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Research Article

Identification of *Parathelphusa* sp. in the Catchment Area of Lake Matano, South Sulawesi, Using Classical Taxonomy and DNA Barcoding

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ABSTRACT

This study aimed to identify and classify *Parathelphusa* sp. in Lake Matano using classical taxonomy and DNA barcoding. Methods included morphological and morphometric analysis, alongside molecular analysis using the *Cytochrome Oxidase Subunit I* (COI) gene and NCBI GenBank BLAST. The results revealed two morphotypes, one identified as *Parathelphusa pantherina*, while the second remained unidentified despite resembling *Parathelphusa pallida*. This research underscores the value of combining DNA barcoding and classical taxonomy (morphological and morphometric) for species identification, offering new insights into the genetic diversity of *Parathelphusa* crabs in the Lake Matano watershed. The results can support conservation, ecosystem management, and the protection of endemic species.

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Freshwater crabs comprise more than 1,500 species in five families, including the speciose family Gecarcinucidae (Pati & Pradhan 2020). These crabs can be an important source of nutrients as they contain vitamins, protein, calcium, and bioactive compounds (Grinang et al. 2017). However, utilization is mostly limited to consumption by local communities, with large species being more popular. Crab species of the family Gecarcinucidae reported from Lake Matano, Sulawesi, Indonesia, include *Nautilothelphusa zimmeri* Balss, 1933, *Parathelphusa pantherina* Schenkel, 1902, *P. pallida* Schenkel, 1902, *P. ferruginea* Chia & Ng, 2006, *Syntripsa matannensis* Schenkel, 1902, and *S. flavichela* Chia & Ng, 2006 (Schubart & Ng 2008; von Rintelen et al. 2012; Sentosa et al. 2017). Of these, five are considered endemic to the Malili ancient lake complex, and have been assessed as endangered in the IUCN Red List (Schubart 2018a, 2018b, 2018c, 2018d, 2018e), while one (*P. pallida*) is endemic to the wider region of Sulawesi and assessed as least concern, despite reports of declining abundance (Esser & Cumberlidge 2008).

Lake Matano, the deepest lake in Southeast Asia and the eighth deepest in the world, is estimated to be around 5 million years old (Adhityatama et al. 2017). The lake has a rich ecosystem of endemic flora and fauna (Achmad et al. 2020) and is designated as a nature reserve (Minister of Agriculture Decree No. 274/Kpts-UM/1979). With a small catchment area (436 km^2) and a surface elevation of 382 m (Crowe et al. 2008), the ecosystem is influenced by geomorphology, human activities, and internal processes (Sulastri et al. 2020). Human activities such as mining and agriculture affect water quality and ecosystems (Hatta et al. 2022). The survey shows that Matano Lake is fed by various rivers with unique catchment area characteristics.

Crabs of the genus *Parathelphusa* play important roles in aquatic ecosystems and are sensitive to environmental quality (Ng 2014). Crab populations in the Malili ancient lake complex are declining due to the introduction of invasive fish species and environmental degradation (Hilgers et al. 2018; Kusumadewi et al. 2024). Invasive flowerhorn hybrid cichlids released between 2005 and 2010 quickly spread and had become the dominant fish species in Lakes Mahalona and Towuti by 2012 (Herder et al. 2012; Haase et al. 2023). Several other invasive fish species have been introduced to Matano Lake, including the striped snakehead (*Channa striata*), tilapia (*Oreochromis* spp.), armoured catfishes (Loricariidae), catfish (*Clarias* spp.) and others; however, the most dominant is the flowerhorn, locally known as louhan (Hedianto & Sentosa 2019; Rahmawati et al. 2025).

Lake Matano, as an ancient lake with high endemic biodiversity, is recognized as a national and global conservation priority (Lukman et al. 2017; Achmad et al. 2020). Science-based conservation of endemic species such as *Parathelphusa* crabs requires ecological and genetic studies, including accurate species identification and distribution data. DNA barcoding techniques can be used to aid in species identification, especially for distinguishing morphologically similar species, in marine and freshwater environments (Hikam et al. 2021). Examples include freshwater shrimps (Jurniati et al. 2020), freshwater crabs (Sinaga et al. 2024), and gastropods (Saleky et al. 2020).

