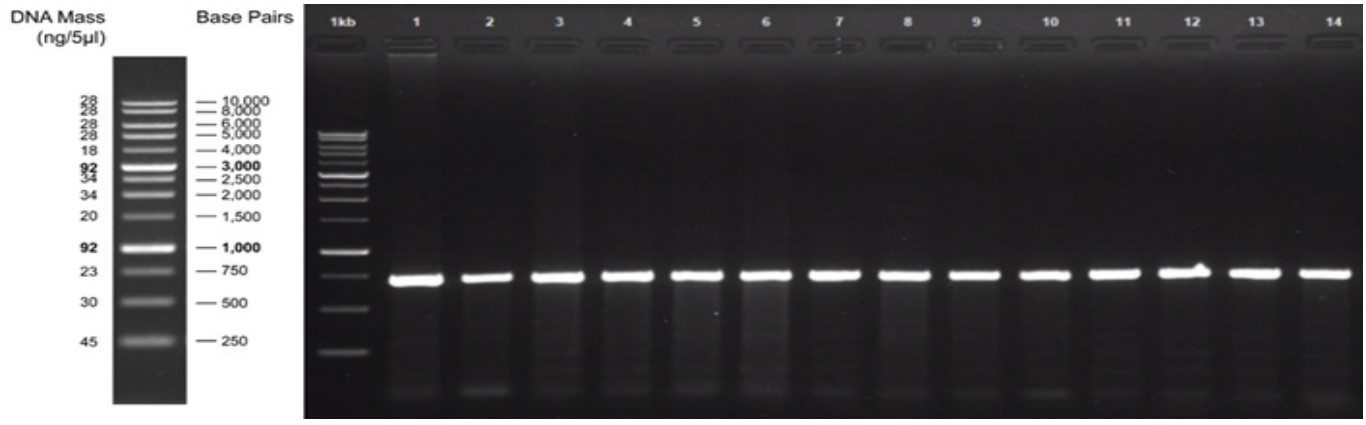

Figure 3. DNA visualization of Lola snail samples with a length of ~700 bp using 1.5% agarose.

(*R. maxima*) also showed proximity to Trochus niloticus (Accepted name: *R. nilotica*). When identified morphologically, the scientific name of Lola snails in the Bangka Belitung Islands is frequently referred to as the species name.

3.1.3.1 Rochia nilotica (Linnaeus, 1716)

The shell of the R. nilotica is large, cumber some, conical, and appears to be sub perforated-sub-perforated. It is covered in a brown or yellowish cuticle, usually missing from the upper whorls. The color under the cuticle is white, longitudinally striped with red, violet, or reddish brown, and maculate or radiately strigate with a lighter shade of the same color. The tower is stringently cone-shaped, peak intense, typically dissolved, whorls at 8–10, the upper ones tuberculate at the stitches, and spirally beaded. The accompanying level on their external surfaces is smooth, isolated by straight stitches; the body-whorl is

Table 3. Sequence of Rochia maxima from Bangka Belitung Islands.

Sequence Result of Rochia maxima (630 bp)						
1	TCCGGATTAG	TAGGAACTGC	TCTTAGACTT	TTAATTCGGG	CCGAGTTAGG	TCAACCCGGT
61	GCGTTACTGG	GGGATGATCA	GCTCTATAAT	GTAATTGTTA	CTGCGCATGC	ATTTGTAATA
121	ATTTTCTTTC	TGGTAATGCC	CTTAATAATT	GGAGGATTTG	GTAACTGGTT	AATTCCTTTAA
182	TGTTGGGAGC	GCCAGACATA	GCATTTCCCC	GGCTTAATAA	TATAAGATTT	TGATTGTTGC
242	CTCCCTCATT	GACATTGCTA	CTGAGGTCGG	CTGCGGTAGA	AAGTGGTGTT	GGTACTGGTT
302	GAACAGTTTA	TCCTCCTCTG	GCTGGAAATT	TGGCACATGC	TGGTGCGTCA	GTTGATCTAG
362	CTATTTTCTC	TCTTCATTTA	GCAGGGGTAT	CCTCTATTTT	GGGTGCTGTTA	ACTTTATTACT
424	ACGGTAATTA	ATATACGTTG	ACATGGAATG	AAATTCGAAC	GATTACCTCT	ATTTGTTTGG
483	TCTGTAAAGA	TTACAGCAAT	TTTGTTGTTG	TTATCCTTGC	CTGTATTAGC	TGGAGCCATTA
543	CTATGCTTCT	GACGGATCGA	AATTTTAACA	CATCTTTTTT	TGATCCAGCC	GGAGGTGGGG
605	ACCCTATTCT	GTATCAGCAT	TTGTTT			

3.1.3 Morphological Analysis

It should be noted that there are morphological differences between R. nilotica and R. maxima (Figure 6) according to George W. Tryon, Jr. and Henry A. Pilsbry in their book *Manual of Conchology; Structural and Systematic Vol. XI. Trochidae (1889):*

Table 4. Sequence of Tectus maximus (EU530150.1).

