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Taxonomic identification of *Valanga* sp. from Cilacap, Central Java (Orthoptera: Acrididae) based on morphometric and DNA barcoding analyses

Original Article

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Abstract:

Valanga is a genus of the Orthoptera: Acrididae, widely distributed across Southeast Asia and the Pacific región. In Indonesia, *Valanga* spp. has been traditionally recognized as the dominant species, yet morphological overlap with other congeners complicates species-level identification. This study employed an integrative taxonomic approach combining morphometric analysis and COI-based DNA barcoding to identify *Valanga irregularis* specimens collected from Cilacap, Central Java. Specimens were collected manually and preserved in 95% ethanol for morphological and molecular analyses. Morphometric data were obtained from key body traits using digital calipers, while DNA was extracted from leg muscle tissue, amplified with universal COI primers, and sequenced by Sanger sequencing. Results revealed pronounced sexual size dimorphism, with females significantly larger and more variable across nearly all measured traits than males. Morphological features such as large body size, shorter antennae relative to body length, and distinct femoral markings were consistent with descriptions of the genus *Valanga*. However, BLAST analysis of COI sequences showed 99.54% similarity with *V. irregularis* from Queensland, Australia, rather than with *V. nigricornis*. Phylogenetic reconstruction using the Maximum Likelihood method (K2P model) confirmed a strongly supported monophyletic clade (>95% bootstrap) between the Cilacap specimens and *V. irregularis*. These findings provide the first molecular evidence of *V. irregularis* in Indonesia, highlighting the importance of combining morphological and molecular approaches to resolve taxonomic ambiguities. The results also expand knowledge on the potential genetic variation and distribution of *Valanga* spp., with implications for biodiversity monitoring and pest management in agricultural systems.

Key words:
Valanga irregularis, sexual size dimorphism, COI gene, morphometrics, phylogenetics

Apstrakt:

Taksonomska identifikacija vrste *Valanga* sp. iz Čilakapa, Centralna Java (Orthoptera: Acrididae) zasnovana na morfometrijskim i DNK barkoding analizama

Valanga je rod iz reda Orthoptera: Acrididae, široko rasprostranjen u jugoistočnoj Aziji i Pacifičkom regionu. U Indoneziji je rod *Valanga* tradicionalno prepoznat kao dominantna vrsta, ali se zbog morfološkog preklapanja sa drugim srodnim vrstama otežava identifikacija na nivou vrste. Ova studija primenila je integrativni taksonomski pristup koji kombinuje morfometrijsku analizu i COI-bazirano DNA barkodovanje kako bi se identifikovali uzorci *Valanga irregularis* sakupljeni u Čilakapu, Centralna Java. Uzorci su prikupljeni ručno i konzervisani u 95% etanolu za morfološke i molekularne analize. Morfometrijski podaci dobijeni su merenjem ključnih telesnih karakteristika pomoću digitalnog šestara, dok je DNK ekstrahovana iz mišićnog tkiva noge, amplifikovana univerzalnim COI prajmerima i sekvencirana Sangerovom metodom. Rezultati su pokazali izražen polni dimorfizam u veličini, pri čemu su ženke bile značajno veće i varijabilnije u gotovo svim merenim osobinama u poređenju sa mužjacima. Morfološke karakteristike kao što su velika telesna veličina, kraće antene u odnosu na dužinu tela i karakteristične oznake na butinama bile su u skladu sa opisima roda *Valanga*. Međutim, BLAST analiza COI sekvenci pokazala je 99,54% sličnosti sa vrstom *V. irregularis* iz Kvinslenda (Australija), a ne sa *V. nigricornis*. Filogenetska rekonstrukcija primenom metode maksimalne verodostojnosti (K2P model) potvrdila je jasno podržanu monofiletsku kladu (>95% bootstrap) između uzoraka iz Čilakapa i *V. irregularis*.Ovi nalazi predstavljaju prvi molekularni dokaz o prisustvu vrste *V. irregularis* u Indoneziji i naglašavaju značaj kombinovanja morfoloških i molekularnih pristupa u rešavanju taksonomskih nejasnoća. Rezultati takođe doprinose boljem razumevanju potencijalne genetičke varijabilnosti i rasprostranjenosti vrsta roda *Valanga*, sa implikacijama za praćenje biodiverziteta i upravljanje štetočinama u poljoprivrednim sistemima.

