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DNA barcoding of cowries (Gastropoda: Cypraeidae) from edge of the Wallace Line, Indonesia

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Abstract

The intertidal zones of Lombok Island, located at the edge of the Wallace Line, represent a biogeographically important transition region that supports high levels of marine biodiversity. This study applied DNA barcoding based on the mitochondrial cytochrome c oxidase subunit I (COI) gene to identify and analyze the phylogenetic relationships of cowries (Gastropoda: Cypraeidae) collected from three coastal localities (Kayangan, Sambelia, and Sekotong). A total of seven cowrie species were confirmed, namely *Bistolida hirundo* (Linnaeus, 1758), *Erronea erronea* (Linnaeus, 1758), *Mauritia arabica* (Linnaeus, 1758), *Monetaria annulus* (Linnaeus, 1758), *M. moneta* (Linnaeus, 1758), *Naria boivinii* (Kiener, 1844), and *N. erosa* (Linnaeus, 1758). In addition, one species from the family Ovulidae, *Calpurnus verrucosus* (Linnaeus, 1758), was included as the outgroup. BLAST analyses revealed high similarity values (>98%) with reference sequences in GenBank, validating the reliability of species-level identification. Genetic distance analysis using the Kimura 2-parameter (K2P) model showed clear interspecific divergence (0.114–0.232), supporting the presence of a “barcode gap” among examined taxa. Phylogenetic reconstruction using the Maximum Likelihood method showed bootstrap support generally exceeding 90%, indicating low interpopulation genetic differentiation and highlighting effective larval dispersal across oceanic regions. Nucleotide composition analysis further confirmed a consistent AT-rich bias (61–63%) typical of gastropod mitochondrial genomes, with subtle interspecific variation potentially useful for molecular diagnostics. This research provides the first DNA barcoding and phylogenetic assessment of cowries from Lombok, enriching the genetic database of Cypraeidae and offering essential baseline data for conservation, biogeographic, and evolutionary studies in the Indo-Pacific marine hotspot.

Keywords: Cowries, DNA Barcoding, Intertidal, Lombok, Wallace Line.

Introduction

The intertidal zone represents a transitional area between marine and terrestrial environments, characterized by high levels of biodiversity driven by variations in environmental factors (Tomanek & Helmuth, 2002). Most intertidal organisms consist of macrozoobenthos, invertebrates inhabiting substrates ranging from hard surfaces to mud, which play an important role as ecological bioindicators (Sahidin et al., 2018; Lim et al., 2020). Previous studies have documented variations in intertidal biota across different ecosystems in both Indonesia and other regions worldwide (Hayward et al., 1999; Tunardi et al., 2018; Candri et al., 2020; Latuconsina

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& Buano, 2021). The presence of intertidal biota in a given habitat can be assessed through both direct and indirect observations (Keeping & Pelletier, 2014). Species identification is traditionally conducted based on morphological characteristics, including shell shape, width, length, coloration, apex, whorl, body whorl, siphonal canal, spire, suture, aperture, and columella (FAO, 1998). However, this method has limitations, particularly at the species level, due to the loss of diagnostic shell traits or the use of dead specimens (Albert et al., 2022). Since the 1990s, molecular approaches have advanced rapidly through the application of PCR and DNA analysis, providing valuable tools to overcome the constraints of morphology and to reconstruct the evolutionary history of complex organisms. Among these, DNA barcoding has become a widely used method, employing the mitochondrial COI gene to accurately discriminate species, including those with incomplete morphological features (Hebert et al., 2003; Waugh, 2007; Jefri et al., 2015). Molecular studies on gastropods have been conducted in various regions (Meyer, 2003; Sun et al., 2016; Ran et al., 2020; Fukunaga et al., 2021; Ma et al., 2023), yet similar research in Indonesia remains limited. Existing studies have primarily focused on Turbinidae, Strombidae, Neritidae, and Bivalvia (Saleky et al., 2016; Viruly et al., 2019; Juniar et al., 2021; Ndobe et al., 2023). To date, no DNA barcoding and phylogenetic analyses have been specifically conducted on cowries, despite the fact that the family Cypraeidae comprises 87 species recorded in Indonesian waters (Soermorumekso, 2014) with relatively comprehensive bioecological studies available (Laimeheriwa, 2017). Field observations indicate a high diversity of cowries in the waters of Lombok; however, molecular-based investigations remain limited. Geographically, Lombok Island is situated at the eastern terminus of the Wallace Line, a major biogeographic boundary that functions as a transitional zone between Indo-Pacific marine regions and acts as a genetic conduit facilitating the transfer of gene flow from the Pacific Ocean to the Indian Ocean. This distinctive geographic setting positions Lombok as a natural laboratory for investigating evolutionary processes, phylogeographic patterns, and adaptive mechanisms in marine organisms. Consequently, DNA barcoding and phylogenetic analyses of cowries from Lombok are expected to substantially enrich existing genetic databases and provide critical support for marine biodiversity conservation, particularly with respect to the genetic resources of molluscs within the family Cypraeidae.