Sequence of Tectus maximus (657 bp)						
1	ACACTTTATTTG	GTTTTAGGTATT	TGATCCGGATTA	GTAGGAACTGCT	CTTAGACTTT	TAATTCGGGCTG
71	AGTTGGGTCAAC	CTGGCGCCTTAC	TGGGGGATGAT	CAGCTCTATAA	TGTAATTGTTA	CTGCGCATG-CATT
141	TGTAATAATTTT	CTTTCTAGTAAT	GCCACTAATAA	TTGGAGGATTTG	GTAACTGGTTA	ATTCCTTTAATG
211	TTGGGAGCGCCA	GACATAGCATTT	CCCCGGCTTAA	TAATATAAGATT	TTGATTGTTGC	CTCCCTCATTGA
281	CATTGCTACTAA	GGTCGGCTGCGG	TAGAAAGTGGT	GTTGGTACTGG	TTGAACAGTTT	ATCCTCCTCT-GGC
351	TGGAAATTTGGC	ACATGCTGGTGC	GTCAGTGGATCT	AGCTATTTTTT	CTCTTCATTTA	GCGGGGGTATCC
421	TCTATTTTAGGT	GCTGTTAACTTT	ATTACTACGGTA	ATTAATATACG	TTGACATGGAA	TGAAATTCGAAC
491	GATTACCTTTAT	TTGTTTGGTCTG	TAAAGATTACA	GCAATTTTGTTG	TTATTATCTTT	GCCTGTGTTAGC
561	TGGAGCCATTAC	TATACTTCTAAC	GGATCGAAATTT	TAACACATCTT	TTTTTGATC-CAG	CCGGAGGTGGG
631	GATCCTATTT	TGTATCAGCA	TTTGTTT			

extended, expanded, and compacted at the insensitive outskirts, pretty much raised underneath, and indented at the hub. A spiral pearly callus penetrates deeply and covers the umbilical tract; a transverse, very oblique aperture; an oblique columella with a strong spiral fold above and a denticle below that extends deeply into the axis.

forms spire whorls that are strictly conical, clearly tuberculate, or plicate, and has a planular body whorl that is not dilated at the periphery; a flat base with a concentrated groove; and a less oblique columella than the type. It exactly resembles an immature specimen of the latter species in its conic shape, flat base, and sculptured spire. However, at the same time, it keeps

