

Morphological and molecular characterization of mole crab (Genus: *Emerita*) in the Cilacap coastlines of Indonesia, with particular focus on genetic diversity of *Emerita* sp. nov.



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Abstract

Abstract. Bhagawati D, Nuryanto A, Winarni ET, Pulungsari AE. 2022. Morphological and molecular characterization of mole crab (Genus: *Emerita*) in the Cilacap coastlines of Indonesia, with particular focus on genetic diversity of *Emerita* sp. nov. *Biodiversitas* 23: 2395-2404. Previous studies reported *Emerita emeritus* is the only species of the Genus *Emerita* inhabiting the coastal ecosystem of the Cilacap District. A recent study reported the presence of suspected new *Emerita* species living on the Cilacap sandy beach but used a small number of specimens and no reports about genetic diversity. This study used more *Emerita* samples than the previous study. This study aimed to identify *Emerita* specimens based on the morphology and the cytochrome c oxidase 1 gene and analyzed the genetic diversity of *Emerita* sp. nov. *Emerita* samples were collected from three different beaches in Cilacap District, Central Java, Indonesia. Morphological identification placed the samples into two different morphotypes. Morphotype A was identified as *Emerita emeritus*. Morphotype B was determined as *Emerita* sp. nov. Molecular data support the placement of *Emerita* samples into *Emerita emeritus*, and *Emerita* sp. nov. *Emerita* sp. nov. has haplotype diversity of 0.857 ± 0.057 , indicating a high genetic diversity. Haplotype H2 was suggested as the most primitive one because other haplotypes radiated from it. This study concluded that two sympatric *Emerita* species inhabit Cilacap coastlines, and *Emerita* sp. nov. has high genetic diversity.

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Morphological and molecular characterization of mole crab (Genus: *Emerita*) in the Cilacap coastlines of Indonesia, with particular focus on genetic diversity of *Emerita* sp. nov.

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Abstract. Bhagawati D, Nuryanto A, Winarni ET, Pulungsari AE. 2022. Morphological and molecular characterization of mole crab (Genus: *Emerita*) in the Cilacap coastlines of Indonesia, with particular focus on genetic diversity of *Emerita* sp. nov. *Biodiversitas* 23: 2395-2404. Previous studies reported *Emerita emeritus* is the only species of the Genus *Emerita* inhabiting the coastal ecosystem of the Cilacap District. A recent study reported the presence of suspected new *Emerita* species living on the Cilacap sandy beach but used a small number of specimens and no reports about genetic diversity. This study used more *Emerita* samples than the previous study. This study aimed to identify *Emerita* specimens based on the morphology and the cytochrome c oxidase 1 gene and analyzed the genetic diversity of *Emerita* sp. nov. *Emerita* samples were collected from three different beaches in Cilacap District, Central Java, Indonesia. Morphological identification placed the samples into two different morphotypes. Morphotype A was identified as *Emerita emeritus*. Morphotype B was determined as *Emerita* sp. nov. Molecular data support the placement of *Emerita* samples into *Emerita emeritus*, and *Emerita* sp. nov. *Emerita* sp. nov. has haplotype diversity of 0.857 ± 0.057 , indicating a high genetic diversity. Haplotype H2 was suggested as the most primitive one because other haplotypes radiated from it. This study concluded that two sympatric *Emerita* species inhabit Cilacap coastlines, and *Emerita* sp. nov. has high genetic diversity.

Keywords: *Albunea*, genetic variation, *Hyppa*, polymorphism, sand crabs

Abbreviations: COI: cytochrome c oxidase 1

INTRODUCTION

Classical taxonomy and systematic utilized morphological data during species characterization (Erlank et al. 2018; Shu et al. 2022). In some animal groups, morphology characteristics are entirely satisfactory (Chan et al. 2016; Mauroka et al. 2018; Korovchinsky 2019). However, in other groups, this character may lead to identification mistakes, especially in groups with limited morphological differences, such as in mole crab from the Genus *Albunea* (Boko and MacLaughlin 2010), cryptic species (Karanovic 2015; Bilgin et al. 2015; Bekker et al. 2016; Kusbiyanto et al. 2020) or group with limited and undeveloped morphological characters, such as egg, larvae, and early juvenile (Ko et al. 2013; Palero et al. 2016; Palecanda et al. 2020).

Mole crabs, locally known as 'yutuk,' belong to Decapoda from the superfamily Hippoidea. It consists of three different families of Albuneidae, Blepharipodidae, and Hippidae, which are divided into *Emerita* and *Hippa* genera. Moreover, ten species have been identified and described under Genus *Emerita* (Boyko and MacLaughlin 2010). This crustacean group is widely distributed over the World (Boyko and MacLaughlin 2010), and the distribution has been elaborated by Mahapatro et al. (2018). In Indonesia, these crabs inhabit sandy coastlines from the

West Coast of Sumatera to Moluccas (Wardiatno et al. 2015; Boyko and Harvey 1999).

Previous studies reported that the three genera of Hippoidea have been described from Indonesia waters (Bhagawati et al. 2016; Pramithasari et al. 2017; Nugroho et al. 2018; Butet et al. 2019; Hartoko et al. 2019; Bhagawati et al. 2020). Other studies described *Emerita emeritus* as the only species of genus *Emerita* found on the southern coastlines of Java (Nugroho et al. 2018; Dewi et al. 2019; Krisanti et al. 2020; Desi et al. 2020), including from Cilacap sandy beaches, such as Widarapayung beach, Sub-district of Binangun (Bhagawati et al. 2016; Haq et al. 2018). However, recent studies observed morphological and molecular deviations in some samples to the *Emerita emeritus* characteristics. The possible presence of the sympatric species complex of the Cilacap coastlines was reported (Nuryanto et al. 2020). Even, Hanim et al. (2017) proposed a scientific name for the new suspected species of *Emerita* from Pangandaran beach, as *Emerita pangandarensis* sp. nov.. Still, the international commission has not approved its zoological nomenclature. However, the studies by Hanim et al. (2017) and Nuryanto et al. (2020) were conducted in few samples and only focused on species identification. These studies did not report genetic diversity in newly suspected *Emerita* species. Molecular characterization was performed in a higher number of specimens and data types. Additionally, it assessed the

genetic diversity of new suspected *Emerita* species collected from the southern coast of Cilacap, Central Java, Indonesia.

Species identification and population genetic studies were conducted using various molecular markers (Nuryanto et al. 2017; Butet et al. 2019; Nuryanto et al. 2019; Elvyra et al. 2020; Riani et al. 2021; Setyaningrum et al. 2022). The cytochrome c oxidase 1 (COI) gene is a common marker used in species determination (Ko et al. 2013; Muchlisin et al. 2013; Dahruddin et al. 2016; Irmawati et al. 2017; Syaifudin et al. 2020) and population genetic studies (Song et al. 2013; Zhang et al. 2014; Fahmi 2015; Nuryanto et al. 2019). Therefore, this research aimed to characterize samples of genus *Emerita* based on morphological and molecular characteristics and assess the genetic diversity using the cytochrome c oxidase 1 gene.

MATERIALS AND METHODS

Research location and sampling sites

The samples of mole crabs were collected from the sandy coastal region of the Cilacap District, Central Java, Indonesia. Additionally, the sampling was carried out in Jetis beach in the Sub-district of Nusawungu as well as Kenari Indah and Widarapayung beaches in the Sub-district of Binangun, Cilacap District, Central Java, Indonesia (Figure 1).