DNA barcoding has not yet been applied to endemic crabs in the watershed of Lake Matano, as previous studies did not cover a broader watershed area, and the available data only pertain to *Parathelphusa* species in the lake (von Rintelen et al. 2012; Sentosa et al. 2017). This study integrates DNA barcoding and classical morphological taxonomy to identify endemic crabs in the Matano watershed. This approach aims to enhance identification accuracy, to improve understanding of biodiversity, and to support sustainable conservation efforts.

In this study, sampling was conducted around the catchment area of Lake Matano, South Sulawesi with morphological analysis conducted at the

Fisheries Biology Laboratory, Faculty of Marine Science and Fisheries, Hasanuddin University. DNA extraction and PCR were carried out at the Biodiversity Laboratory of Indonesia (BIONESIA), Ubung Kaja, Denpasar City, Bali, while DNA sequencing was carried out at PT Genetics Science, Jakarta. Endemic crabs were collected from sites in six rivers around Lake Matano (Figure 1) with the help of local fishermen. Each specimen was photographed and stored in a labelled bag containing 96 % ethanol. The samples were then stored in a cool box with ice cubes and brought to the laboratory.

Upon arrival at the Fisheries Biology Laboratory, Hasanuddin University, tissue samples were taken from three specimens for genetic analysis. Body tissues were taken from the right side of the abdomen using sterile forceps and put into 1.5 mL micro tubes containing 96 % absolute ethanol, then taken to the Bionesia Laboratory in Denpasar, for DNA barcode analysis. Morphometric measurements (Figure 2) were carried out at the Fisheries Biology Laboratory using digital callipers with an accuracy of 0.1 mm following references (Keenan et al. 1998; Junardi et al. 2020). Morphological analysis and identification of *Parathelphusa* specimens referred to (Chia & Ng 2006).

Genomic DNA was extracted from each sample using the Geneaid Tissue Genomic DNA Extraction kit following the manufacturer's protocol. Crab tissue samples were placed in a microcentrifuge with GT buffer and proteinase, incubated, and underwent a process of lysis, binding, DNA purification by washing in a GS column, and final elution using Elution Buffer/TE at 60 °C. Fragments of the target *cytochrome oxidase subunit I* (COI) gene (barcode DNA) were amplified via PCR using forward LCO1490 and reverse HCO2198 primers (Folmer et al. 1994) following the BIONESIA protocol. The PCR profile included denaturation, annealing process, and extension steps. PCR products were verified through electrophoresis on 1 % agarose gel