Ključne reči:
Valanga irregularis, polni dimorfizam u veličini, COI gen, morfometrija, filogenetika

Introduction

The genus *Valanga* (Orthoptera: Acrididae) is widely distributed across Southeast Asia and the Pacific Islands, including Indonesia, Malaysia, Singapore, the Philippines, as well as parts of southern Thailand, Cambodia, and Vietnam (Hochkirch et al., 2018). On the island of Java, grasshoppers are found in nearly all regions, particularly in the teak forests of Central and East Java. Since the Dutch colonial era, there have been numerous reports of grasshopper outbreaks that caused significant agricultural losses in Cilacap and surrounding areas over many years (Aji, 2023).

In Indonesia, the wood grasshopper, commonly recognized as *Valanga nigricornis*, is the most frequently encountered species, documented in forests of Java, Sumatra, Kalimantan, and extending to the Malay Peninsula (Asmaliyah et al., 2019). In contrast, *Valanga irregularis*, a giant grasshopper native to the tropical and subtropical regions of Australia (Australian Government, 2019; Bussiness Queensland, 2022), has never been reported from the Indonesian archipelago. However, these two species exhibit considerable morphological similarities that often lead to taxonomic misidentification, particularly in the absence of molecular data (Anonymous, 2016; Direktorat Jenderal Perkebunan, 2021).

Traditional taxonomy, which relies solely on external morphological traits, is often constrained by intraspecific variation and sexual dimorphism (Mohr et al., 2024). These factors make species recognition within closely related taxa particularly challenging. Consequently, molecular analysis has emerged as a reliable complementary tool. DNA barcoding, particularly targeting the mitochondrial cytochrome c oxidase subunit I (COI) gene, has proven effective for accurate species identification across a wide range of animal taxa (Odah, 2023; Alam et al., 2024).

As demonstrated by Hebert et al. (2003) and standardized by Folmer et al. (1994), the COI gene has become the universal molecular marker for distinguishing species. Within Orthoptera, DNA barcoding has successfully clarified taxonomic ambiguities, revealed cryptic species, and supported biodiversity assessments (Ragazzini et al., 2025). Nevertheless, the application of molecular taxonomy in *Valanga* spp. from Indonesia remains limited. At present, only a few *Valanga* COI sequences from Indonesia are available in public databases, thereby restricting regional comparative studies and efforts to document species distribution.

Cilacap, located in southern Central Java, has a long history of grasshopper outbreaks dating back to the colonial era. Yet, scientific studies integrating both morphological and molecular data on local grasshopper populations remain scarce. This lack of baseline data poses significant challenges for both pest management and ecological studies. In addition, *Valanga* spp., particularly *V. nigricornis*, have been traditionally used as food in several regions of Indonesia. Grasshoppers are consumed fried as local snacks and even processed into flour for food fortification. This demonstrates that the species is not only ecologically important, but also carries notable socio-economic value (Iwansyah et al., 2024; Sarjan et al., 2021).

Given the limitations of morphology-based identification and the ecological as well as socio-economic significance of this species, the present study combines morphometric and COI-based DNA barcoding analyses to identify *Valanga* specimens collected in Cilacap, Central Java. Furthermore, this study was conducted as a preliminary step for subsequent research focusing on utilization of *Valanga* exoskeletons as a natural source of chitin. Accurate species identification is essential prior to biochemical extraction processes, as chitin content and structural characteristics may vary among species. Understanding the exact *Valanga* species used will thus ensure reproducibility and reliability in future chitin-related studies (Chapman, 2013; Pratiwi, 2014).

In addition, the *Valanga* grasshopper undergoes a hemimetabolous life cycle with three main stages: egg, nymph, and adult. Females deposit eggs in the soil during the rainy season, which later hatch into nymphs resembling miniature adults. The nymphs pass through several instar stages, gradually developing wings and reproductive organs, before reaching adulthood (Resh & Carde, 2009). The complete life cycle duration can range from several months to over a year, depending on environmental conditions such as temperature and humidity. This understanding of the *Valanga* life cycle also supports effective pest management and sustainable harvesting strategies for potential chitin-based applications (Abenaim & Conti, 2025).