Mole crabs sampling

Emerita specimens were collected manually using two traditional fishing gears called “sodo nets” and “sorok bamboo” (Figure 2). Furthermore, local fishers performed samples collection and handling. Abdominal tissue samples were cut off for approximately 5 mm² and preserved using 96% alcohol in 2 ml screw lid tubes.

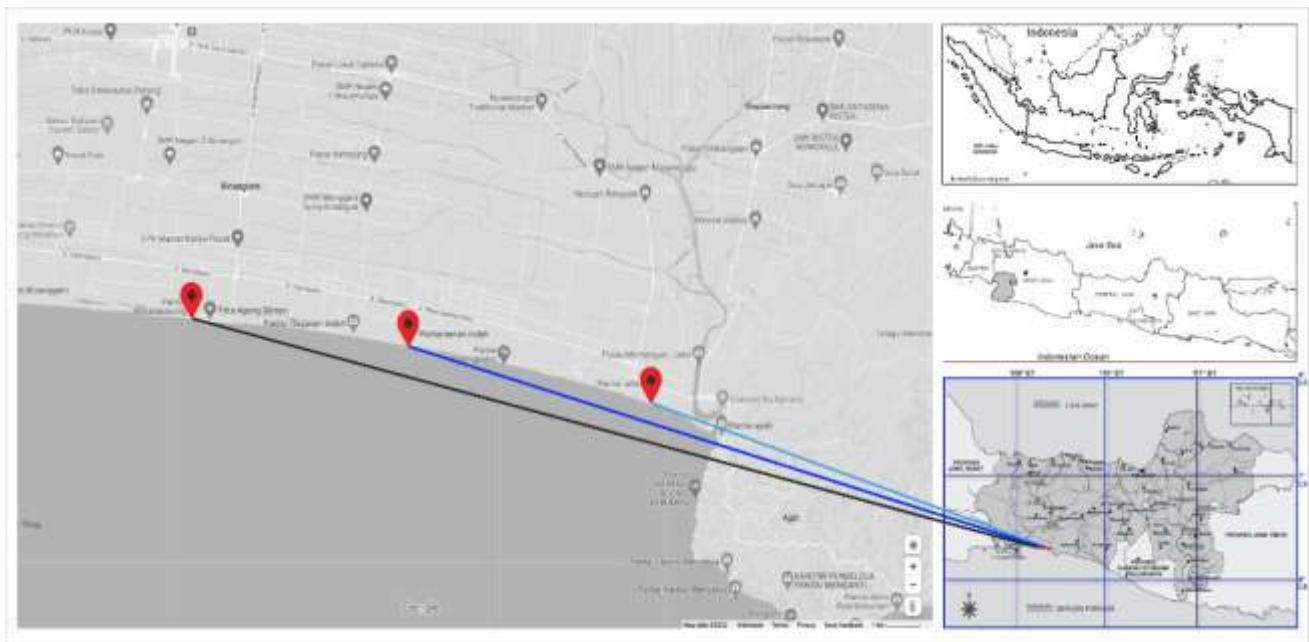


Figure 1. Sampling location map of *Emerita* at Jetis, Kenari Indah and Widarapayung Beaches (source: google maps, modified by S.S. Asmarani 2022)



Figure 2. Fishing gears for collecting mole crab (*Emerita*) samples. A. sodo nets. B. sorok bamboo

Procedures

Morphological characterization

Freshly collected crabs were brought to Animal Taxonomy Laboratory, Faculty of Biology Jenderal Soedirman University. The samples were washed thoroughly using freshwater, and morphological characterization was carried out based on the diagnostic character essential for identifying crustaceans. According to Ng (1998), several diagnostic characteristics for identifying crustaceans are carapax, anterolateral side, dorsal surface, frontal side, buccal cavern/mouthpart, and locomotion (dactyl and pereopod), abdominal segments, and gonopods.

Observations on the genus *Emerita* were performed by referring to the diagnostic character used by Sankolli (1965), Haig (1986); Boyko and Harvey (1999), Osawa and Chan (2010), Wardiatno et al. (2015) and Bhagawati et al. (2016, 2020). These characteristics are the color and shape of the carapax; the position, number, and shape of the slits (Carapace Groove/CG) on the carapax surface; spines on the anterior carapax; a curved shape of the margin on the latero-anterior; and the shape and number of fine spines on the latero-anterior portion. Carapax height measurements were conducted on the front, middle, and back of the body, with the shape and size of the eyestalk. The merus distal and dactyl form on the maxilliped-3 and the first pereopod, while spines and hairs form on the margin of the first pereopod dactyl. Pleopods are formed in the abdominal segment as pleural.

DNA isolation and marker amplification

Genomic DNA was isolated from abdominal tissue samples using the Quick-DNA™ Miniprep Plus kit from Zymo's research. The processes were conducted based on the procedures provided by the company. The extracted DNA was migrated in 1% agarose electrophoresis and stained using ethidium bromide. The COI gene marker fragments were amplified using FishF2 and FishR2 primers (Ward et al. 2005) in Primus 25 Peqlab Thermocycler. Subsequently, the amplification reactions consisted of 1x buffer PCR, 2 mM MgCl₂, 0.2 mM of each primer, 0.2 mM dNTP mix, 1 U Taq polymerase, and 2.0 ng/μL template DNA. The final volume to 50 μL of the mixtures was adjusted by adding DNA-RNA-free water. The pre-denaturation step at 95°C started thermal cycles for 4 minutes. The amplification reactions were performed for 35 cycles with denaturation steps that lasted for 30 seconds at 95°C, followed by annealing at 53°C for 120 seconds, and terminated by extension steps 60 for minutes at 72°C. Additionally, a final elongation step terminated the cycles after 5 minutes, at 72°C. The amplified COI marker was stained using ethidium bromide in 1.5% agarose gel and documented using the GelDoc apparatus (BioRad).

Marker sequencing and editing

Nucleotide sequencing of the used marker was conducted in the Molecular Genetic Laboratory of PT Genetika Science Indonesia Jakarta, according to the Sanger method. The study obtained consensus and multiple

alignments by assembling the forward and reverse sequences using ClustalW ver.1.4 in Bioedit (Hall 2011). In addition, it obtained haplotype and Arlequin data files from its generating process in DnaSP 6 (Rozas et al. 2017).

Data analysis

The taxonomic status of *Emerita* samples was delineated based on sequence homology to the conspecific relative available in GenBank. This test was carried out using an essential local alignment search tool (BLAST). This study also used genetic distance, genetic divergence or a gap of 5% (Candek and Kuntner 2015; Setyaningrum et al. 2022). Variance analysis and fixation statistic (Fst) were conducted in Arlequin 3.5 (Excoffier and Lischer 2010) to estimate significant genetic divergence between the morphotypes. The diversity data was evaluated using Haplotypes (h) and nucleotide (π) diversities, calculated using Arlequin 3.5. Similarly, the neutrality of the used COI marker was tested using Fs and D values (Excoffier and Lischer 2010). Evolutionary relationships among haplotypes were estimated based on haplotype networks reconstructed using the median-joining method in NETWORK software (Bandelt et al. 1999).

