



NOTE

New sightings reported in western Indonesia and a preliminary study of *Hippa ovalis* distribution in Indonesian waters

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ABSTRACT: Species distribution data is essential to understand the patterns of biodiversity, determine areas for conservation, and measure the impact of habitat loss and climate change. In this study, we reported a preliminary study about the distribution pattern of a Hippidae family member, *Hippa ovalis*. A few reports about *H. ovalis* in Indonesia have been found, but their distribution patterns remain unknown. The samples were collected from 2018 to 2021; 10 specimens were collected from western and eastern Indonesia. The specimens were identified using morphological and molecular (the COI gene) tools. Our samples primarily included *H. ovalis*. Gene tree and genetic distance were used to determine the distribution pattern of *H. ovalis* and to analyze its haplotype network. We found seven haplotypes of *H. ovalis* among our samples, three shared and four unique. Genetic similarity shows that the western and eastern populations have a close relationship, and we hypothesize that no or minimum barrier can be found among the populations. Furthermore, this widespread dispersal of *H. ovalis* is probably due to pelagic larval duration and ocean current, particularly the Indonesian Through Flow.

KEY WORDS: Distribution pattern, mole crab, new report, Wallacea.

INTRODUCTION

Species distribution data is essential for understanding biodiversity patterns, determining conservation priority areas, and measuring the impact of habitat loss and climate change (Zhao *et al.*, 2020). The distribution of species is influenced by several factors, including the environmental barrier. Considering that the environmental barrier in the marine realm is weaker than that in the terrestrial realm (Myers, 1997), animals that inhabit the marine realm can disperse to a wider area than those that inhabit the land. This phenomenon affects the distribution pattern of marine organisms. One marine organism that lacks distributional data is the hippoid crab (*Hippa ovalis*). This taxon has two life phases: pelagic larva (juvenile phase) and benthos (adult phase), which could affect their dispersal ability, affecting their distribution pattern.

Species of Superfamily Hippoidea is predominantly distributed on tropical beaches (Boyko and Harvey, 1999), although some could also be found on subtropical beaches (Ríos-Elósegui and Hendrickx, 2014). In general, the distribution pattern of these organism are limited to the sandy beaches of coastal areas (Subramoniam and Gunamalai, 2003). Although their presence is well known in Indonesia among the locals, studies on sand crabs are still lacking (Wardiatno *et al.*, 2015). Kumar *et al.*, (2018) indicated that the ability of species from the superfamily Hippoidea to adapt to and burrow in sand habitat leads to their limited collection and distribution records.

Superfamily Hippoidea in Indonesia has two families: Hippidae and Albuneidae. The members of the Hippidae family in Indonesia include the species of the genera

Hippa (Fabricius, 1787) and *Emerita* (Scopoli, 1777; Ardika *et al.*, 2015). *Hippa ovalis*, found in Indonesia, belongs to the family Hippidae. This species is previously known as *Recipes ovalis* (Milne-Edwards, 1862) or *Recipes celebensis* (Thallwitz, 1891). The original distribution of *H. ovalis* spans from the eastern coast of Africa (Réunion Island), where its type locality is contained (Milne-Edwards, 1862), to Papua New Guinea (Boyko and McLaughlin, 2010). This species can also be found in Timor (De Man, 1895-1898), Taiwan (Osawa *et al.*, 2010). In Indonesia, *H. ovalis* is only reported in the eastern and central parts of Indonesia, namely, Sulawesi (Thallwitz, 1891; Wardiatno *et al.*, 2015), Maluku Islands (De Man, 1895-1898, Br Silaban *et al.*, 2020), Bali, (Wardiatno *et al.*, 2015) and the southern coast of Java (Darusman *et al.*, 2015). There is a limited research publication regarding the distribution of *H. ovalis* on the western side of Indonesia. Since this species is known to have a wider distribution from the eastern coast of Africa (Indian Ocean) and Papua New Guinea (Pacific Ocean), the earlier known limited distribution along the Indonesian coast was questionable. Thus, this study aims to update a new distribution note in the western part of Indonesia, which expands the currently known distribution of *H. ovalis* in Indonesia.