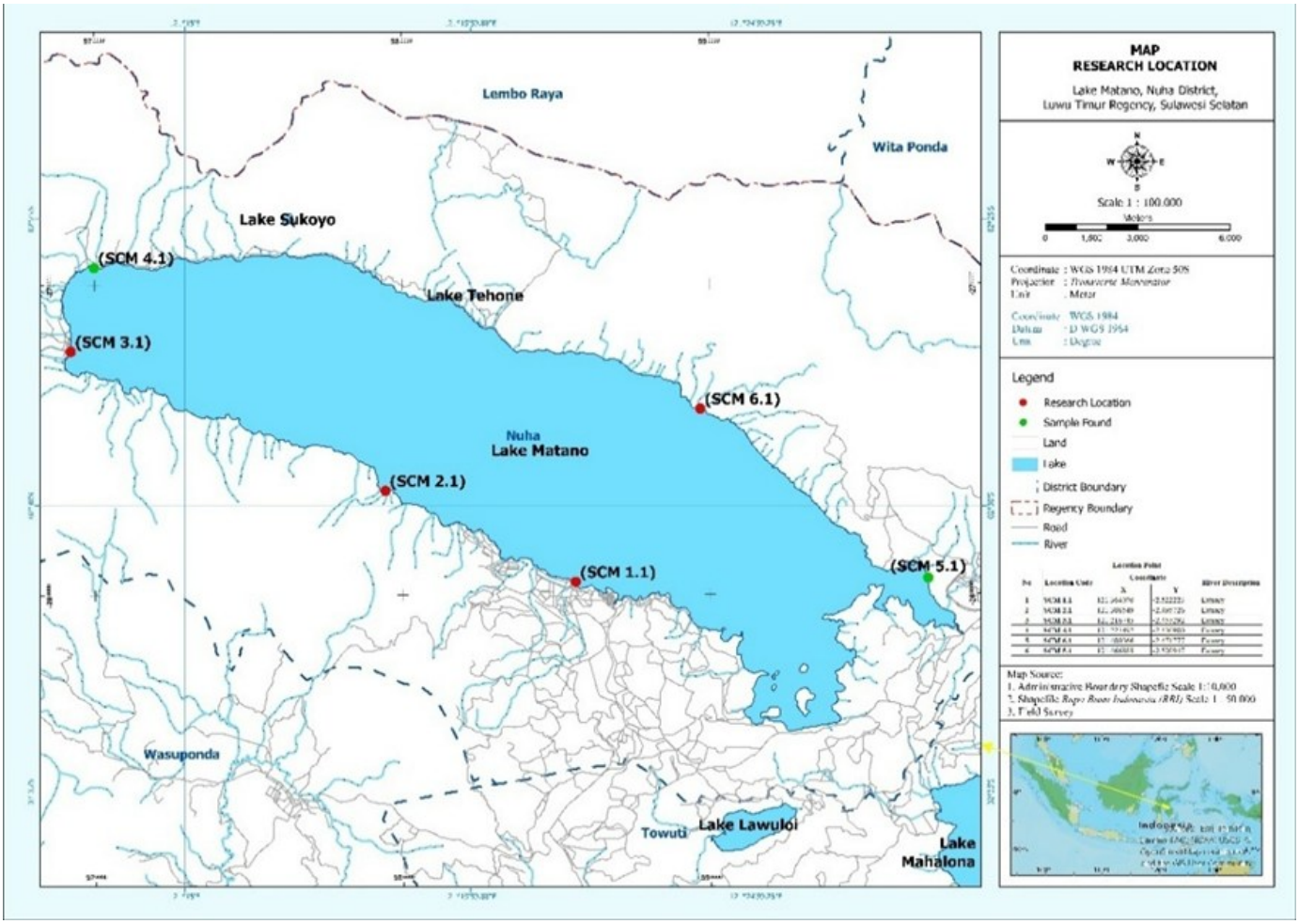

Figure 1. Research sites in the Lake Matano watershed.

with Nucleic Acid Gel Stain (GelRed®), then sent for Sanger sequencing, using a Capillary Electrophoresis Sequencer at PT Genetika Science in Jakarta.

Figure 2. Morphometric parameters of *Parathelphusa* sp. from Lake Matano watershed. Abbreviations: CL= Carapace length, CW= Carapace width, PCW= Posterior carapace width, FW= Frontal width, SL= Sternum length, SW= Sternum width, CaL= Carpus length, PrW= Propodus width, ChL= Chela length, MPrL= Major propodus length, and TL= Total width.

Morphological and morphometric data were analyzed descriptively in Microsoft Excel 2021. Chromatograms from Sanger sequencing were processed in MEGA 11 (Tamura et al. 2021) and the nucleotide sequences of each specimen were cleaned, aligned, and concatenated to generate DNA barcodes. Homologous sequences were obtained from the NCBI GenBank using the online nucleotide Basic Local Alignment Search Tool (BLAST) (NCBI, https://blast.ncbi.nlm.nih.gov) with default parameters, then aligned using the ClustalW routine in MEGA 11. Phylogenetic trees were constructed using the Neighbour-Joining method with the Kimura 2 parameter model and 1000 bootstrap replicates (Kimura 1980) and edited using the IToL Version 5 online tool (Letunic & Bork 2021).