RESULTS AND DISCUSSION

Taxonomic status

Morphological identification

A total of 17 individual *Emerita* samples were analyzed during the study. Morphological identification separated the samples into two different morphotypes. The first (A) and second (B) morphotypes consisted of 3 and 14 individuals, respectively (Figures 3A and 3B). However, they have similar general morphological characteristics that lead to Genus *Emerita* placement. The body of the *Emerita* crab is light, dark to blackish gray, with a slightly cylindrical shape with a wider distal carapace area. The eyestalk is long and slender, extending beyond the second antenna segment. The antennae are very long with hairy setae, and the segment on the second antenna consists of 3 horn-like and median spines. There are two oblique elongated protrusions with distinct spines that can be moved at the edges. The carapace has 3 frontal lobes, with the median very pointed and triangular, separated from the lateral lobe. The surface of the carapace has visible line-shaped slits located post-frontal and post-gastric. The latero-frontal margin has fine spines with sparse hairs. It has a short abdomen with a long telson, almost half the carapace length. The first pereopods were simple with an oval, lamellate dactyl, less than twice the width. Dactylus of the first pereopod with 4-5 rigid spines is found in the distal half of the lower margin, while 1-3 with 2 spines is in the tip.

The morphotypes A and B were differentiated by the following characteristics. The frontal part of the carapace showed differences in the shape and length of the spines at the base of the second antenna segment, the shape of a hollow between the three spines at the tip of the carapace, and the post-frontal and post-gastric cleft forms (Figure 3).

Individuals with morphotype A have eye stalks longer than the spines at the second antenna base (Figure 3A). In contrast, morphotype B has eye stalks almost the same length as the spines at the second antenna base. Another performance is the concave shape between the three spines on the frontal carapace. Morphotype A does not form an angle, while B forms a curve. The shape of the gap found in the post-frontal area is a straight line, neat and flat in morphotype A, but it is elevated in morphotype B with a curved line in the post-stomach. In morphotype A, the arch is not too deep, and its carapace's right and left ends have a thin curved slit. In contrast, morphotype B has a narrower curved line.

Based on the latero-frontal section on body height, morphotype A had a flatter body shape than B (Figure 4.). There are differences in the spines at the second antenna base from the lateral side between morphotypes A and B. Furthermore, morphotype A has slightly curved outer spines, while B tends to be straight. The latero-frontal margin of the carapace, which contains fine spines with sparse hairs between the two morphotypes, has different spine shapes, arch, and the number of spines. The tip of the spine is not sharp; hence, when touched, it feels like a smooth protrusion. The anterior end of the margin does not have spines and has a shorter size than that of morphotype B. The shape of the posterior carapace margin curve in morphotype A is more prominent without spines. In contrast, it is more sloping in morphotype B, which has fine spines.

Morphotypes A and B had different shapes on the distal part of the merus of the third maxilliped (Figure 5). Sankolli (1965), Kazmi and Siddiqui (2006), Boyko (2002), and Bhagawati et al. characterize morphotype A as having features similar to *Emerita emeritus* (Linnaeus, 1756) (2016; 2020). Morphotype A has the first pereopod dactyl oval, measuring less than twice the largest width. There are distinct spines on margins and occupy nearly the distal third of the lower part. Morphotype B has the character of the first pereopod dactyl, which is similar to morphotype A. However, the spines on the margins are smaller and possess the same size (Figure 6).

Based on their morphological characteristics, morphotypes A and B have many similarities (*Emerita*) and differences, suggesting the occurrence of new species. However, it has been well-known that mole crabs from the superfamily Hippoidea show high variability in morphology (Poore 2004; Ahyong et al. 2009; Schnabel and Ahyong 2010). This condition may lead to misidentification when performed based on morphological characters. Molecular data confirmed the possible occurrence of Sympatric species of *Emerita emeritus* in the Cilacap coastlines (Nuryanto et al. 2020) inferred from several specimens. Therefore, further study is still needed using more samples to strengthen the data on new *Emerita* species in the areas.

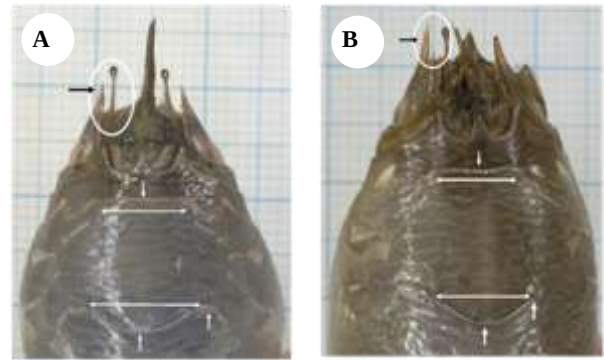


Figure 3. Frontal carapace on morphotype A and morphotype B

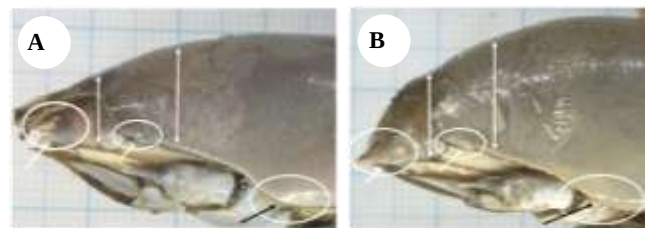


Figure 4. Latero-frontal carapace in morphotype A and morphotype B

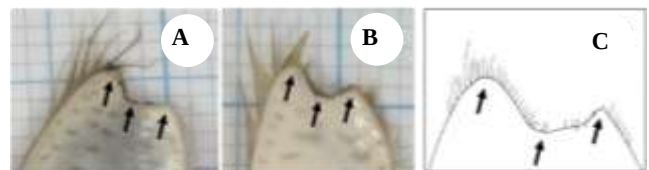


Figure 5. The distal part of the merus of the third maxilliped: Morphotype A; Morphotype B; and C. schematic of *Emerita emeritus* (Linnaeus 1756.), ovigerous females from Madras (Sankolli 1965)

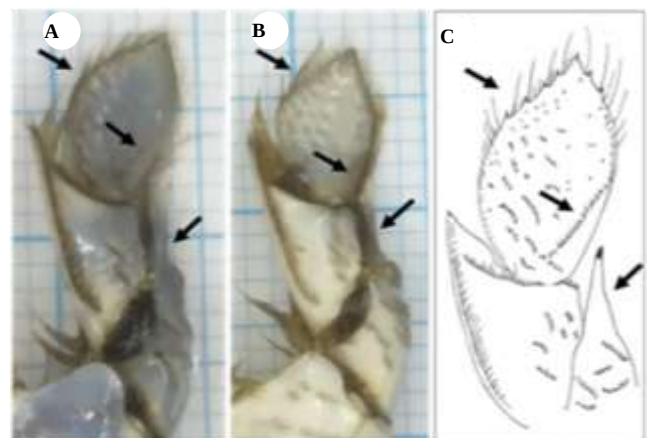


Figure 6. First pereopod on morphotype A, morphotype B, and schematic of *Emerita emeritus* (Linnaeus 1756.), ovigerous females from Madras (Sankolli 1965)

Molecular characterization

Sequence identity tests to the closest relative in GenBank revealed that three individuals (K11, K13, and WP9) of the morphotype A have high sequence identities to *Emerita emeritus* KR047035 ranging from 96.12% to 96.25%. In contrast, the sequence identities to *Emerita* sp. ranged from 85.60% to 85.74%. The remaining 14 individuals of the morphotype B showed low identities to *Emerita emeritus* KR 047035 in GenBank, ranging between 84.78% and 86.87%. The sequence identity of the remaining 14 specimens of the morphotype B to *Emerita* sp. MZ571198 was high ranging from 98.83 to 100% (Table 1).

Genetic distance and genetic gap

Table 2 summarizes the genetic distance and gap between morphotype A and *E. emeritus* KR047035 and morphotype B and *Emerita* sp. MZ571198. The genetic gap was estimated based on the difference between the maximum and the minimum genetic distance of species.