Materials and Methods

Sampling and morphometric analysis

Specimens of *Valanga* spp. were collected from Cilacap, Central Java (7°36’53.7”S, 108°57’37.8”E) in May 2024 (**Fig. 1**). Sampling was conducted manually during the daytime when adults were most active, and specimens were subsequently preserved in 95% ethanol. Morphological characters measured included body length, antenna length, thorax length, foreleg, midleg, hindleg length, as well as forewing length and width. Measurements were taken using a digital caliper with a precision of ±0.01 mm.

Fig. 1. Sampling location in Cilacap, Central Java, Indonesia.

DNA barcoding analysis

Total DNA was extracted from the 95% ethanol-preserved leg muscle tissue of the wood grasshopper using a commercial spin-column kit. PCR amplification was conducted using DNA barcoding with the mitochondrial cytochrome oxidase I (COI) gene as a universal primer with LCO1490 (5'-GGT CAA CAA ATC ATA AAG ATA TTG G-3') and HC02198 (5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3') (Folmer et al., 1994).

The DNA extraction was performed according to the protocol for the Tissue Genomic Mini Kit (GT100, Geneaid). Amplification was performed using MyTaq HS Red Mix 2× in a total reaction volume of 40 µL, consisting of 17 µL ddH_2O, 20 µL MyTaq HS Red Mix 2×, 2 µL DNA template, and 1.5 µL of each primer (10 µM). PCR amplification was conducted using a TPersonal thermocycler (Biometra) with the following conditions: initial denaturation at 95 °C for 3 minutes, followed by 35 cycles of denaturation at 95 °C for 20 seconds, annealing at 50 °C for 30 seconds, extension at 72 °C for 20 seconds, and a final extension at 72 °C for 1 minute. The amplicon was sent to First Base C.O. Laboratory (Malaysia) for sequencing. DNA sequences were obtained in chromatogram format and edited using Geneious Prime version 2025.0.3. Sequences generated with the reverse primer were reverse-complemented and subsequently assembled with forward sequences, resulting in bidirectional alignments. Species identification was performed by comparing the nucleotide sequences against reference databases using the BLAST (Basic Local Alignment Search Tool) algorithm. Searches were conducted in both the Barcode of Life Data System (BOLD; www.boldsystems.org) and GenBank (NCBI; www.blast.ncbi.nlm.nih.gov) (Tallei & Kolondam, 2015).

Results

Morphological analysis

Valanga sp., commonly known as the wood grasshopper, is a member of the family Acrididae widely distributed across Southeast Asia. The head bears antennae shorter than the body length and large compound eyes, as shown in **Fig. 2**.

The *Valanga* sp. specimens collected from Cilacap exhibited a distinct femoral pattern on the hind legs. This pattern was characterized by a series of transverse dark markings that contrasted with the predominantly yellowish-brown background color of the femur (**Fig. 3**). Such markings were consistently observed across the examined individuals and were especially visible when the grasshoppers perched on host plant leaves, with the hind femur fully exposed.

The presence of this femoral pattern supports the morphological conformity of the Cilacap Specimens with diagnostic descriptions of the genus *Valanga.* In particular, the marked bands of the femur provide an additional diagnostic trait that complements other external characters such as large body size, antennae shorter than body length, and dull greenish-brown coloration.