Three samples of *Parathelphusa* sp. were recovered from the six study sites in the Lake Matano catchment: one from SCM 5.1 and two from SCM 4.1. Based on morphology referring to Chia and Ng (2006), two specimens showed typical features of *Parathelphusa pantherina* (Figure 3A) while one specimen (Figure 3B) most closely resembled *Parathelphusa pallida*, but morphological differences prevented definitive identification.

Figure 3. Morphology of *Parathelphusa* crabs from the Matano watershed: (A) *P. pantherina*. (B) *Parathelphusa* sp.

The morphometric characteristics of the three *Parathelphusa* specimens are presented in Table 1. For *P. pantherina*, comparative data from a previous study on the same species are also shown in Table 1.

The DNA barcodes obtained from the three crab specimens were 672 bp long (Table 2). Two sequences had over 99 % identity with the NCBI GenBank reference sequence of *P. pantherina* accession KF201113.1, collected from Matano Lake (Poettinger & Schubart 2014). No GenBank accession was close (>98 % identity) to the third sequence. The barcoded DNA sequences have been deposited in NCBI GenBank under submission number SUB14896961, accession numbers PQ662808- PQ662810.

A phylogenetic tree constructed using DNA barcodes from this study and homologous sequences from GenBank (Figure 4) shows two specimens in the *P. pantherina* clade while the third specimen is nested in the genus *Parathelphusa* but does not cluster with any GenBank accessions.

Morphological analysis of *Parathelphusa* sp. showed interspecies variation at the two Lake Matano watershed Sites. Two specimens from SCM 4 were confirmed as *P. pantherina*, while a specimen from SCM 5 resembled *P. pallida* more closely than other congeneric species described to date, but had black spots, unlike the description of *P. pallida* (Chia & Ng 2006). *P. pallida* is characterized by a body without black spots, while the specimen found in SCM 5 had clearly visible black spots on its carapace. Such differences could be influenced by genetic factors, nutrition, environmental conditions, and development (Song et al. 2022). DNA barcoding showed that the SCM 5 specimen was closer to *Parathelphusa ferruginea* than *P. pallida* based on the BLAST results, but did not cluster with either of these species in the phylogenetic analysis. Based on the morphological description of *P. ferruginea* by (Chia & Ng 2006), this species has a rusty red colour, a rough and wrinkled carapace surface, an "H"-shaped central depression, and an expanded claw size. These characteristics differ significantly from the specimen found in SCM 5, which more closely resembles *P. pallida*.

Parathelphusa crabs collected from the catchment area (DTA) of Lake Matano (Table 1) were within but towards the lower end of the carapace width size range previously reported for *P. pantherina* from Lake Matano (Sentosa et al. 2017). This indicates that these individuals may still be in relatively early growth stages. Meanwhile, the *Parathelphusa* sp. specimen from site SCM 5 had a carapace width of 54.5 mm, much larger than *P. pantherina*

Table 1. Morphometric characters of *Parathelphusa pantherina* and *Parathelphusa* sp. from Lake Matano DTA.

NO.	Character	Code	Measurements (mm)		Sentosa et al. 2017 (mm)
			Parathelphusa pantherina	*Parathelphusa* sp.	*Parathelphusa pantherina*
1	Carapace Width	CW	25.6 - 29.2	54.5	16.6 - 33.3
2	Carapace Length	CL	20.9 - 25.0	45	-
3	Posterior Carapace Width	PCW	11.6 - 16.7	27	-
4	Frontal Width	FW	11.6 - 16.7	21.8	-
5	Sternum Length	SL	9.3 - 14.6	45	-
6	Sternum Width	SW	16.3 - 18.8	38	-
7	Carpus Length	CaL	7.0 - 12.5	32.7	-
8	Major Propodus Length	MpL	16.3 - 27.1	51	-
9	Propodus Width	PW	4.7 - 10.4	20	-
10	Chela Length	ChL	11.6 - 16.7	24	-
11	Total width	TL	4.3 - 4.8	5.5	-

Table 2. Closest NCBI GenBank Accessions (BLAST Nukleotida results) for DNA Barcode Sequences of *Parathelphusa* spp. from the Lake Matano Watershed.