Material and Methods

Time and Study Areas

The study was conducted during March–April 2024 in the intertidal zone at three locations in Lombok Island: (1) Kayangan District, North Lombok; (2) Sambelia District, East Lombok; and (3) Sekotong District, West Lombok (Figure 1).

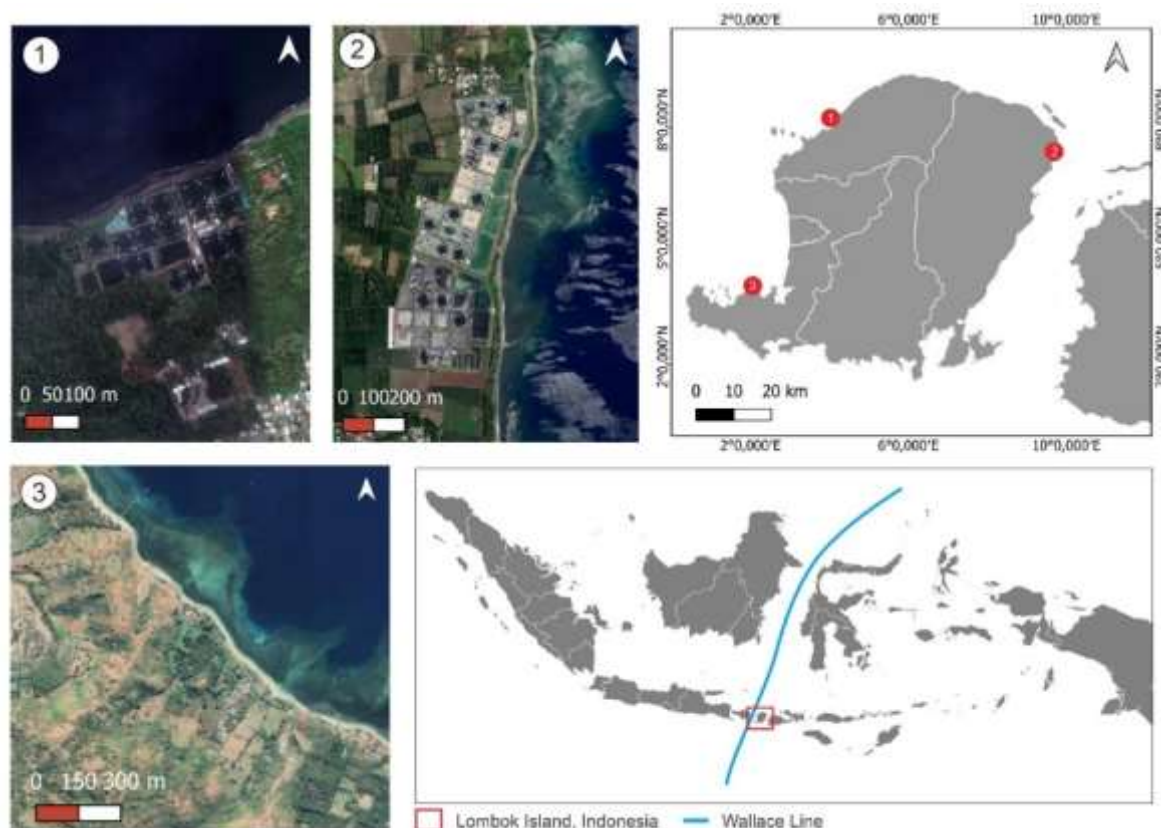


Figure 1. Sampling sites for cowries research are located on Lombok Island, Indonesia.