METHODS

Sample Collection and Identification

Sample collection was conducted in 2018–2021 (Table 1; Fig. 1), containing ten specimens. The specimens were deposited in the Animal Physiology and

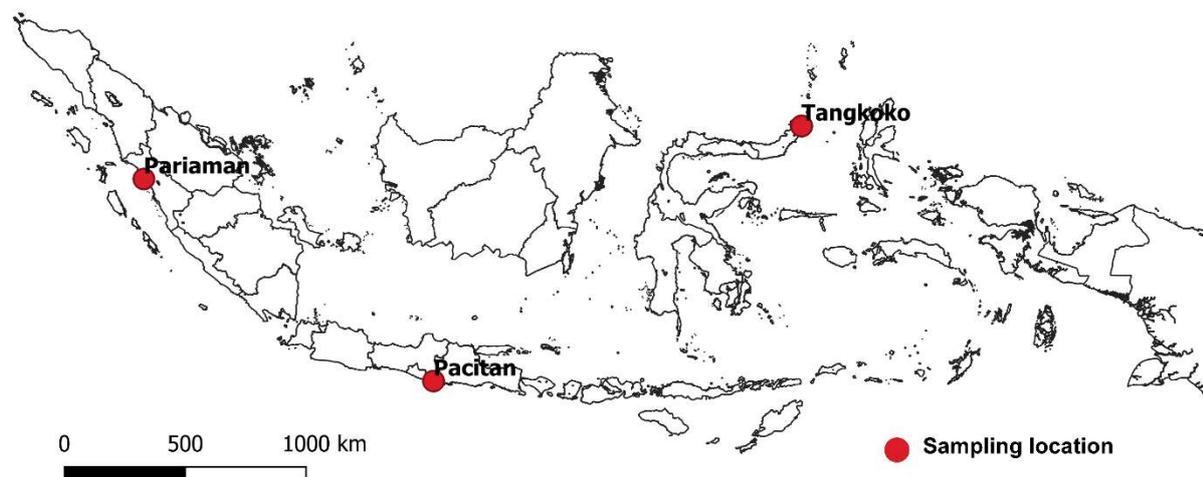


Fig 1. Sampling location of *Hippa ovalis* in Indonesia

Table 1. *Hippa ovalis* sampling location on the Indonesian water in this study.

No.	Date	Location	Total samples
1	May 2018	Pariaman, West Sumatra	3
2	February 2020	Tangkoko, North Sulawesi	5
3	January 2021	Pacitan, East Java	2

Table 2. Sequences of *Hippa ovalis* for data analysis

No	Sequence name	Accession No.	References
1	Pariaman 2	ON306443	This study
2	Pariaman 5	ON306442	
3	Pariaman 6	ON306441	
4	Pacitan 2	ON306440	
5	Pacitan 6	ON306439	
6	Tangkoko 1	ON306438	
7	Tangkoko 2	ON306437	
8	Tangkoko 3	ON306436	
9	Tangkoko 4	ON306435	
10	Tangkoko 5	ON306434	
11	voucher MZB Cru 4118_Bali	KR046034.1	Wardiatno <i>et al.</i> , 2015
12	isolate 7_Cilacap	MG930988.1	Bhagawati, published on Genbank

Behavior Lab at the Department of Biology, IPB University. The specimens were photographed using a Nikon Coolpix B700 camera and then drawn on a HUION Canvas Pro 13 tablet. In addition, the specimens were identified based on their morphological traits and compared with the identification keys established by Boyko and Harvey (1999) and Osawa *et al.*, (2010). The characters, such as carapace length and width, are measured using a caliper. We also used a short fragment of the COI gene as a molecular marker to confirm the morphological identification results. The short fragment of the COI gene can identify an organism up to species level. This method is known as DNA barcoding (Hebert *et al.*, 2003).