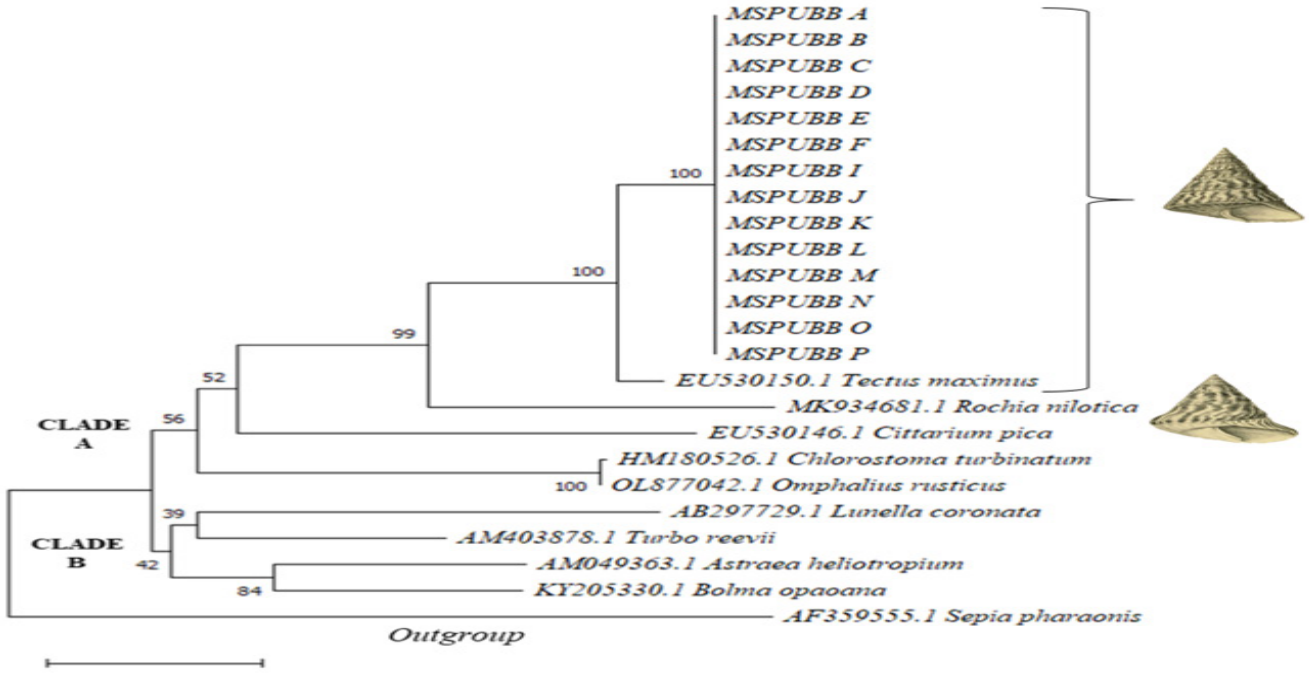

Figure 4. Phylogenetic tree of Lola snail found in Bangka Belitung Islands.

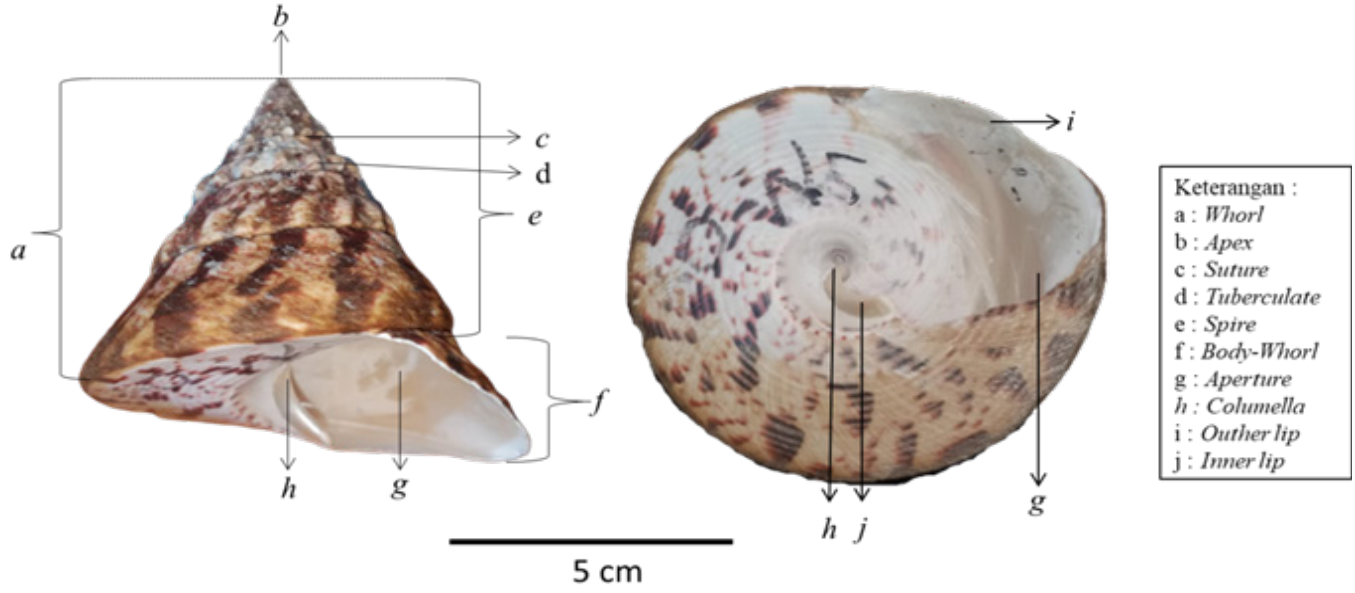

Figure 5. Lola snail samples were found in Bangka Belitung Islands.

3.1.3.2 Rochia maxima (Koch, 1844)

The shell is lighter than that of *R. nilotica*; it

these characteristics as adults. Lola snails from Bangka Belitung Islands and their morphology can be seen in Figure 5 and morphological differences between *R.*

Nilotica (left) and *R. maxima* (right) in Figure 6.