Cowrie Sampling and Preparation

Cowrie gastropod specimens were randomly collected from various species across the three study sites. Phenotypic identification was conducted based on diagnostic features following (FAO, 1998); including morphometric traits such as shell shape, coloration, and sculpture, with additional reference to online taxonomic databases: SeaLifeBase (<https://www.sealifebase.ca/>), Molluscabase (<https://www.molluscabase.org/>), and the World Register of Marine Species (WoRMS; <https://www.marinespecies.org/>). Sampling was carried out during the lowest tidal phase within the designated intertidal zones of the three locations. Each specimen was photographed for documentation, after which approximately 5–10 g of foot tissue was excised and preserved in absolute ethanol 96% (Meyer, 2003; Pu et al., 2019; Ma et al., 2023).

Molecular Character Analysis

Molecular analyses were performed at the Immunology Laboratory, Faculty of Mathematics and Natural Sciences, University of Mataram. Prior to DNA extraction, tissue samples were rinsed with distilled water to remove residual ethanol, followed by grinding in liquid nitrogen (N₂) until homogenized (Bressan et al., 2014). DNA extraction was conducted using a modified cetyltrimethylammonium bromide (CTAB) protocol (Winnepennickx et al., 1993). The extraction procedure involved the addition of CTAB buffer to the samples, followed by sonication, centrifugation, and repeated purification with chloroform:isoamyl alcohol (24:1) until a clear supernatant was obtained. DNA was then precipitated with cold isopropanol to form visible strands, centrifuged at 4°C, and the resulting pellet washed with 70% ethanol. After discarding the ethanol and allowing the pellet to dry overnight, the DNA was resuspended in 60 µL of nuclease-free water. The mitochondrial cytochrome oxidase subunit I (COI) gene was targeted for amplification by polymerase chain reaction (PCR) using the primers LCO1490 and HCO2198 (Folmer et al., 1994). DNA concentration and purity were determined with a NanoPhotometer®, and PCR reactions were carried out using AB1 master mix. The thermal cycling conditions were as follows: initial denaturation at 94°C for 3 min; denaturation at 95°C for 30 s (30 cycles); annealing at 52°C for 1 min; extension at 72°C for 1 min; and a final extension at 72°C for 10 min.

Electrophoresis

PCR products were visualized through agarose gel electrophoresis. A 2% agarose gel was prepared with ethidium bromide (10 µL) as the staining agent. A 5 µL aliquot of each PCR product was loaded into the wells, and electrophoresis was carried out at 90 V for 35 min. The resulting DNA bands were observed under a UV transilluminator. Successful amplification was indicated by a single clear band of approximately 600–700 base pairs (bp), confirming the product's suitability for sequencing (Wittmeier & Hummel, 2022; Suyatno et al., 2025).

DNA Sequencing

PCR products showing clear electrophoresis bands were subjected to DNA sequencing, conducted by 1st Base through PT. Genetika Science Indonesia, using the Sanger sequencing method with chain-terminator chemistry (BigDye® Terminator v3.1) on an automated capillary genetic analyzer from Applied Biosystems (Sanger et al., 1977).

Bioinformatic Analysis

The resulting DNA sequences were processed and aligned using MEGA XII (Molecular Evolutionary Genetics Analysis). Sequences were edited and aligned with ClustalW in order to assess nucleotide variability (Kumar et al., 2024). High-quality sequences were compared against available databases using the Basic Local Alignment Search Tool (BLAST) at the National Center for Biotechnology Information (NCBI, USA; www.ncbi.nlm.nih.gov) to determine similarity with existing cowrie sequences. Phylogenetic relationships were inferred using the Maximum Likelihood (ML) method implemented in PhyML 3.0. The best-fit nucleotide substitution model (TN93+G+I) was selected based on model selection analysis. Equilibrium base frequencies were optimized using maximum likelihood, with the proportion of invariable sites estimated at 0.597. Rate heterogeneity among sites was modeled using a discrete gamma distribution with four rate categories (Γ), and the gamma shape parameter was estimated at 1.404 (Lefort et al., 2017). Node support was assessed by 1000 bootstrap replications to evaluate the robustness of phylogenetic clades (Efron et al., 1996). Genetic distances among species were calculated using the K2P model, which differentiates between transition and transversion substitutions with greater accuracy. Additionally, nucleotide composition was analyzed to determine the proportions of A, T, G, and C bases. This information is important, as nucleotide composition patterns can reflect species-specific molecular characteristics and provide additional support for phylogenetic interpretation (Prasetya & Saefuddin, 2011; Nishimaki & Sato, 2019; Kaur, 2021).