Genetic divergence

Variance analysis and F_{st} value indicated that the two morphotypes showed significant genetic differences with a p -value of 0.005 (Table 3). The significant genetic difference between the two indicated that both belong to two different species, proved by the BLAST result.

Amino acid composition

The morphotypes were also subjected to amino acid composition comparison to define molecular divergence, as summarized in Table 4.

This research delineated the samples of morphotype A as *Emerita emeritus*. This is due to the strong genetic and conspecific identities of 96.12% to 96.25% and 85.60% to 85.74% for *Emerita* sp (MZ571198). Morphotype A was delineated into *E. emeritus* because genetic divergence within species may range from 0% to 4.6% (da Silva et al. 2011) or higher (Weis et al. 2014). Genetic divergence between morphotype A and *Emerita emeritus* KR047035 was below 4.6% (da Silva et al. 2011). The highest value was 3.88%, within the allowable range of 4% to 5%, as a moderate level of genetic identity for species delineation (Jeffery et al. 2011). This study has selected the value because the mutation rate of the COI gene is species-specific (Karanovic et al. 2015; Palecanda et al. 2020). A genetic threshold between 4% and 5% is permissible for genetic species determination, although additional considerations should be accounted for (Higashi et al. 2011; Jeffrey et al. 2011). Previous studies also utilized a genetic threshold of 5% during species determination (Candek and Kuntner 2015; Kusbiyanto et al. 2020; Riani et al. 2021).

The remaining 14 samples were identified as *Emerita* sp. nov. because of their high genetic identity (98.83% to 100%) to *Emerita* sp. MZ571198. In contrast, morphotype B had a low genetic identity (84.78% to 86.87%) to *Emerita emeritus* KR047035. This value is widely used as a genetic threshold in species delineation during animal barcoding (Hubert et al. 2010; Candek and Kuntner 2015).

The division of morphotypes A and B into two distinct species is due to a genetic distance ranging from 16.80% to 19.00%, with a genetic gap of 13.6% (Table 2). Moreover, the two morphotypes also showed significant genetic variances and fixation index ($p=0.0059$, Table 3) with different compositions of nucleotide content, especially in Adenine (A) and Thymine (T) composition (Table 4). Amino acid AT was higher than GC in both morphotypes, but the content of A and T was different. The phenomena were also reported in fish (Elvyra et al. 2020). The molecular difference observed in this study is in line with morphotypes A and B morphology. Therefore, morphotypes A and B delineated as *Emerita emeritus* and *Emerita* sp. nov. was reliable.

This study also proved that the COI gene is a good marker for taxonomic identification at the species level. The COI gene's reliability as a barcode is highly variable among animal species (Balkhis et al. 2011; Sachithanandam et al. 2012; Winarni et al. 2021). Similar phenomena were also reported from several locations across Indonesia (Muchlisin et al. 2013; Irmawati et al. 2017; Pramono et al. 2017) and other regions (Aquilino et al. 2011; Triantafyllidis et al. 2011).

Historical demography and genetic diversity of *Emerita* sp. nov.

Historical demography

Tajima's D value was -1.563 ($p=0.044$). That statistically significant results assumed that the used COI marker was under selection pressure. Instead of accepting selection pressure on the used marker, the negative sign of the D value indicated a recent population bottleneck and neutrality of the marker (Tajima 1989; Jong et al. 2011). The negative symptoms and non-significant F_s (-1.580 , $p=0.147$) could assume that the marker was neutral and indicated a population bottleneck (Table 5). The assumption was based on the fact that F_s values are believed to be more sensitive than Tajimas' D . According to Jong et al. (2011) and Mohammed et al. (2021), the sensitivity of F_s values because it is calculated based on nucleotide diversity. A similar phenomenon was also reported in fish (Setyaningrum et al. 2022). Therefore, the used COI marker could be assumed as a neutral marker for assessing the genetic diversity of the *Emerita* sp. population in the Cilacap coastlines.

Table 1. The BLAST parameters of *Emerita* samples from Cilacap coastlines to their conspecific relatives in GenBank

Samples	<i>Emerita emeritus</i> KR047035			<i>Emerita</i> sp. MZ571198		
	Coverage	Expect Value	Genetic identity (%)	Coverage	Expect Value	Genetic identity (%)
K1 (A)	100	0.00	96.12	99	0.00	85.74
K3 (A)	100	0.00	96.12	99	0.00	85.74
WP9 (A)	99	0.00	96.25	100	0.00	85.60
J3 (B)	96	2e179	86.87	100	0.00	98.83
J4 (B)	97	2e-125	84.78	99	0.00	99.15
J6 (B)	99	0.00	86.48	100	0.00	99.84
J7 (B)	99	0.00	86.44	100	0.00	99.16
J8 (B)	99	0.00	86.45	99	0.00	100
K14 (B)	99	0.00	86.48	100	0.00	99.84
K15 (B)	99	0.00	86.32	100	0.00	99.67
WP3 (B)	99	0.00	86.32	100	0.00	99.51
WP5 (B)	98	0.00	86.64	99	0.00	99.83
WP8 (B)	99	0.00	86.42	100	0.00	99.85
CLPE8* (B)	99	0.00	86.84	100	0.00	99.84
CLP4* (B)	98	2e-169	86.57	100	0.00	99.82
CLP11* (B)	98	5e-171	86.75	100	0.00	100
CLP15* (B)	98	5e-171	86.75	100	0.00	100

Table 2. Genetic distance and gap within and among species (%)

Population	<i>Emerita emeritus</i>	<i>Emerita</i> sp.
<i>Emerita emeritus</i>	0.00-3.20	16.80-19.00
<i>Emerita</i> sp.	16.80-0.190	0.00-1.70
The gap between <i>E. emeritus</i> and <i>Emerita</i> sp.	16.80-3.20 = 13.6	

Table 4. Amino acid composition of each morphotype (%)

Nucleotide	Morphotype	
	Morphotype A	Morphotype B
A	24.34	19.60
T	29.72	33.41
G	27.39	28.93
C	18.54	18.05

Table 3. Variance and Fst analysis indicate significant genetic divergence between two *Emerita* morphotypes

Source of variation	d.f	Sum of squares	Variance components	Percentage of variation
Between morphotypes	1	1.303	0.143 ^{Va}	26.53
Within morphotypes	17	6.750	0.397	73.47
Total	18	8.053	0.540	
Fixation index (Fst):	0.265			
p-value (Va and Fst)	0.0059			

Table 5. Species, number of individuals (N), number of haplotypes (nhp), haplotype diversity (h), nucleotide diversity (μ), Tajima'D, and Fu's Fs values

Species	N	nhp	h	μ	D	p-sig.	Fs	p-sig.
<i>Emerita</i> sp. nov	15	7	0.857 ± 0.057	0.005 ± 0.003	-1.563*	0.044	-1.580 ^{ns}	0.147