3.2.1 Molecular Identification

Some of the *Rochia maxima* (previous name: *Tectus maximus*) sequences were not deposited in GenBank, therefore 99-100% match is not always possible. According to Madduppa, *et al.* (2020) the similarity limit is accepted at >96% for species differentiation. The results of the molecular identification of the Cytochrome Oxidase Subunit 1 gene in Lola snail samples using the BLAST program integrated on the GenBank website were identified as *Rochia maxima* species (Koch, 1844). The following are the results of the visualization of the Lola snail agarose gel sample (Figure 3 and Table 2). The sequencing results of the Lola snail samples (Table 3) had a high similarity in query cover values asto *Rochia maxima* species (Table 4). According to Madduppa *et al.* (2020), the query cover value and the level of similarity indicate that the samples, therefore, belonged to that species. So, based on the molecular results, the samples belong to *Rochia maxima* species.

present study used the identification results from other researchers as a reference when determining the Lola snail species in the Bangka Belitung Islands.

3.2.2 Phylogenetic Analysis

The phylogenetic tree reconstruction using DNA sequences was based on the species *R. maxima* and various other species, such as *R. nilotica*, Cittarium pica, *Chlorostoma turbinatum*, *Omphalius rusticus*, *Lunella coronata*, *Turbo reevii*, *Astraea heliotropium*, *Bolma opaoana*, and *Sepia pharaonis*. *Sepia pharaonis* species was employed as an outgroup. According to the findings, all samples from the Bangka Belitung Islands formed a clade with *Rochia maxima* species.

The phylogenetic tree identifies two main clades, namely clades A and B. Clade A includes the Tegulidae family, and clade B includes the Turbinidae family from the Genbank Sequence. Species belonging to clade A are *Rochia maxima*, *Rochia nilotica*, *Cittarium pica*, *Chlorostoma turbinatum*, and

Figure 6. Morphological differences *R. nilotica* (left) and *R. maxima* (right) (Source: Tryon and Pilsbry, 1889).

The morphological and molecular identification had the same outcome, namely *Rochia maxima*. In the Decree of the Director General of Conservation of Natural Resources and Ecosystems No. SK.2/KSDAE/KKH/KSA.2/1/2022 regarding Quotas for Taking Natural Plants and Catching Wild Animals for the 2022 Period, the Lola snail species is classified under the name of *Rochia nilotica*. However, that name differs from the identification made by researchers. According to Saleky and Merly (2021), morphological identification has shortcomings because the morphology of gastropods is similar at the genus level, and they have a modified shell type, which can result in errors. The

Omphalius rusticus. While species belonging to clade B are *Lunella coronata*, *Turbo reevii*, *Astraea heliotropium*, and *Bolma opaoana*. The phylogenetic tree shows a separation between the ingroup (Gastropods) and the outgroup (Cephalopods). *Rochia maxima* form a monophyletic clade within clade A with a high bootstrap value (100%). According to the phylogenetic tree analysis, the sample codes MSPUBB_A to MSPUBB_P had a high bootstrap value (100%) for *Rochia maxima* (Koch, 1844) with a similarity value of 96.48–96.89%. In addition, the closest kinship of the identified samples is Trochus niloticus (*Rochia niloti-*

ca), with a high bootstrap value (99%) and a similarity of 87.31%. Meanwhile, the bootstrap value of the Lola snail sequence with samples in clade B was 41%. This indicates that clade B is distantly related compared to clade A.

Smaller genetic distances indicate fewer base-pair differences and higher morphological similarities between species. *Rochia maxima* and *Tectus maximus* had the smallest genetic distance, indicating a close familial relationship, whereas *Rochia maxima* and *Trochus niloticus* had the highest genetic distances, indicating significant genetic differences between the two species (Table 1). The identical matter was reported by Williams *et al.* (2008), who declared that *R. maxima* and *R. nilotica* have the same morphology and are considered similar but genetically distinct. This study evidence that molecular identification, particularly through the use of DNA barcodes for the mt-COI gene, can be used as a method to identify species of Lola species that exhibit nearly identical morphology across species (Simbolon and Aji, 2021).

Various environmental factors can have an impact on genetic distance variations. Genetic drift and natural selection are two factors that can affect these variations (Freeland, 2012). Furthermore, variances in geography and environmental factors can lead to alterations in morphology and phylogeny (Twindiko *et al*., 2013). High genetic similarity is characterized by high morphological similarity, leading to common morphological misidentification of species (Simbolon *et al*., 2021). Molecular identification of species using DNA barcoding reveals species with high morpholog ical similarity (cryptic species), allowing for more accurate species identification. However, the effectiveness of molecular identification heavily relies on the availability of sequence data stored in the GenBank (Fahmi *et al*., 2016). Therefore, it is crucial to conduct both morphological and molecular identification simultaneously to ensure a more precise and reliable identification process.