Results and Discussion

The BLAST analysis of mitochondrial COI sequences reliably confirmed the taxonomic identity of cowrie specimens collected from the intertidal zones of Kayangan, Sambelia, and Sekotong, Lombok Island. Query coverage values (91–99%) and high sequence similarity (>98%), combined with consistently low E-values (0.0), indicate strong concordance with reference sequences in GenBank and support the robustness of species-level identification (Harvey et al., 2015; Leray et al., 2019) (Table 1). A total of eight species were identified, comprising *Mauritia arabica* (Linnaeus, 1758), *Naria erosa* (Linnaeus, 1758), *Monetaria annulus* (Linnaeus, 1758), *M. moneta* (Linnaeus, 1758), *Naria boivinii* (Kiener, 1844), *Erronea erronea* (Linnaeus, 1758), *Bistolida hirundo* (Linnaeus, 1758),

and *Calpurnus verrucosus* (Linnaeus, 1758) (outgroup), occurred across multiple sampling sites, suggesting broad ecological tolerance within Lombok's intertidal habitats (Figure 2). This distribution pattern is consistent with previous records from Lombok and surrounding regions (Meyer, 2003; Mujiono, 2020; Candri et al., 2024; Jefri et al., 2025). In contrast, the detection of *B. hirundo* and *C. verrucosus* exclusively at Sekotong highlights localized variation in species composition among coastal sectors. While the occurrence of *C. verrucosus* has been reported previously (Meyer, 2003) the present record provides the most recent confirmation of *B. hirundo* from Lombok, supported by both morphological characters and DNA barcoding. All identified species are currently categorized as Not Evaluated (NE) under the IUCN Red List, reflecting a substantial lack of conservation assessment for cowries in the Indo-Pacific region despite their recognized ecological roles and commercial importance in the ornamental shell trade (Peters et al., 2013). Overall, the integration of DNA barcoding and BLAST analysis provided high-resolution and reliable species identification of cowries from Lombok's intertidal zone. These results establish a verified taxonomic baseline for the region and offer essential reference data to support future phylogenetic, biogeographic, and conservation-oriented studies.



Figure 2. Sample of cowries collected from the intertidal waters of Lombok Island, Indonesia.

Table 1. List of the BLAST result and IUCN status of cowries obtained from the intertidal waters of Lombok Island, Indonesia.

Sample code	Species	Sites	Query cover (%)	E. Value	Per. Ident	Accession number	IUCN Status
MBS_CYP_01	<i>Mauritia arabica</i>	Kayangan	97%	0.0	99.85%	NC072227	NE
MBS_CYP_05	<i>Naria erosa</i>	Kayangan	91%	0.0	99.84%	DQ207058	NE
MBS_CYP_06	<i>Monetaria annulus</i>	Kayangan	95%	0.0	99.84%	MZ560054	NE
MBS_CYP_11	<i>Naria boivinii</i>	Kayangan	91%	0.0	100.00%	AY161667	NE
SBL_CYP_01	<i>Naria erosa</i>	Sambelia	98%	0.0	99.39%	NC072231	NE
SBL_CYP_04	<i>Monetaria annulus</i>	Sambelia	99%	0.0	98.33%	LC469295	NE
SBL_CYP_07	<i>Monetaria moneta</i>	Sambelia	96%	0.0	99.55%	NC072229	NE
SBL_CYP_10	<i>Erronea erronea</i>	Sambelia	97%	0.0	99.69%	NC066082	NE
SBL_CYP_11	<i>Erronea erronea</i>	Sambelia	97%	0.0	99.08%	NC066082	NE
SKT_CYP_01	<i>Mauritia arabica</i>	Sekotong	91%	0.0	99.84%	AY161698	NE
SKT_CYP_06	<i>Monetaria moneta</i>	Sekotong	98%	0.0	99.55%	NC072229	NE
SKT_CYP_16	<i>Calpurnus verrucosus</i>	Sekotong	99%	0.0	99.54%	PQ450686	NE
SKT_CYP_19	<i>Bistolida hirundo</i>	Sekotong	91%	0.0	98.86%	AY161773	NE

NE; Not Evaluated

Genetic Distance of Cowries from Lombok Island Intertidal Waters

Pairwise genetic distances among cowrie species from the intertidal waters of Lombok Island, together with reference sequences retrieved from the National Center for Biotechnology Information (NCBI), are summarized in Table 2. Genetic distances were estimated using the Kimura 2-parameter (K2P) model based on mitochondrial COI gene sequences, a widely accepted marker for DNA barcoding and phylogenetic inference (Austerlitz et al., 2009). The inclusion of conspecific sequences from different Indo-Pacific regions (Table 3) enables a broader assessment of genetic divergence at both intra and interspecific levels.