Note: *significant, ns: not significant

Genetic diversity

Multiple sequences alignment resulted in a total of 418 bp COI gene fragments from 14 individuals *Emerita* sp. nov. collected from the coastlines of Jetis, Sub-district of Nusawungu, Kenari Indah and Widarapayung, Sub-district of Binangun, Cilacap District, Central Java, Indonesia. Furthermore, 12 out of 418 bp were polymorphic, resulting in 7 haplotypes, and the haplotype diversity was 0.857 ± 0.057 (Table 5). This data indicates that the *Emerita*

sp. nov. population in the Cilacap coastlines has high genetic diversity. The nucleotide diversity value (μ) was 0.005 ± 0.003 , which revealed low nucleotide diversity and a relatively low rate of evolution in the *Emerita* sp. nov. population on the Cilacap coastlines. The haplotype network (Figure 3) shows that haplotypes were separated by 2 to 7 mutation steps. However, the mutation was widely distributed in the population, as indicated by high haplotype diversity (0.857 ± 0.057). High haplotype

diversity assessed using the COI gene was widespread in animal phyla (Dorn et al. 2011; Dung et al. 2013; Song et al. 2013; Zhang et al. 2014; Nuryanto et al. 2019). At the same time, low haplotype diversity was also common in animal populations (Setyaningrum et al. 2022). The COI gene's study may show a complex pattern of diversity levels, even within species (Pavesi et al. 2011; Parmaksiz and Eksi 2017). The phenomena are also observed in population studies using other markers, such as microsatellite (Esa and Rahim 2013; Gouskov et al. 2016; Abbas et al. 2017; Achrem et al. 2017; Cheng et al. 2017) and d-loop (Zhong et al. 2013; Liu et al. 2016; Lau et al. 2018; Parmaksiz 2019; Ariyaraphong et al. 2021; Zhang et al. 2022).

This study cannot be compared with previous results because there is no population genetic study on mole crabs, especially on the presumable *Emerita* sp. nov. The only population study was conducted by Pramithasari et al. (2017), who compared mole crabs (*Albunea symmysta*) populations in Java and Sumatra. However, their study used morphological data, and the comparison to Pramithasari et al. (2017) was not congruent. This fact implies that more studies on the population genetics of mole crabs are needed.

Evolutionary relationships among *Emerita* sp. nov. individuals

The evolutionary process of the *Emerita* sp. nov. population on the southern coast of Cilacap is presented in the haplotype network (Figure 7). Star-like haplotype network in Figure 7 showed that haplotype 2 was the most primitive. Meanwhile, H2 was the center of the network, and other haplotypes evolved from (H2) as the most abundant (Balkhis et al. 2011; Song et al. 2012). The result contradicted the general acceptance that primitive haplotype has the highest abundance in the population (Adamson et al. 2012; Barasa et al. 2014; Baisvar et al. 2018, 2019). The low frequency of H2 observed was assumed because of the small population (14 individuals). However, this assumption should be proven based on a further study using a high number of analyzed individuals.

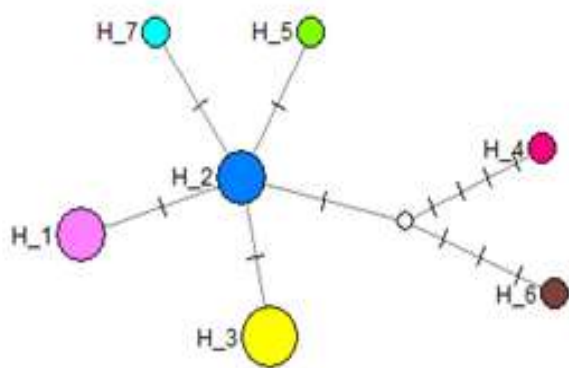


Figure 7. Haplotype networks indicating evolutionary relationships among *Emerita* sp. nov. individuals

According to the analyzed data, this study concluded that mole crabs (Genus *Emerita*) in the Cilacap coastlines consisted of two distinct sympatric species (*Emerita emeritus* and *Emerita* sp. nov.). *Emerita* sp. nov. had high haplotype diversity and was more abundant than *Emerita emeritus*. As a result, comprehensive research in terms of sampling site, number of samples, and other biological characteristics are needed to provide complete information for sympatric and taxa species of *Emerita* sp. nov.

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REFERENCES

- Abbas K, Xiaoyun Z, Weimin W. 2017. Microsatellite markers reveal genetic differentiation of Chinese dojo loach *Misgurnus anguillicaudatus* in the Yangtze River basin. *Turkish J Fish Aquat Sci* 17: 1167-1177. DOI: 10.4194/1303-2712-v17_6_10.
- Achrem M, Skuza L, Kirczuk L, Domagala J, Pilecka-Rapacz M, Czerniawski R. 2017. Assessment of genetic variability in common whitefish from the catchment area of the Oder River using microsatellite markers. *Acta Biologica* 24: 5-13. DOI: 10.18276/ab.2017.24-01.
- Adamson EAS, Hurwood DA, Mather PB. 2012. Insights into historical drainage evolution based on the phylogeography of the chevron snakehead fish (*Channa striata*) in the Mekong Basin. *Freshwater Biol* 57: 1-19. DOI: 10.1111/j.1365-2427.2012.02864.x.
- Ahyong ST, Schnabel KE, Maas EW. 2009. Anomuran phylogeny: New insights from molecular data. In: *Decapod Crustacean Phylogenetics*. CRC Press, Boca Raton. DOI: 10.13140/2.1.2705.5684.
- Aquilino SVL, Tango JM, Fontanilla IKC, Pagulayan RC, Basiao ZU, Ong PS, Quilang JP. 2011. DNA barcoding of the ichthyofauna of Taal Lake, Philippines. *Mol Ecol Resour* 11 (4): 612-619. DOI: 10.1111/j.1755-0998.2011.03000.x.
- Ariyaraphong N, Laopichienpong N, Singchat W, Panthum T, Ahmad SF, Jattawa D, Duengkhae P, Muangmai N, Suwanasopee T, Koonawootrittriron S, Srikulnath K. 2021. High-Level gene flow restricts genetic differentiation in dairy cattle populations in Thailand: Insights from large-scale Mt D-loop sequencing. *Animals* 11: 1680. DOI: 10.3390/ani11061680.
- Baisvar VS, Kumar R, Singh M, Kushwaha B. 2019. Cytochrome c oxidase i gene-based genetic divergence and molecular phylogeny among the species of fish Genus *Channa*. *Proc Nat Acad Sci India Sec B Biol Sci* 89 (4): 1455-1463. DOI: 10.1007/s40011-018-01070-w.
- Baisvar VS, Singh M, Kumar R. 2018. Population structuring of *Channa striata* from Indian waters using control region of mtDNA. *Mitochondrial DNA Part A* 30 (3): 414-423. DOI: 10.1080/24701394.2018.1532416.
- Balkhis ABS, Firdaus A, Jamsari J, Hwai TS, Yasin Z. 2011. Evidence of geographical structuring in the Malaysian Snakehead, *Channa striata*, based on a partial segment of the CO1 gene. *Genet Mol Biol* 34 (3): 520-523. DOI: 10.1590/S1415-47572011005000016.
- Bandelt HJ, Foster P, Rohl A. 1999. Median-joining networks for inferring intraspecific phylogenies. *Mol Biol Evol* 16 (1): 37-48. DOI: 10.1093/oxfordjournals.molbev.a026036.