DNA Barcoding specimens from Matano DTA			Closest NCBI GenBank Accession			
Specimen ID	Station	Length (bp)	Species Name	Accession Number	Query Cover (%)	Identity (%)
UNH24-MAT020	SCM 5	672	*Parathelphusa ferruginea*	KF201127.1[a]	97 %	97.13 %
UNH24-MAT021	SCM 4	672	*P. pantherina*	KF201113.1[a]	97 %	99.84 %
UNH24-MAT022	SCM 4	672	*P. pantherina*	KF201113.1[a]	97 %	100 %

[a] (Poettinger & Schubart 2014)

from site SCM 4 in the Lake Matano watershed. To identify this species, additional references are required due to the lack of comparative data from previous studies. Lake crabs tend to be larger due to pressure (von Rintelen et al. 2012). Morphometric measurements of SCM 4 only included carapace width, but DNA barcoding confirmed it as *P. pantherina*, while SCM 5 requires further study for accurate identification. The mtDNA COI gene is a common molecular marker for species identification of freshwater crabs (Waugh 2007; Paransa et al. 2024). In this study, the 672 bp fragment of the COI gene was used to identify crabs in the Lake Matano DTA, resulting in two genotypes, only one of which was identified to the species level (Table 2). DNA barcode-based identification using BLAST matched the morphological results for specimens from site SCM 4, with a high identity (99.83-100 %) with the closest GenBank *P. pantherina* accession, KF201113 (Poettinger & Schubart 2014). Meanwhile, the DNA barcode of SCM 5 could not be identified based on current GenBank accessions. The closest match was *P. ferruginea* accession KF201127, from a river in the Lake Lantoa watershed (Poettinger & Schubart 2014), differing from *P. pallida* by nearly 3 %, while intraspecific genetic variation in the COI marker is typically less than 3 % in crabs (Hidayani et al. 2020).

The phylogenetic tree (Figure 4) supports the morphological and molecular (BLAST) identification of the two SCM 4 specimens as *P. pantherina*, as the sequences form a monophyletic group (clade) with other *P. pantherina* sequences in GenBank, well separated from other species groups within the genus. Meanwhile, specimen SCM 5 formed a separate clade (labelled *BIOSUB284 001 Parathelphusa* sp.), with closest kinship to another singlet, *Parathelphusa* sp., GenBank accession KF201089.1 from Lemolemo River in the Towuti Lake watershed (Poettinger & Schubart 2014). Both singlets are