Table 2. Intra and inter species sequence divergences of cowries obtained from the intertidal waters of Lombok Island and NCBI.

No.	Species	Intra species	Inter species						
			1	2	3	4	5	6	7
1	<i>Bistolida hirundo</i>	0,014							
2	<i>Calpurnus verrucosus</i>	n/c	0,205						
3	<i>Erronea erronea</i>	0,026	0,114	0,224					
4	<i>Mauritia arabica</i>	0,053	0,158	0,230	0,184				
5	<i>Monetaria annulus</i>	0,008	0,184	0,236	0,188	0,219			
6	<i>Monetaria moneta</i>	0,007	0,232	0,301	0,223	0,216	0,162		
7	<i>Naria boivinii</i>	0,001	0,207	0,236	0,201	0,227	0,156	0,181	
8	<i>Naria erosa</i>	0,098	0,182	0,252	0,166	0,219	0,182	0,186	0,159

Intraspecific genetic divergence was consistently low across all examined taxa, ranging from 0.001 in *Naria boivinii* to 0.098 in *Naria erosa*. The relatively high intraspecific divergence in *Naria erosa* (0.098) likely reflects deep phylogeographic structure or cryptic mitochondrial lineages across its wide Indo-Pacific range rather than misidentification alone (Hebert et al., 2003; Meyer & Paulay, 2005; Sun et al., 2012; Karnaver et al., 2023). Particularly low values were recorded for *Monetaria moneta* (0.007), *M. annulus* (0.008), and *N. boivinii* (0.001), indicating strong genetic cohesion within species despite the incorporation of sequences originating from geographically distant localities (Table 3).

Table 3. Cowries sequence data downloaded from the National Center for Biotechnology Information (NCBI).

No.	Species	Sites	Accession number	References
1	<i>Monetaria moneta</i>	China	MN389074	(Ran et al., 2020)
2	<i>Monetaria moneta</i>	India	KU324888	(Karnaver et al., 2023)
3	<i>Monetaria moneta</i>	French Polynesia	KT290127	(Ardura et al., 2015)
4	<i>Monetaria annulus</i>	China	MN389075	(Ran et al., 2020)
5	<i>Monetaria annulus</i>	Australia	KT754015	(Couto et al., 2016)
6	<i>Naria boivinii</i>	Philippines	DQ207051	(Meyer & Paulay, 2005)
7	<i>Naria boivinii</i>	Japan	DQ207050	(Meyer & Paulay, 2005)
8	<i>Naria erosa</i>	India	KU324891	(Karnaver et al., 2023)
9	<i>Naria erosa</i>	China	DQ324053	(Ma et al., 2023)
10	<i>Mauritia arabica</i>	Hongkong	PP652042	(McIlroy et al., 2024)
11	<i>Mauritia arabica</i>	Tanzania	DQ207102	(Meyer & Paulay, 2005)
12	<i>Mauritia arabica</i>	Thailand	DQ207101	(Meyer & Paulay, 2005)
13	<i>Bistolida hirundo</i>	Papua New Guinea	DQ207213	(Meyer & Paulay, 2005)
14	<i>Bistolida hirundo</i>	Thailand	DQ207212	(Meyer & Paulay, 2005)
15	<i>Errosaria erronea</i>	China	JF693397	(Sun et al., 2012)
16	<i>Errosaria erronea</i>	Singapore	DQ207342	(Meyer & Paulay, 2005)
17	<i>Errosaria erronea</i>	Australia	DQ207341	(Meyer & Paulay, 2005)