- Barasa JE, Abila R, Grobler JP, Dangasuk OG, Njihira MN. 2014. Genetic diversity and gene flow in *Clarias gariepinus* from Lakes Victoria and Kanyaboli, Kenya. *Afr J Aquatic Sci* 39 (3): 287-293. DOI: 10.2989/16085914.2014.933734.
- Bekker EI, Karabanov DP, Galimov YR, Kotov AA. 2016. DNA barcoding reveals high cryptic diversity in the North Eurasian *Moina* species (Crustacea: Cladocera). *PLoS ONE* 11 (8): e0161737. DOI: 10.1371/journal.pone.0161737.
- Bhagawati D, Winarni ET, Nuryanto A. 2020. Molecular barcoding reveals the existence of mole crabs *Emerita emerita* in North Coast of Central Java. *Biosaintifika* 12 (1): 104-110. DOI: 10.15294/biosaintifika.v12i1.20497.
- Bhagawati D, Anggoro S, Zainuri M, Sya'rani L. 2016. Ethnotaxonomical study of mole crab (Crustacea: Hippidae) on coastal community of Cilacap. *Biosaintifika* 8 (2): 222-230. DOI: 10.15294/biosaintifika.v8i2.6491.
- Bilgin R, Utkan MA, Kalkan E, Karhan SU, Bekbolet M. 2015. DNA barcoding of twelve shrimp (Crustacea: Decapoda) from Turkish sea reveals cryptic diversity. *Mediterr Mar Sci* 16 (1): 36-45. DOI: 10.12681/mms.548.
- Boyko CB, McLaughlin PA. 2010. Annotated checklist of anomuran decapod crustaceans of the world (exclusive of the Kiwaoidea and families Chirostylidae and Galatheididae of the Galatheoidea) Part IV – Hippidae. *Raffles Bull. Biol* 23: 139-151.
- Boyko CB. 2002. A worldwide revision of the recent and fossil sand crabs of the Albuneidae Stimpson and Blepharipodidae, new family (Crustacea: Decapoda: Anomura: Hippidae). *Bull Am Museum Nat History* 272: 1-396. DOI: 10.1206/0003-0090(2002)272<0001:AWROTR>2.0.CO;2.
- Boyko CB, Harvey AW. 1999. Crustacea Decapoda: Albuneidae and Hippidae of the tropical Indo-West Pacific region, in Crosnier A. (eds.). *Résultats des Campagnes MUSORSTOM. Mémoires du Muséum National d'Histoire Naturelle* 20 (180): 379-406.
- Butet NA, Dewi IABP, Zairion, Hakim AA. 2019. Species validation of mole crabs based on molecular marker of 16s rRNA from Bantul and Purworejo waters. *J Trop Fish Manag* 3 (2): 28-35. [Indonesian]
- Candek K, Kuntner M. 2015. DNA barcoding gap: Reliable species identification over morphological and geographical scales. *Mol Ecol Resour* 15 (2): 268-277. DOI: 10.1111/1755-0998.12304.
- Chan BKK, Chen H-N, Dando PR, Southward AJ, Southward EC. 2016. Biodiversity and biogeography of Chthamalid barnacles from the North-Eastern Pacific (Crustacea Cirripedia). *PLoS ONE* 11 (3): e0149556. DOI: 10.1371/journal.pone.0149556.
- Cheng F, Zhao S, Schmidt BV, Ye L, Hallerman EM, Xie S. 2017. Morphological but no genetic differentiation among fragmented populations of *Hemiculter leucisculus* (Actinopterygii, Cyprinidae) from a lake complex in the middle Yangtze, China. *Hydrobiology* 809: 6. DOI: 10.1007/s10750-017-3464-0.
- Dahrudin H, Utama A, Busson F, Sauri S, Hanner R, Keith P, Hadiaty R, Hubert N. 2016. Revisiting the ichthyodiversity of Java and Bali through DNA barcodes: Taxonomic coverage, identification accuracy, cryptic diversity, and identification of exotic species. *Mol Ecol Resour* 17 (2): 288-299. DOI: 10.1111/1755-0998.12528.
- da Silva JM, Creer S, dos Santos A, Costa AC, Cunha MR, Costa FO, Carvalho GR. 2011. Systematic and evolutionary insights derived from mtDNA COI barcode diversity in the Decapoda (Crustacea: Malacostraca). *PLoS ONE* 6 (5): e19449. DOI: 10.1371/journal.pone.0019449.
- Desi T, Suryanti, Widayanti N. 2020. Habitat preference and abundance of mole crab based on sea tides in coastal area of Kebumen District, Aquasains 9 (1): 893-901. [Indonesian]
- Dewi WK, Suaryanti S, Purnomo PW. 2019. Habitat preferences and abundance of mole crab at spring and neap tide in coastal area of Purworejo Central Java, Indonesia. *Intl J Appl Environ Sci* 14 (4): 383-394.
- Dorn A, Ng'oma E, Janko K, Reichwald K, Polacik M, Platzer M, Cellerino A, Reichard M. 2011. Phylogeny, genetic variability and colour polymorphism of an emerging animal model: the short-lived annual *Nothobranchius* fishes from southern Mozambique. *Mol Phylogenet Evol* 61: 739-749. DOI: 10.1016/j.ympev.2011.06.010.
- Dung DT, Hop, NT, Thakham U, Waikagul J. 2013. Genetic differences among Vietnamese *Haplorchis taichui* populations using the COI genetic marker. *J Helminthol* 87: 66-70. DOI: 10.1017/S00222149X12000041.
- Elvyra R, Solihin DD, Affandi R, Junior MZ, Suhendra M. 2020. Molecular characteristics and phylogenetic relationships of silurid catfishes (*Kryptopterus*, *Ompok*, and *Phalacrognathus*) from the Kampar River, Indonesia, based on the cytochrome b gene. *Biodiversitas* 21 (8): 3539-3546. DOI: 10.13057/biodiv/d210816.
- Erlank E, Koekemoer LL, Coetzee M. 2018. The importance of morphological identification of African anopheline mosquitoes (Diptera: Culicidae) for malaria control programmes. *Malaria J* 17: 43. DOI: 10.1186/s12936-018-2189-5.
- Esa Y, Rahim KAA. 2013. Genetic structure and preliminary findings of cryptic diversity of the Malaysian mahseer (*Tor tambroides* Valenciennes: Cyprinidae) inferred from mitochondrial DNA and microsatellite analyses. *BioMed Res Intl* 2013: 170980. DOI: 10.1155/2013/170980.
- Excoffier L, Lischer HEL. 2010. Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Mol Ecol Resour* 10 (3): 564-567. DOI: 10.1111/j.1755-0998.2010.02847.x.
- Gouskov A, Reyes M, Wirthner-Bitterlin L, Vorburger C. 2016. Fish population genetic structure shaped by hydroelectric power plants in the upper Rhine catchment. *Evol Appl* 9: 394-408. DOI: 10.1111/eva.12339.
- Hall T. 2011. BioEdit: An important software for molecular biology. *GERF Bull Biosci* 2 (1): 60-61. DOI: 10.1017/S0317167100012865.
- Haig J. 1974. A review of the Australian crabs of Family Hippidae (Crustacea, Decapoda, Anomura). *Memoirs Queensland Museum* 17 (1): 175-189.
- Hanim N, Farajallah A, Putri V, Wardiatno Y, Perwitasari F, Suman A. 2017. *Emerita pangandaranensis* sp. nov., a new sand crab (Anomura, Hippidae) from the South Coast of Java, Indonesia. *Arpha Preprints*. DOI: 10.3897/arpha.preprints.e81075.
- Hartoko A, Muskananfolo MR, Latifah N, Sulardiono B, Suprpto D, Rudiyanto S. 2019. Coastal sediment and benthic crustacean *Emerita emerita*, *Albunea symmista*, *Hippa adactyla* of South Coast Central Java Indonesia. *Intl J Appl Environ Sci* 14 (5): 523-539.
- Haq M, Irmansyah, Maddu A, Riyanto B, Wardiatno Y, Zakiah AFN. 2018. Exploration of composition, elements, and microstructure of body and shell on tropical mole crab (*Emerita emerita*). *IOP Conf Ser Earth Environ Sci* 187: 012021. DOI: 10.1088/1755-1315/187/1/012021.
- Higashi R, Tsukagoshi A, Kimura H, Kato K. 2011. Male dimorphism in a new interstitial species of the genus *Microloxoconcha* (Podocopa: Ostracoda). *J Crustacean Biol* 31 (1): 142-152. DOI: 10.1651/09-3234.1.
- Hubert N, Delieu-Trottin E, Irisson JO, Meyer C, Planes S. 2010. Identifying coral reef fish larvae through DNA barcoding: A test case with the families Acanthuridae and Holocentridae. *Mol Phylogenet Evol* 55: 1195-1203. DOI: 10.1016/j.ympev.2010.02.023.
- Irmawati I, Tresnati J, Nadiarti, Fachrudin L, Arma NR. 2017. Identification of wild stock and the first generation (F1) of domesticated snakehead fish, *Channa* spp. using partial Cytochrome C Oxidase Subunit I (COI) gene. *Jurnal Iktiologi Indonesia* 17 (2): 165-173. DOI: 10.32491/jii.v17i2.356. [Indonesia]
- Jeffery NW, Elias-Gutierrez M, Adamowicz SJ. 2011. Species diversity and phylogeographical affinities of the Branchiopoda (Crustacea) of Churchill, Manitoba, Canada. *PLoS ONE* 6 (5): e18364. DOI: 10.1371/journal.pone.0018364.
- Jong MA, de Wahlberg N, van Eijk M, Brakefield PM, Zwaan BJ. 2011. Mitochondrial DNA signature for range-wide populations of *Bicyclus anynana* suggests a rapid expansion from recent refugia. *PLoS ONE* 6 (6): e21385. DOI: 10.1371/journal.pone.0021385.
- Karanovic I. 2015. Barcoding of ancient lake Ostracods (Crustacea) reveals cryptic speciation with extremely low distances. *PLoS ONE* 10 (3): e0121133. DOI: 10.1371/journal.pone.0121133.
- Kazmi QB, Siddiqui FA. 2006. An illustrated key to the Malacostraca (Crustacea) of northern Arabian Sea Part VI: Decapoda Anomura. *Pakistan J Mar Sci* 15 (1): 11-79.
- Ko H-L, Wang Y-T, Chiu T-S, Lee M-A, Leu M-Y, Chang K-Z, Chen W-Y, Shao K-T. 2013. Evaluating the accuracy of morphological identification of larval fishes by applying DNA barcoding. *PLoS ONE* 8 (1): e53451. DOI: 10.1371/journal.pone.0053451.
- Korovchinsky NM. 2019. Morphological assessment of the North Eurasian interspecific hybrid forms of the genus *Bythotrephes* Leydig, 1860 (Crustacea: Cladocera: Cercopagididae). *Zootaxa* 4550 (3): 340-356. DOI: 10.11646/zootaxa.4550.3.3.
- Krisanti M, Ramadhan BF, Mashar A, Butet NA, Hakim AA, Wardiatno Y. 2020. Mole crab phylogenetics relationship analysis in