DNA Extraction, Amplification, and Sequencing

The genomic DNA from telson muscle tissues was

extracted using the DNA extraction kit GENE AID Genomic DNA Mini Kit (Tissue), following the manufacturer's protocol. The upper part of the COI gene fragment near the 5' end was amplified in vitro using polymerase chain reaction (PCR) with a Biometra Thermal Cycler. The COI gene fragment was amplified using the primers under PCR following Wardiatno *et al.*, (2015). The amplicons obtained from PCR were then sent to commercial sequencing facilities to be sequenced using the Sanger method with Applied Biosystem Big Dye® terminator kit v.3.1.

Data Analysis

For data analysis, we used the data set shown in Table 2. The genetic diversity in this study was calculated based on nucleotide variation and haplotype diversity using DNASP 5 (Librado and Rozas 2009). The distribution pattern was observed using the haplotype relationship network (Bandelt *et al.*, 1999). The genetic distance was determined by applying the pairwise distance method with a Kimura-2 parameter model using MEGA 7 to determine the proximity of the haplotype (Kumar *et al.*, 2016).

RESULTS

Morphological characteristics of *Hippa ovalis*

Systematics (Boyko and Harvey 1999):
 Infraorder ANOMURA Macleay 1838;
 Family HIPPIDAE Stimpson 1858;
 Genus *Hippa* Fabricius 1787;
Hippa ovalis Milne Edwards 1862

Based on the morphological traits, we confirmed that our specimens are *H. ovalis* (Fig. 2). Key diagnostics features are: the frontal margin of the carapace has two lobes, which are usually separated by a low rounded lobe; the submarginal of the carapace has 40–55 setose pit rows;

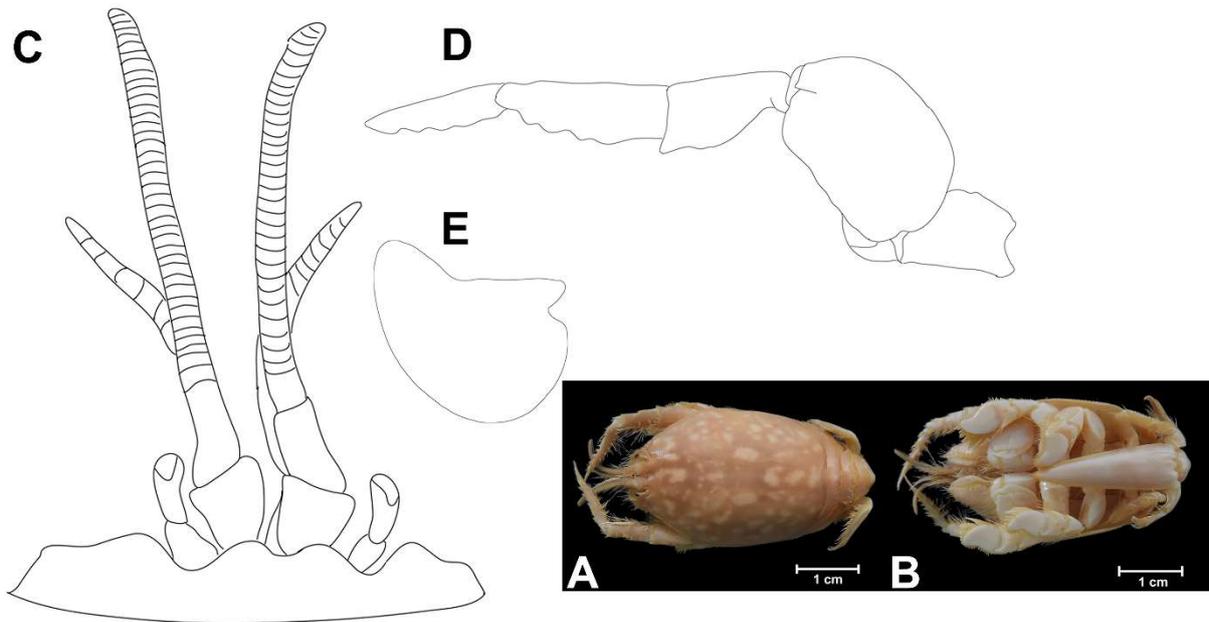


Fig 2. Morphological characteristic of *Hippa ovalis*, **A.** dorsal view, **B.** ventral view, **C.** Frontal carapace margin, **D.** First pereiopod, **E.** Dactylus of the second pereiopod.