These results support the robustness of COI barcoding for reliable species level identification in cowries and are consistent with previous molecular studies on marine gastropods (Sun et al., 2016; Ge et al., 2021). In contrast, interspecific genetic distances were substantially higher, ranging from 0.114 to 0.232. The lowest interspecific divergence was observed between *Erronea erronea* and *Bistolida hirundo* (0.114), suggesting a relatively close evolutionary relationship between these taxa. Conversely, the highest genetic distance (0.232) was detected between *B. hirundo* and *Monetaria moneta*, reflecting pronounced evolutionary separation consistent with their assignment to distinct genera. Most interspecific comparisons exceeded 0.15, indicating clear genetic discontinuities among species (Ge et al., 2021). Comparisons among genera, including *Bistolida*, *Monetaria*, *Mauritia*, *Erronea*, and *Naria*, consistently yielded high divergence values (0.114–0.232), providing strong evidence for a distinct “barcode gap” separating intra and interspecific variation. This pattern reinforces the effectiveness of COI sequences in discriminating closely related cowrie species and confirms the presence of well-defined genetic boundaries within the family Cypraeidae (Hebert et al., 2003; Dominici et al., 2020). Overall, the genetic distance matrix derived from Lombok specimens and NCBI reference sequences demonstrates both fine scale genetic uniformity within species and substantial divergence among genera. These findings highlight the utility of COI based genetic distance analysis for resolving taxonomic relationships and elucidating evolutionary patterns of cowries inhabiting Lombok’s intertidal zone. Moreover, the observed levels of divergence contribute valuable insights into biodiversity structure within the Indo-Pacific marine hotspot, emphasizing the biogeographic significance of Lombok Island at the edge of the Wallace Line (Zhao et al., 2025).

Phylogenetic Relationships of Cowries from Lombok Island

The Maximum Likelihood (ML) phylogenetic tree provides a robust framework for elucidating evolutionary relationships among cowrie species collected from the intertidal waters of Lombok Island in comparison with conspecific sequences from other Indo-Pacific regions (Figure 3). The tree was rooted using *Calpurnus verrucosus* as an outgroup, enabling clear interpretation of interspecific and intergeneric relationships within the family Cypraeidae (Simone, 2004; Dominici et al., 2020). Overall, Lombok cowrie specimens clustered within their respective species level clades, with node support values ranging from moderate to high, indicating generally reliable phylogenetic signal consistent with morphological identification. *Monetaria moneta* specimens from Lombok grouped with sequences from India, China, and French Polynesia, forming a cohesive clade supported by moderate bootstrap values, which reflects a broad Indo-Pacific distribution accompanied by relatively low intraspecific divergence. Similarly, *Monetaria annulus* from Lombok clustered with conspecific sequences from China and Australia, supported by high bootstrap values, indicating strong genetic cohesion across geographically distant populations (Heyden et al., 2014; Bowen et al., 2016; Rieder et al., 2025; Song et al., 2025). Within the genus *Naria*, Lombok specimens of *N. erosa* and *N. boivinii* each formed distinct monophyletic clades together with sequences from India, China, Japan, and the Philippines. These clades were supported by moderate to high bootstrap values, suggesting the persistence of well-defined mitochondrial lineages across the Indo-Pacific, while also indicating some degree of phylogeographic structuring within *Naria* species (Simone, 2004; May et al., 2023). A comparable pattern was observed in *Mauritia arabica*, where Lombok specimens clustered with conspecifics from Hong Kong, Thailand, and Tanzania, supported by moderate to high node confidence and reflecting genetic continuity across a wide geographic range (Patiluna & Demayo, 2015). The clustering of *Bistolida hirundo* and *Erronea erronea* further supports this overall pattern, with Lombok specimens grouping with conspecific sequences from Southeast Asia, Papua New Guinea, and Australia. Although bootstrap support varied among nodes, the absence of deep mitochondrial subdivision suggests limited intraspecific divergence despite broad geographic separation (Mujiono, 2015; Latupeirissa et al., 2020; Tan & Low, 2022). Taken together, the phylogenetic reconstruction indicates that cowries from Lombok are genetically consistent with their Indo-Pacific conspecifics, supporting accurate taxonomic placement and suggesting generally low interpopulation genetic differentiation. This pattern is consistent with effective dispersal and connectivity, likely facilitated by the planktonic larval stage of cowries, which enables long-distance gene flow across ocean basins (Passamonti, 2015; Tay et al., 2023). Lombok’s position near the Wallace Line may further enhance connectivity by functioning as a transitional biogeographic corridor where Indo-Pacific marine lineages converge (Lourie & Vincent, 2004; Aryanti & Gradstein, 2007), while continuous larval transport may mitigate genetic drift and maintain genetic cohesion across populations (Eldon et al., 2016).