- Parangkusumo and Ketawang Beach Waters. IOP Conf Seri Earth Environ Sci 420: 012018. DOI: 10.1088/1755-1315/420/1/012018.
- Kusbiyanto, Bhagawati D, Nuryanto A. 2020. DNA barcoding of crustacean larvae in Segara Anakan, Cilacap, Central Java, Indonesia using cytochrome c oxidase gene. Biodiversitas 21 (10): 4878-4887. DOI: 10.13057/biodiv/d211054.
- Lau J-S, Ransangan J, Rodrigues KF. 2018. Genetic diversity and population structure of the Asian green mussel (*Perna viridis*) in the waters of Sabah, Malaysia, based on mitochondrial DNA D-Loop sequences. Turkish J Fish Aquatic Sci 18: 109-117. DOI: 10.4194/1303-2712-v18_1_12.
- Liu J, Ding X, Zeng Y, Yue Y, Guo X, Guo T, Chu M, Wang F, Han J, Feng R, Sun X, Niu C, Yang B, Guo J, Yuan C. 2016. Genetic diversity and phylogenetic evolution of Tibetan sheep based on mtDNA D-Loop sequences. PLoS ONE 11 (17): e0159308. DOI: 10.1371/journal.pone.0159308.
- Mahapatro D, Karna SK, Mohanty SK, Mohanty B, Muduli PR, Pattnaik AK, Nanda S. 2018. First record of a burrowing mole crab *Emerita emerita* (Decapoda: Anomura: Hippidae) from Chilika Lake, East coast of India. Indian J Geo-Mar Sci 47: 109-113.
- Mauroka N, Ohtsuki H, Makino W, Urabe J. 2018. Rediscovery after almost 120 years: Morphological and genetic evidence supporting the validity of *Daphnia mitsukurii* (Crustacea: Cladocera). Zool Sci 35 (5): 468-475. DOI: 10.2108/zs170081.
- Mohammed MA, Nuryanto A, Kusmintarsih ES. 2021. Genetic differentiation of dengue vector *Aedes aegypti* in the small geographical scale of Banyumas District, Indonesia, based on Cytochrome Oxidase I. Biodiversitas 22 (2): 675-683. DOI: 10.13057/biodiv/d220219.
- Muchlisin ZA, Thomy Z, Fadli N, Sarong MA, Siti-Azizah MN. 2013. DNA barcoding of freshwater fishes from Lake Laut Tawar, Aceh Province, Indonesia. Acta Ichthyologica et Piscatoria 43 (1): 21-29. DOI: 10.3750/AIP.2013.43.1.04.
- Ng PKL. 1998 Crabs. In: Carpenter KE, Niem VH (eds.). FAO species identification guide for fishery purposes. The living marine resources of the Western Central Pacific. Cephalopods, crustaceans, holothurians, and sharks. Rome, FAO.
- Nugroho S, Suryanti S, Rudyanti S. 2018. Distribution pattern of mole crab (Hippidae) based on the substrat's salinity in Pagak Beach, Ngombol Sub-district, Purworejo District, Central Java. Indonesian J Fish Sci Technol 14 (1): 16-22. DOI: 10.14710/ijfst.14.1.16-22. [Indonesia]
- Nuryanto A, Bhagawati A, Rukayah S, Rahayu DRUS, Wibowo DN. 2020. Molecular barcoding reveals possible existence of sympatric species of *Emerita emerita* in south coast of Cilacap Central Java. IOP Conf Ser Earth Environ Sci 593: 012014. DOI: 10.1088/1755-1315/593/1/012014.
- Nuryanto A, Komalawati N, Sugiharto. 2019. Genetic diversity assessment of *Hemibagrus nemurus* from rivers in Java Island, Indonesia using COI gene. Biodiversitas 20 (9): 2707-2717. DOI: 10.13057/biodiv/d200936.
- Nuryanto A, Pramono H, Sastranegara MH. 2017. Molecular identification of fish larvae from East Plawangan of Segara Anakan, Cilacap, Central Java, Indonesia. Biosaintifika 9 (1): 33-40. DOI: 10.15294/biosaintifika.v9i1.9191.
- Osawa M, Boyko CB, Chan T Y. 2010. Part I Hiipoidea (mole crabs). In: Chan TY (eds.). Crustacean fauna of Taiwan: Crab-like Anomurans (Hippoidea, Lithodoidea, and Porcellanidae). National Taiwan University, Keelung, Taiwan.
- Palecanda S, Feller KD, Porter ML. 2020. Using larval barcoding to estimate stomatopod species richness at Lizard Island, Australia, for conservation monitoring. Sci Rep 10: 10990. DOI: 10.1038/s41598020-67696-x.
- Palero F, Genis-Armero R, Hall MR, Clark PF. 2016. DNA barcoding the phyllosoma of *Scyllarides squammosus* (H. Milne Edwards, 1837) (Decapoda: Achelata: Scyllaridae). Zootaxa 4139 (4): 481- 498. DOI: 10.11646/zootaxa.4139.4.2.
- Parmaksiz A. 2019. Population genetic diversity of yellow barbell (*Carasobarbus luteus*) from Kueik, Euphrates, and Tigris Rivers based on mitochondrial DNA D-loop sequences. Turkish J Fish Aquatic Sci 20 (1): 79-86.
- Parmaksiz A, Eksi E. 2017. Genetic diversity of the cyprinid fish *Capoeta trutta* (Heckel, 1843) populations from Euphrates and Tigris rivers in Turkey based on mtDNA COI sequences. Indian J Fish 64 (1): 18-22. DOI: 10.21077/ijf.2017.64.1.62396-03.
- Pavesi L, De Mattheis E, Tiedemann R, Ket maier V. 2011. Temporal population genetics and COI phylogeography of the sandhopper *Macrorchestia remyi* (Amphipoda: Talitridae). Zool Stud 50 (2): 220-229.
- Poore G. 2004. Marine Decapod Crustacea of Southern Australia: A Guide to Identification. CSIRO Publishing, Australia.