Morphometric data from *Valanga* sp. specimens collected in the teak forest of Kubangkangkung,

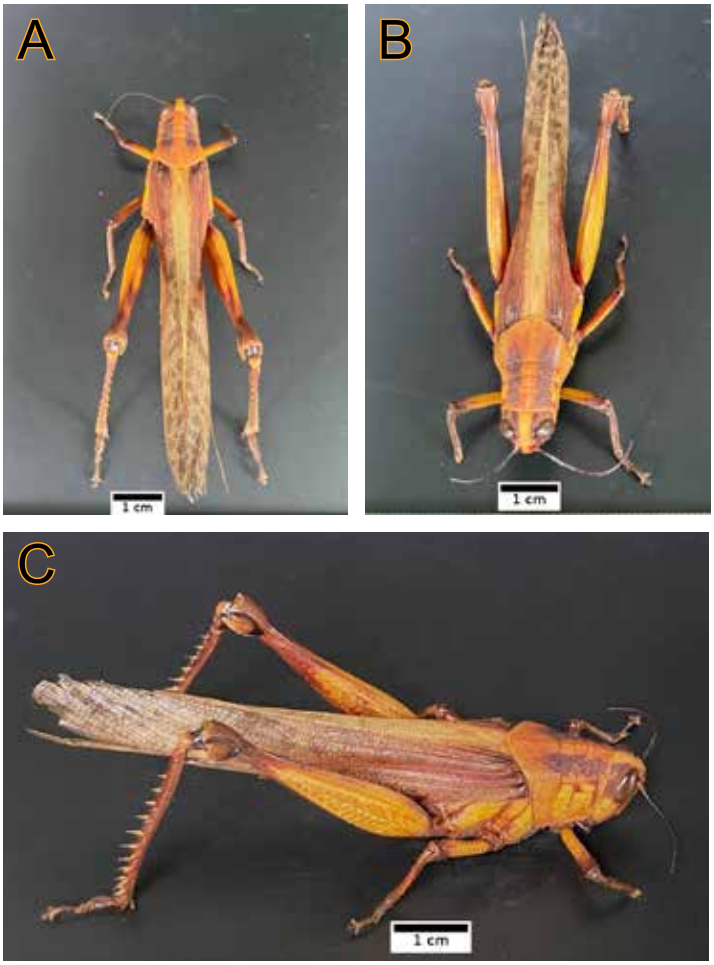

Fig. 2. Adult female *Valanga* specimens: **A**: dorsal view, **B**: frontal view **C**: lateral view

Fig. 3. The arrow shows the femoral pattern on the *Valanga* specimen

Cilacap, revealed distinct sexual dimorphism in several body characters. Based on measurements of 12 individuals, male body length ranged from 52.14 to 58.02 mm, while female body length ranged from 59.77 to 64.05 mm. The average body length of males was 55.84 mm and of females 61.57 mm. Mean values of key morphological traits in male and female *Valanga* adults are presented in **Tab. 1**.

The adult male *Valanga* specimens examined exhibit a fairly uniform overall size: body length clusters tightly between 52 mm and 58 mm, with the central half of individuals falling near 55–57 mm. Wing length mirrors this consistency, spanning about 50–57 mm, underscoring a proportional relationship between thoracic bulk and flight surfaces. Antennae and hind legs show the greatest relative variability; antenna length ranges from about 16 mm to 19 mm, while hind-leg length extends from 27 mm up to just below 29 mm, hinting at functional flexibility in sensory reach and jumping power. In contrast, fore- and mid-legs are compact and tightly grouped (approximately 6–8 mm), suggesting stabilizing selection for locomotor support rather than propulsion. Wing width remains the narrowest dimension (around 7–9 mm) yet displays only modest spread, reflecting conservative wing-loading demands. Altogether, the male *Valanga* imago presents as a moderately large grasshopper with consistent core body and wing proportions, overlaid by subtle but discernible individual differences in appendages that may influence sensory performance and escape mechanics.

The adult female *Valanga* grasshoppers in this sample are conspicuously larger than their male counterparts and exhibit greater size variability across several traits. Body length ranges from 60 mm to 64 mm, confirming a consistent female-biased dimorphism in overall stature. Wings scale proportionally: their lengths hover around 58–60 mm and widths center near 9 mm, yielding broader flight surfaces that could support the heavier female thorax and abdomen. Antennae range widely—from about 17 mm to 24 mm—suggesting that, while females generally possess longer sensory organs, they also tolerate greater individual divergence in antennal size. Hind-leg length spans roughly 29 mm up to nearly 38 mm, marking it as the