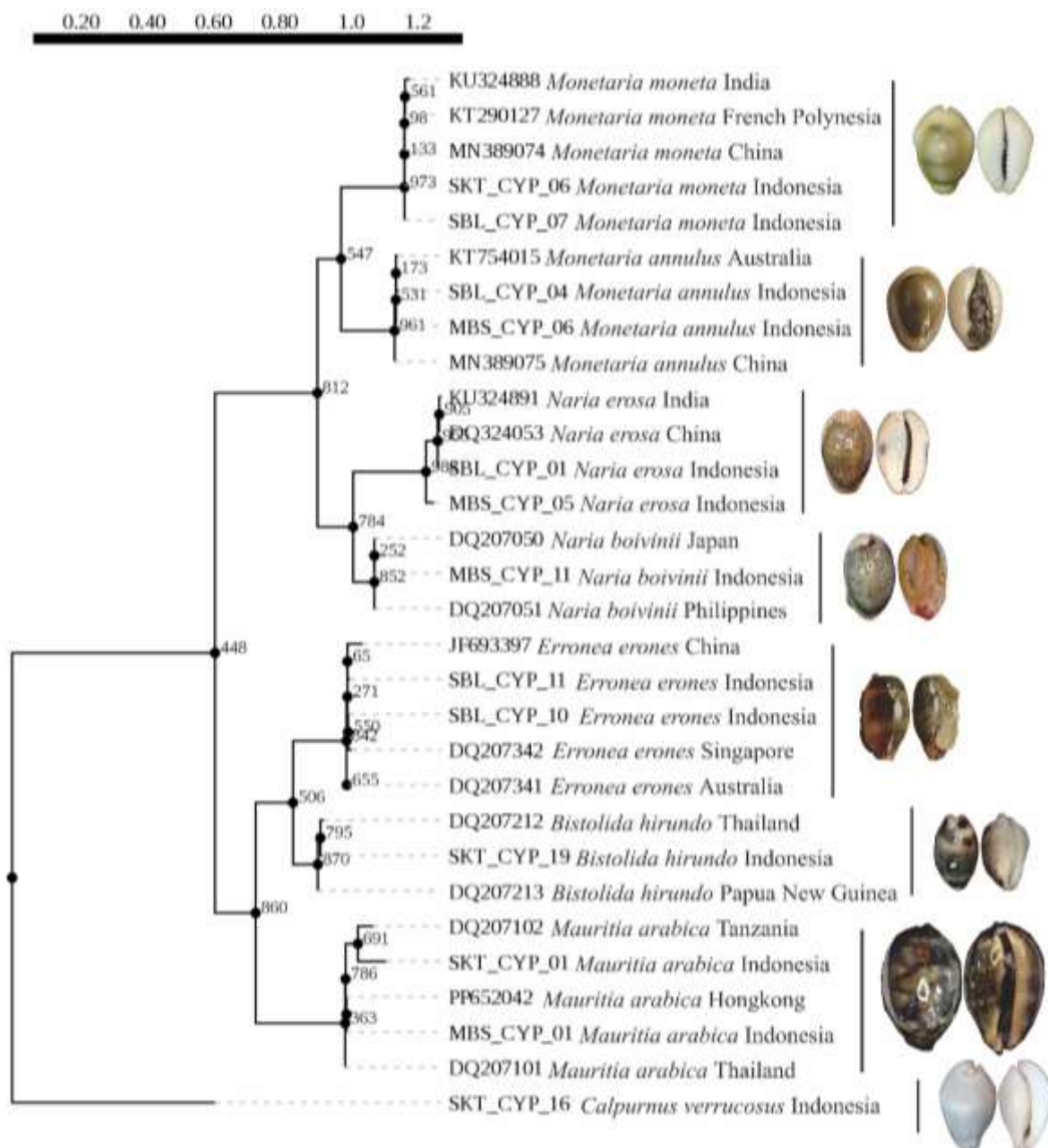


Figure 3. Maximum likelihood phylogenetic tree based on 30 COI sequences of cowries distributed in the intertidal waters of the Lombok Island, Indonesia, reconstructed using PhyML 3.0 (1000 bootstrap).