3.2.3 Morphological analysis

R. maxima has a lighter shell than *R. nilotica*, a clear conical shape, and a circle on the body that does not widen at the edges. Zoologists stated that *R. maxima* is a primitive form of *R. nilotica* (Tryon and Pilsbry, 1889). However, a study by Williams *et al.* (2008) stated that *R. maxima* and *R. nilotica* have the same morphology and are considered similar but genetically different. It is hoped that the clarification of the Lola snail species in this study can be used to specifically determine the conservation status and catching quo ta for Lola snails from the Bangka Belitung Islands.

A brief communication with Mr. Bunjamin Dharma (2022) as a Board of Advisors in the Indonesian Malacological Society showed that the key-difference between *R. nilotica* and *R. maxima* is that the former's shell of *R. nilotica* is thick and heavy, with a balanced height and diameter ratio, a concave last whorl, a curved periphery, and a slightly convex base. The shell of *R. maxima* is thin and relatively light, taller than wide, its whorl is flat, the periphery is angular, and the bottom is flat. The initial oversight was made by Tryon and Pilsbry (1889), who classified *R. maxima* as a variation of *R. nilotica*, however, a recent study stated that both of the species are distinct.

3.2.4. Management of the Lola snail

The Tectus (recent name: *Rochia*) is a large reef snail that is commonly caught in tropical waters, where it is high value and durable quality make it an attractive source of income for island communities (Pakao *et al*., 2009). After rapid geographical extension around the world in the 1930s and 1940s, the rise in global demand for *Rochia* shells quickly raised serious concerns about the conservation of this resource in the global market (Dumas *et al*., 2017). Historical evidence of *Rochia's* vulnerability to overfishing and the application of increasingly stringent fisheries regulations have led to severe stock collapse, sometimes to the brink of local extinction (Purcell *et al*., 2004).

The government has laid out steps regarding the conservation of Lola snails, which is planned in the National Action Plan (*Rencana Aksi Nasional or RAN*). The RAN for Lola Conservation was inspired by several issues described in the RAN for Lola Conservation Period I: 2016–2020, such as the lack of information regarding the status of the Lola snail population in nature, indications of a decline in the Lola snail population, and habitat damage. The purpose of the National Action Plan is based on Government Regulation No. 60 of 2007 concerning the Conservation of Fish Resources. In this regulation, species conservation is defined as an act of utilizing, preserving, and protecting fish resources to ensure the availability, existence, and sustainability of various types of fish for present and future generations. The RAN Lola Conservation emphasizes the importance of Rochia nilotica species, which is a well-known type of Lola snail in Indonesia. In the RAN Lola Conservation, no management or conservation plans are lined out relating

to the Rochia maxima species. The clarification of the Lola snail species in this study serves as a reference in determining the conservation status of Lola snailsnails and the catch quota from the Bangka Belitung Islands so that the type of information submitted is according to the data generated.

4. Conclusion

Lola snails originating from the Bangka Belitung Islands (Nasik Strait, Rebo Waters, and Ketawai Island) were identified as *Rochia maxima*, not to be *Rochia nilotica* species, based on molecular and morphological identification. Even though they both have the same morphological form, they are genetically different. The clarification of the Lola snail species in this study serves as a reference in determining the conservation status of Lola snails and the catch quota from the Bangka Belitung Islands so that the type of information submitted is according to the data generated. Moreover, it is hoped that the existence of the Lola snail in nature can continue to be sustainable. In addition, further research is needed regarding the sustainable of Lola snails since its current exploitation is massive.

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Authors' Contributions

All authors have contributed to the final manuscript. The contribution of each author as follow, SA, OS, FR and DW; collected the data, drafted the manuscript, and designed the figures. DP, DA and UYA; devised the main conceptual ideas and critical revision of the article. All authors discussed the results and contributed to the final manuscript.

Conflict of Interest

The authors declare that they have no competing interests.

Declaration of Artificial Intelligence (AI)

The author(s) affirm that no artificial intelligence (AI) tools, services, or technologies were employed in the creation, editing, or refinement of this manuscript. All content presented is the result of the independent intellectual efforts of the author(s), ensuring originality and integrity.

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