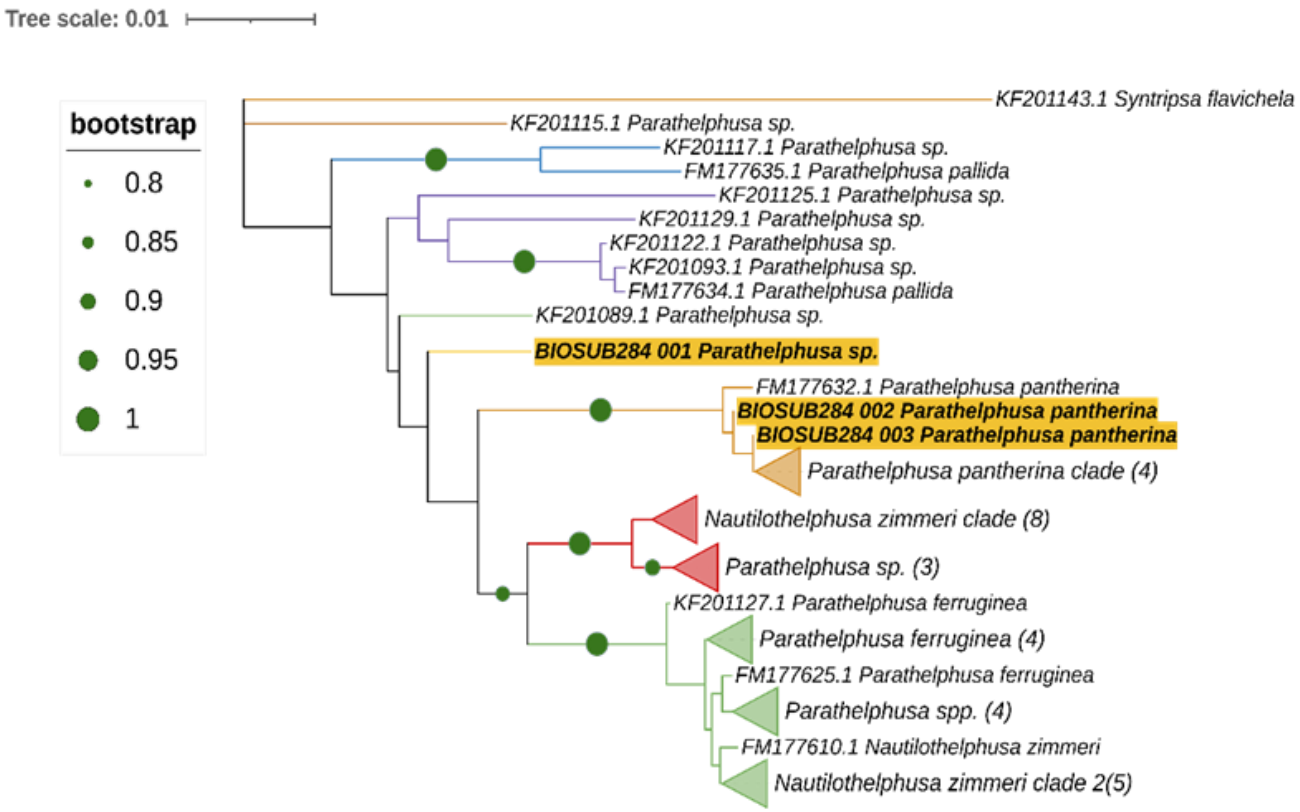

Figure 4. Phylogenetic tree based on COI DNA barcodes of *Parathelphusa* crabs from Lake Matano (yellow highlights) and nearby GenBank accessions homologous to *Sytripsa flavichela* as outgroups.

clearly separated from the clades containing *P. ferruginea* accessions, an apparent contradiction with the BLAST results, as well as clades containing *P. pantherina* and *P. pallida*. Several other separate clades were also identified as *Parathelphusa* sp. (Figure 4), suggesting the identity of these sequences was not yet known when submitted to GenBank. The outgroup, *Syntripsa flavichela*, plays an important role in identifying primitive and derivative characters and in determining the starting point in the construction of the phylogenetic tree (Subari et al. 2021).

This study on freshwater crabs in the Danau Matano watershed identified two sympatric species of the genus *Parathelphusa*. Morphological and genetic analyses (DNA barcoding) identified specimens from site SCM 4 as *P. pantherina*. Based on morphology, the specimen from SCM 5 most closely resembled *P. pallida*, though with some differences, while the DNA barcode nested in the genus *Parathelphusa* but differed from all current COI GenBank accessions. This unidentified taxon may be a new or poorly documented species within the genus *Parathelphusa*. These findings add to the evidence for undescribed species in the genus *Parathelphusa*, as discussed by Poettinger and Schubart (2014), and highlight the need for further research on freshwater crab diversity using integrated morphological and molecular taxonomy approaches, in particular in the Malili ancient lakes of Sulawesi.

AUTHORS CONTRIBUTION

A.A.H., N.N. and A.M.M.: planned the research and contributed to the manuscript including final edits. A.W.M.: collected and analyzed the data and wrote the draft manuscript. A.A.M.: provided materials and contributed to the manuscript.

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CONFLICT OF INTEREST

All authors declare no conflict of interest.

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