Nucleotide Composition of Cowrie Sequences

The nucleotide composition of cowrie sequences from intertidal habitats of Lombok is summarized in Table 4. Across all species and sampling sites, sequence length was conserved at 585 bp, with slight variations in base composition among taxa. Overall, thymine (T) exhibited the highest frequency (ranging from 30.94% in *N. erosa* from Kayangan to 38.46% in *B. hirundo* from Sekotong), followed by adenine (A: 22.22–25.81%) and cytosine (C: 17.44–25.13%). Guanine (G) consistently displayed the lowest frequency (17.95–22.22%). The observed AT-rich bias (approximately 61–63% across samples) is typical of invertebrate mitochondrial genomes and reflects evolutionary constraints on codon usage and replication efficiency. Notably, *B. hirundo* exhibited the highest T content (38.46%), which may suggest lineage-specific nucleotide substitution patterns, while *N. boivini* from Kayangan demonstrated the highest C content (24.10%), indicating compositional heterogeneity even among closely related taxa (Li et al., 2025). The consistency of nucleotide bias across species underscores the conserved nature of mitochondrial coding regions, yet the subtle interspecific differences may provide informative molecular markers for species-level discrimination within cowries (Matumba et al., 2020). Such variation in nucleotide composition has been widely recognized as influencing phylogenetic signal and codon preference in marine

gastropods (Gu et al., 2025), further supporting the utility of COI sequences in molecular taxonomy and biodiversity assessments of Lombok's intertidal ecosystems.

Table 4. Nucleotide composition of cowrie sequences from intertidal of Lombok, Indonesia

Sample code	Species	Sites	T(U)	C	A	G	Total
SKT CYP 19	<i>Bistolida hirundo</i>	Sekotong	38.46	17.44	23.76	20.34	585
SKT CYP 06	<i>Monetaria moneta</i>	Sekotong	31.97	25.13	23.25	19.66	585
SKT CYP 01	<i>Mauritia arabica</i>	Sekotong	36.07	19.49	22.22	22.22	585
SBL CYP 11	<i>Erronea erronea</i>	Sambelia	37.44	18.29	24.44	19.83	585
SBL CYP 10	<i>Erronea erronea</i>	Sambelia	37.61	17.78	24.44	20.17	585
SBL CYP 07	<i>Monetaria moneta</i>	Sambelia	31.97	25.13	23.25	19.66	585
SBL CYP 04	<i>Monetaria annulus</i>	Sambelia	32.82	23.42	25.47	18.29	585
SBL CYP 01	<i>Naria erosa</i>	Sambelia	31.62	24.27	24.96	19.15	585
MBS CYP 11	<i>Naria boivinii</i>	Kayangan	31.79	24.10	25.13	18.97	585
MBS CYP 06	<i>Monetaria annulus</i>	Kayangan	32.82	23.42	25.81	17.95	585
MBS CYP 05	<i>Naria erosa</i>	Kayangan	30.94	24.79	25.47	18.80	585
MBS CYP 01	<i>Mauritia arabica</i>	Kayangan	35.73	19.66	23.76	20.85	585

Conclusion

This study represents the first DNA barcoding and phylogenetic assessment of cowries (Cypraeidae) from Lombok Island, located at the edge of the Wallace Line. Using the mitochondrial COI gene, eight species were successfully identified with high sequence similarity (>98%) to reference data in GenBank, confirming the reliability of molecular identification. Genetic distance analysis revealed a clear interspecific “barcode gap” (0.114–0.232), while phylogenetic reconstruction demonstrated strong clustering of Lombok specimens with Indo-Pacific conspecifics, supported by high bootstrap values (>90%). Although based on a single mitochondrial marker, these patterns are consistent with limited genetic structuring across regions and suggest potential connectivity among Indo-Pacific populations, possibly mediated by planktonic larval dispersal. Nucleotide composition analyses further revealed an AT-rich bias characteristic of gastropod mitochondrial genomes, with minor interspecific variation that may have diagnostic value. Overall, this study enriches the genetic reference data for Cypraeidae and provides essential baseline information for future multi-locus or genomic studies aimed at testing hypotheses on population connectivity, phylogeography, and conservation of marine biodiversity within the Indo-Pacific region.

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