Table 1. Average morphometric characters of *Valanga* spp. adults

Sex	Body length	Antenna length	Foreleg length	Midleg length	Hindleg length	Forewing length	Forewing width
Male	55.84	17.17	7.03	6.77	28.82	53.25	8.37
Female	61.57	20.56	7.55	8.71	35.15	58.09	9.11

most variable appendage and hinting at functional differences in jumping or escape performance among females of the same population. In contrast, fore- and mid-legs remain more tightly clustered, yet even these medians exceed those of males, mirroring the overall up-scaling of the female body plan. Altogether, the pattern reflects a typical orthopteran sexual dimorphism: females are not only larger in every measured dimension but also harbor broader phenotypic spread in the structures most closely tied to mobility and sensory exploration.

The boxplots in **Fig. 4** provide a comparative overview of morphometric variation between male and female *Valanga* spp. specimens across six measured traits. Female *Valanga* imagoes are unmistakably larger and more variable than males across nearly every measured trait. Whereas male body length centers at about 56 mm with a narrow spread, female bodies extend to roughly 62 mm on average and span a broader 60–64 mm range, signaling marked sexual size dimorphism. Wing length follows the same pattern: males cluster near 53 mm, while females hover around 59 mm, and females also carry wider wings, reaching past 10 mm versus the male ceiling of about 9 mm, indicating proportionally broader flight surfaces to support greater mass. Antennae reveal the sharpest contrast in variability: male lengths tighten around 17 mm, while female lengths stretch from the high teens into the mid-twenties, suggesting heightened sensory investment and individual divergence among females. Leg dimensions echo the theme; male hind legs group near 29 mm, whereas female hind legs range from 29 mm to nearly 38 mm, highlighting stronger variation in jumping structures. Even the more conservative fore- and mid-legs sit higher for females, mirroring their overall up-scaled body plan. In short, males exhibit compact, tightly regulated morphometrics, while females combine universal up-scaling with greater spread, especially in the antennae and hind legs, reflecting the dual pressures of larger body size and diversified functional demands.