- Pramithasari FA, Butet NA, Wardiatno Y. 2017. Variation in morphometric characters in four sand crab (*Albunea symmista*) populations collected from Sumatra and Java Island, Indonesia. Trop Life Sci Res 28 (1): 103-115. DOI: 10.21315/tlsr2017.28.1.7.
- Pramono TB, Arfiati D, Widodo MS, Yanuhar U. 2017. Identifikasi ikan Genus *Mystus* dengan pendekatan genetik. Jurnal Sumberdaya Akuatik Indopasifik 1 (2): 123-132. DOI: 10.30862/jsai-fpik-unipa.2017.Vol.1.No.2.34. [Indonesia]
- Riani S, Prabowo RE, Nuryanto A. 2021. Molecular characteristics and taxonomic status of morphologically similar barnacles (*Amphibalanus*) assessed using the cytochrome c oxidase 1 gene. Biodiversitas 22 (3): 1456-1466. DOI: 10.13057/biodiv/d220349.
- Rozas J, Ferrer-Mata A, Sanchez-DelBarrio JC, Guirao-Rico S, Librado P, Ramos-Osins SE, Sanchez-Gracia A. 2017. DnaSP 6: DNA sequence polymorphism analysis of large data sets. Mol Biol Evol 34 (12): 3299-3302. DOI: 10.1093/molbev/msx248.
- Sachithanandam V, Mohan PM, Muruganandam N, Chaaithanya IK, Dhivya P, Baskaaran R. 2012. DNA barcoding, phylogenetic study of *Epinephelus* spp. from Andaman coastal region, India. Indian J Geo-Mar Sci 41 (4): 203-211.
- Sankolli KN. 1965. On a new species of *Emerita* (Decapoda, Anomura) from India, with a note on *Emerita Emeritus* (L.). Crustaceana 8: 48-54. DOI: 10.1163/156854065X00541.
- Schnabel KE, Ahlyong ST. 2010. A new classification of the Chirostyloidea (Crustacea: Decapoda: Anomura). Zootaxa 2687: 56-64. DOI: 10.11646/zootaxa.2687.1.4.
- Setyaningrum N, Lestari W, Krismono, Nuryanto A. 2022. Genetically continuous populations of Striped Snakehead (*Channa striata*) in the Cingcingguling River fragmented by Sempor Reservoir, Central Java, Indonesia. Biodiversitas 23 (1): 222-230. DOI: 10.13057/biodiv/d230128.
- Shu Q-H, Li S-D, Tian M, Meng Y, He S-M-Q, Zhu M, Wang M-M, Wang W-L. 2022. Morphological and molecular characterization of *Paragonimus skrjabini* complex from Yunnan, China: A brief report. Acta Parasitologica 67: 316-321. DOI: 10.1007/s11686-021-00461-w.
- Song LM, Munian K, Rashid ZA, Bhassu S. 2013. Characterisation of Asian snakehead murrel *Channa striata* (Channidae) in Malaysia: An insight into molecular data and morphological approach. Sci World J 2013: 917506. DOI: 10.1155/2013/917506.
- Syaifudin M, Wijayanti M, Dwinanti SH, Muslim, Mahendra M, Marlina S. 2020. DNA barcodes and phylogenetic of striped snakehead and ocellated snakehead fish from South Sumatra, Indonesia. Biodiversitas 21 (3): 1227-1235. DOI: 10.13057/biodiv/d210350.
- Tajima F. 1989. Statistical method for testing then mutation hypothesis by DNA polymorphism. Genetics 123: 585-595. DOI: 10.1093/genetics/123.3.585.
- Triantafyllidis A, Bobori D, Koliamitra C, Gbandi E, Mpanti M, Petriki O, Karaiskou N. 2011. DNA barcoding analysis of fish species diversity in four north Greek lakes. Mitochondrial DNA 22 (SUPPL. 1): 37-42. DOI: 10.3109/19401736.2010.542242.
- Ward RD, Zemlak TS, Innes BH, Last PR, Hebert PDN. 2005. DNA barcoding Australia's fish species. Philos Trans R Soc Lond B Biol Sci 360 (1462): 1847-1857. DOI: 10.1098/rstb.2005.1716.
- Wardiatno Y, Ardika PU, Farajallah A, Butet NA, Mashar A, Kamal MM, Renjana EA. 2015. Biodiversity of Indonesian sand crabs (Crustacea, Anomura, Hippidae) and assessment of their phylogenetic relationships. AACL Bioflux 8 (2): 224-235.
- Weis M, Macher JN, Seefeldt MA, Leese F. 2014. Molecular evidence for further overlooked species within the *Gammarus fossarum* complex (Crustacea: Amphipoda). Hydrobiol 721 (1): 165-184. DOI: 10.1007/s10750-013-1658-7.
- Winarni ET, Kusbiyanto, Nuryanto A. 2021. Estimating crustacean species utilize Segara Anakan Estuary Cilacap, Indonesia, as nursery ground through DNA barcoding. J Hunan Univ Nat Sci 48 (10): 275-282.
- Zhang W, Jiang S, Salumy KR, Xuan Z, Xiong Y, Jin S, Gong Y, Wu Y, Qiao H, Fu H. 2022. Comparison of genetic diversity and population structure of eight *Macrobrachium nipponense* populations in China

- based on D-loop sequences. Aquaculture Rep 23: 101086. DOI: 10.1016/j.aqrep.2022.101086.
- Zhang G-H, Yuan Z-J, Zhang C-X, Yin K-S, Tang M-J, Guo H-W, Fu J-Y, Xiao Q. 2014. Detecting deep divergence in seventeen populations of tea geometrid (*Ectopis obliqua* Prout) in China by COI mtDNA and cross-breeding. PLoS ONE 9 (6): e99373. DOI: 10.1371/journal.pone.0099373.
- Zhong L, Song C, Wang M, Chen Y, Qin Q, Pan J, Chen X. 2013. Genetic diversity and population structure of yellow catfish *Pelteobagrus fulvidraco* from five lakes in the middle and lower reaches of the Yangtze River, China, based on mitochondrial DNA control region. Mitochondrial DNA 24 (5): 552-558. DOI: 10.3109/19401736.2013.770491.