Table 3. Measurement of *Hippa ovalis* carapace.

No Specimens	Sex	Carapace	
		width (mm)	length (mm)
1	Tangkoko 1 male	22.125	26.000
2	Tangkoko 2 male	20.250	25.075
3	Tangkoko 3 male	17.325	21.250
4	Tangkoko 4 ovigerous female	24.075	30.050
5	Tangkoko 5 ovigerous female	24.450	32.450
6	Pacitan 2 ovigerous female	27.180	33.530
7	Pacitan 6 male	18.740	23.970
8	Pariaman 2 non-ovigerous female	24.250	29.275
9	Pariaman 5 non-ovigerous female	20.450	26.000
10	Pariaman 6 non-ovigerous female	23.000	28.150

the flagellum of the antenna consists of two pairs, a pair above and a pair below, which was shorter; the flagellum of the antenna is composed of three articles; the dactyl of pereiopod I have a subcylindrical shape, and the dactyl of pereiopod II has a slightly concave margin (Fig. 2C-E). The carapace length and width of our *Hippa ovalis* specimens are presented in Table 3.

Haplotype and its Relationship Network

The obtained COI fragment of *H. ovalis* was 590 bp long. In these gene fragments, we found seven clustered haplotypes of Indonesian *H. ovalis* with a haplotype diversity value (H_d) of 0.894, which indicates high genetic diversity. Then, we drew the relationship of these haplotypes (Fig. 3). Three shared haplotypes are identified: H-1, which is shared between Tangkoko (Sulawesi) and Pariaman (Sumatra); H-4, which is shared

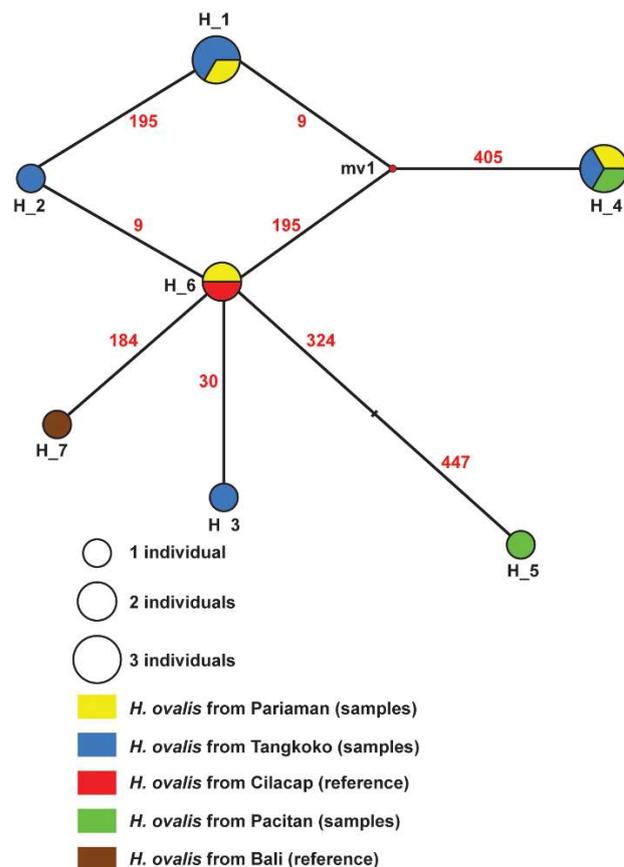


Fig 3. Haplotype network of *Hippa ovalis* from Indonesia.