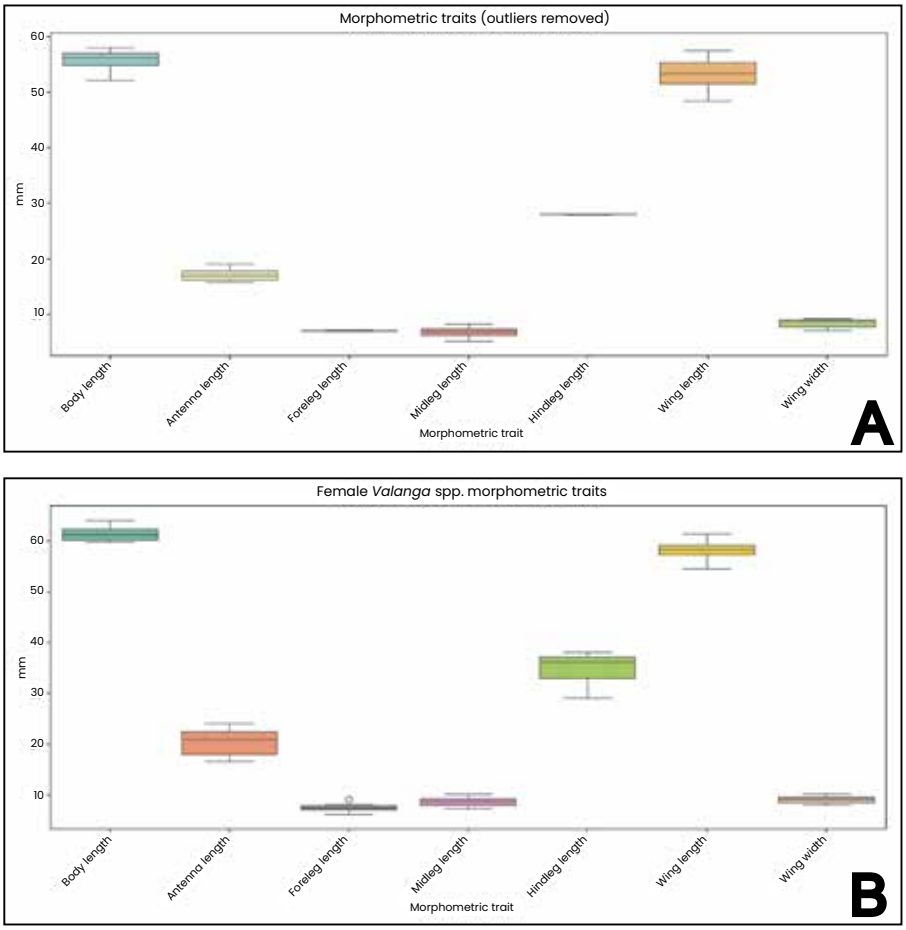

Fig. 4. Boxplots overview of morphometric variation in *Valanga* sp.: **A**: male specimens, **B**: female specimens

DNA barcoding analysis

The PCR products produced a single band of ~710 bp when visualized on 0.8% agarose gel electrophoresis, indicating successful

amplification of the target fragment. After sequencing and editing, a clean COI sequence of 658 bp was obtained and used for downstream analyses (**Fig. 5**).

The sequence was then trimmed and formatted in FASTA to serve as the primary dataset for downstream molecular identification and comparative analysis. The resulting FASTA sequence is presented below:

A A C T T T A T A C T T T A T A T T T G
G A G C T T G A G C A G G A A T A G T A
G G A A C A T C T A T A A G A A T A C T
T A T T C G T G C C G A A T T A G G A C
A A C C A G G A T C A C T A A T T G G G
G A T G A T C A A A T T T A T A A T G T
C A T C A T T A C A G C C C A T G C A T
T T G T A A T A A T T T T C T T C A T G
G T A A T G C C A A T T A T A A T T G G
T G G A T T T G G T A A T T G A C T A G
T A C C A C T A A T A A T T G G T G C A
C C A G A T A T A G C A T T C C C A C G
A A T A A A C A A T A T A A G T T T T T
G A T T A C T A C C T C C A T C A T T A
A C A C T C C T T C T T A C G T C C T C
T A T A G T A G A T A A T G G T G C T G
G T A C A G G A T G A A C A G T T T A C
C C C C C A C T A G C A G G A G C T A T
T G C A C A T G G C G G A G C A T C T G
T A G A T C T A G C A A T T T T T T C A
C T A C A C C T A G C A G G T G T A T C
C T C A A T T C T T G G T G C A G T A A
A C T T T A T T A C A A C A G C A A T T
A A T A T A C G A T C A G A A A G T
A T A A C T C T A G A T C A A A C A C C T T
T A T T T G T T T G A T C T G T A G C T
A T T A C A G C C C T T C T C C T T C T
T C T A T C A C T C C C T G T T C T A G
C A G G A G C T A T T A C T A T A T T A
C T T A C A G A C C G A A A T T T A A A
T A C A T C A T T T T T T G A C C C T G
C A G G T G G G G G T G A T C C A A T T
C T A T A T C A A C A T T T A T T T

The obtained sequence was subsequently compared with publicly available reference datasets using BLAST in GenBank and the Barcode of Life Data System (BOLD). The analysis of the *Valanga* sp. specimen from Cilacap exhibited 99.54% similarity with *V. irregularis* (Accession No.: HQ969563.1) from Queensland, Australia. Additionally, it showed 98.78% similarity to a specimen from Papua New Guinea, while similarity with *Austracris guttulosa* was only 97.11% (**Tab. 2**).

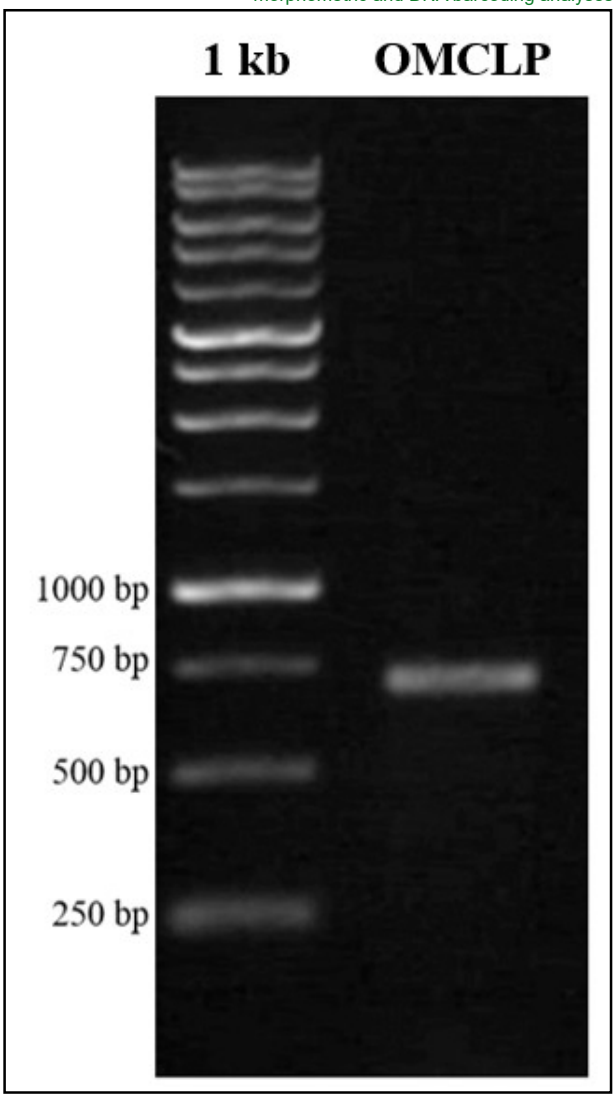

Fig. 5. Detection of DNA band through 0.8% agarose gel electrophoresis

Table 2. Percentage similarity of Valanga sp. from Cilacap with reference species.

No.	Specimen ID (Location)	Reference Species	Similarity (%)
1	OMCLP (Cilacap)	*Valanga irregularis* (HQ969563.1, Queensland, Australia)	99.54
2	GU115848.1 (Papua New Guinea)	*Valanga* sp. (Papua New Guinea)	98.78
3	GU115847.1 (Australia)	*Austracris guttulosa*	97.11
4	GU116334.1 (Galápagos Island)	*Schistocerca literosa*	91.03
5	HQ260647.1 (China)	*Locusta migratoria*	83.74

These results indicate that the *Valanga* specimen from Cilacap is genetically very close to *V. irregularis*. Several minor variations (single nucleotide polymorphisms, SNPs) were also detected in the sequence, reflecting natural intraspecific variation. A summary of sequence alignment results is provided in **Tab. 2.**

Phylogenetic relationships between the Cilacap *Valanga* specimens and international references were reconstructed using the Maximum Likelihood (ML) method based on the Kimura 2-Parameter (K2P) evolutionary model. Branch support was tested with 1,000 bootstrap replications to ensure robust phylogenetic estimation (Hebert et al., 2003).

The phylogenetic tree (**Fig. 6**) shows that the OMCLP specimen from Cilacap clusters tightly with *V. irregularis* from Queensland, Australia (HQ969563.1). This grouping forms a monophyletic clade with very strong bootstrap support (>95%), confirming a highly reliable evolutionary relationship between these populations. This finding aligns with previous reports demonstrating the utility of COI-based DNA barcoding in revealing geographic variation among insect populations (Folmer et al., 1994; Hebert et al., 2003).

The close clustering of OMCLP with reference *V. irregularis* indicates that the Cilacap specimens are genetically part of *V. irregularis*. The high genetic similarity supports the hypothesis of a broad Indo-Australasian distribution of *V. irregularis*, possibly shaped by historical ecological factors such as landmass shifts and past climate change (Hebert et al., 2003).

In another part of the tree, *Valanga* from Papua New Guinea separated from the *V. irregularis* clade with higher genetic divergence, yet still formed a closely related sister group. Bootstrap support for this clade was moderately strong (87%), suggesting that genetic differentiation between Papua New Guinea and Cilacap/Australia populations has occurred, while maintaining a close evolutionary relationship (Folmer et al., 1994).