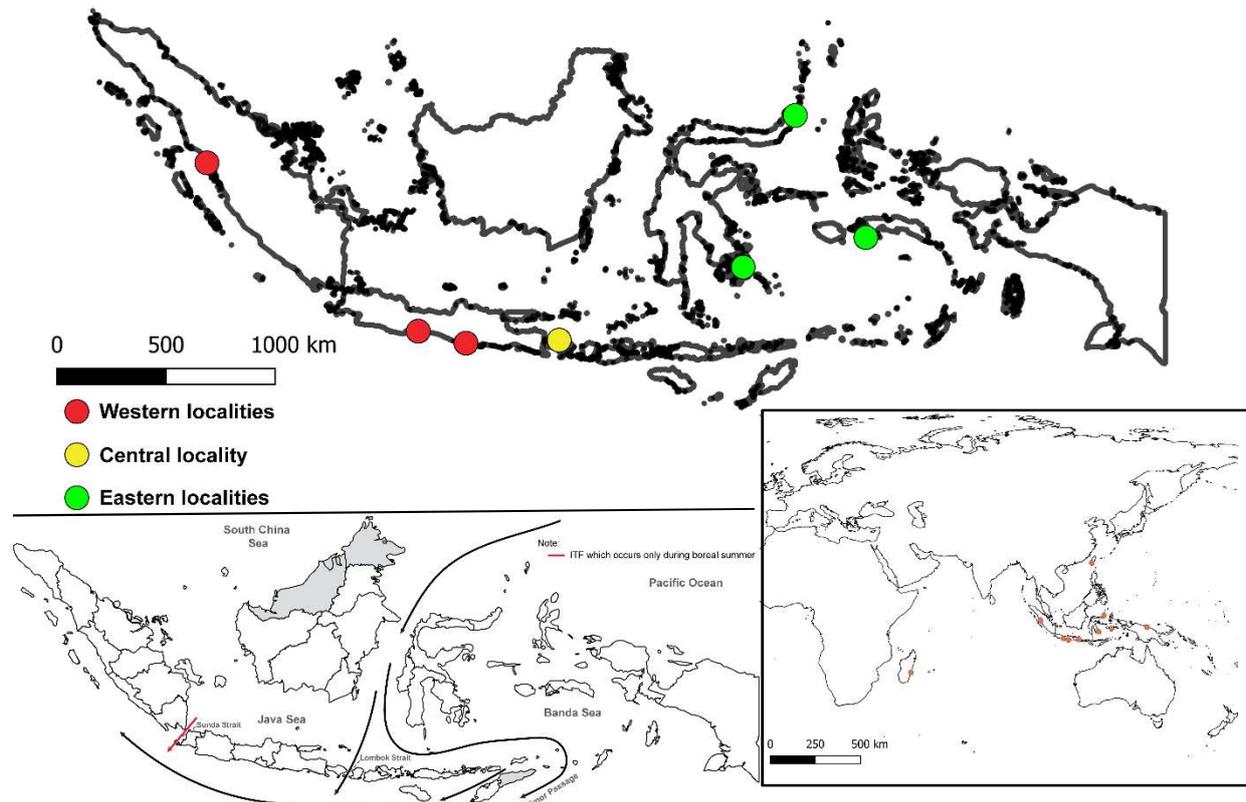


Fig. 4. The distribution of *Hippa ovalis* **A.** In Indonesia. **B.** Global distribution. **C.** Indonesian Throughflow (reproduced based on Makarim *et al.*, 2019).

by Tangkoko (Sulawesi), Pariaman (Sumatra), and Pacitan (Java); and H-6, which is shared between Cilacap (Java) and Pariaman (Sumatra). H-4 has a high frequency, shared by three samples from three distant locations. H-4 is connected to five out of eight connections, represented by a black bar (Fig. 3). The other haplotypes, such as H-2, H-3, H-5, and H-7, are unique to each of their locations.

The genetic distance results (ranging between 0.000 and 0.007) indicated that all samples were almost genetically identical. The genetic similarity indicated that gene flows could be found between the western and eastern populations. We hypothesized that no or minimum biogeographical barrier could be found in *H. ovalis* distribution along the Indonesian coast.

DISCUSSION

The 10 mole crab specimens used in this study were confirmed to be *H. ovalis* based on morphological characteristics and molecular data. In this study, we recorded a new finding about the distribution area of *H. ovalis*, Pariaman (Sumatra Island) and Pacitan (Java Island) in West Indonesia. This finding enriches the former information on the distribution area of *H. ovalis*, which was previously recorded only in East and Central Indonesia (Wardiatno *et al.*, 2015) (Fig. 4A).

We found seven haplotypes of *H. ovalis* in Indonesia,

three of which are shared, and four are unique to their locations. The haplotypes H-1, H-4, and H-6 of *H. ovalis* are shared between West and East Indonesia. In addition, the species' genetic distance and gene tree topology show a close relationship among these three locations. This relationship indicates that the environmental barrier of *H. ovalis* is minimal. The connectivity between the eastern and western populations of *H. ovalis* in Indonesia was surprising, as the Indonesian Archipelago is a significant biogeographically barrier between the Indian and Pacific Oceans, which is known as marine Wallace's Line (Barber *et al.*, 2000). We hypothesized that this connectivity might be due to its pelagic larva duration of hippoid crab and Indonesian ocean current.

The pelagic larva enables the species to move up to thousands of kilometers in the sea (Scheltema, 1986). Thus, the pelagic larva of *Hippa* may disperse among various places in Indonesia by drifting with the ocean current. We also hypothesized that the pelagic larval duration (PLD) of the *Hippa* life phase promotes the wide distribution of this species. The PLD of the *Hippa* genus lasts for about 59–82 days (Hanson, 1969). Larval duration could be used to measure the dispersal potential of benthic organisms (Weersing and Toonen, 2009).

Ocean currents can also affect the direction of larvae dispersal (Sanvicente-Añorve *et al.*, 2018). The Indonesian Throughflow Water (ITF) is the primary



current in Indonesia which flows from the Pacific Ocean to the Indian Ocean (Gordon, 2005; Sprintall *et al.*, 2009). The Pacific Ocean waters enter Indonesia primarily through the Makassar Strait, with minor contributions through the Lifamatola Strait, the South China Sea, and the Karimata Strait. Most Pacific Ocean waters reach the Indian Ocean through the Lombok, Ombai, and Timor Straits, and some exit through the Sunda Strait in summer. Recently, the ITF has been found to reach Sumatra (Fig. 4C) (Makarim *et al.*, 2019).

We hypothesized that the shared haplotype among the populations from Pariaman, Pacitan, and Tangkoko in H-4 and Pariaman and Tangkoko in H-1 occurs because of the ITF. The haplotype H-6 shared between Pariaman and Cilacap also occurs possibly because of the ITF, which can reach Sumatra directly from the south of Java during the summer boreal monsoon. Our results showed that *H. ovalis* from Indonesia could be panmictic, which implies the absence of restrictions or barriers; therefore, there are gene flows which connecting all populations. This result shows a current connection between West and East Indonesia. We expect the ITF could be a facilitating factor of *H. ovalis* dispersal, as it connects several places within this species distribution range, such as Taiwan (the South China Sea), Indonesia, Papua New Guinea (the Pacific Ocean), and East Africa (the Indian Ocean) (Fig. 4B). Further research is necessary to study the global distribution of *H. ovalis* using more samples and to involve more expansive study areas.

From this study, we hypothesized that *Hippa ovalis* in Indonesia have a wider distribution area than previously thought. This species is found in western and eastern Indonesia beyond Wallace's Line. This broad distribution ability can be attributed due to the species' pelagic larval duration and the Indonesian Throughflow.

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