Other genera, such as *A. guttulosa* and *Schistocerca literosa*, were positioned significantly apart from the *Valanga* clade, with greater genetic distances and lower bootstrap support. This separation confirms that evolutionary divergence at the genus level is substantial, consistent with previous findings on the diversification within the subfamily Cyrtacanthacridinae (Song & Wenzel, 2008; Song, 2010)

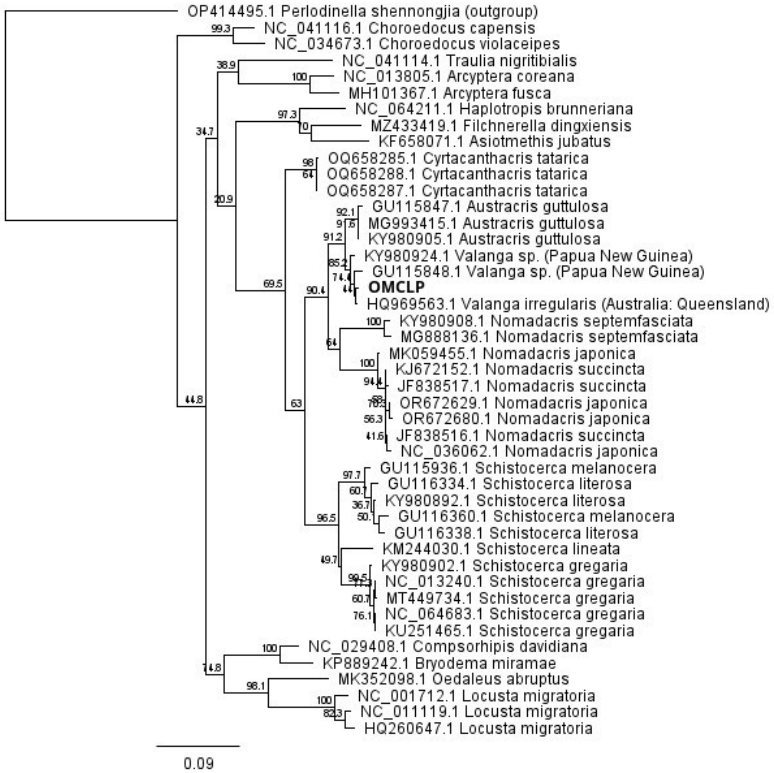

Fig. 6. Phylogenetic tree reconstruction of *Valanga* spp. based on COI gene sequences.

Discussion

Morphologically, the collected specimens conformed to the diagnostic features of the genus *Valanga*, which is characterized by large body size, antennae shorter than body length, and body coloration dominated by greenish-brown to dull yellow tones with distinctive femoral markings. The morphometric data revealed that females consistently had longer bodies, antennae, legs, and wings than males. These findings demonstrated apparent sexual dimorphism, consistent with previous morphological descriptions of wood grasshoppers reported by Triplehorn & Jhonson (2005) and Beutel et al. (2014). This morphological conformity strengthens the identification of the Cilacap specimens as belonging to the genus *Valanga*, while simultaneously providing evidence of intraspecific variation that is consistent with patterns reported in other Acrididae (Cisneiros et al., 2012; Suganya et al., 2021).

The morphometric data highlighted significant differences between males and females, a phenomenon commonly known

as sexual size dimorphism (SSD). Females were consistently larger than males in body length, wing length, and hind leg length. The average measurements obtained were consistent with the general pattern observed in Acrididae, where larger female size is associated with reproductive strategies that enhance ovarian capacity and the ability to produce more eggs (Hochkirch & Gröning, 2008). Such an SSD has also been described as a widespread evolutionary strategy among Orthoptera, indicating intense selection pressures favoring increased female size for reproductive success (Whitman, 2008).

Antenna length exhibited striking variability. Males possessed relatively uniform antennae averaging around 17 mm, whereas females displayed broader variation, ranging from 18 mm to 25 mm. This variability may be linked to differences in ecological and sensory functions between the sexes. Longer and more variable antennae in females may increase sensitivity to environmental cues, for example, in selecting appropriate oviposition sites, while the relatively uniform antennae of males may reflect their reliance on orientation during mate searching. This suggests that antennal dimorphism is not merely a morphometric phenomenon but also has ecological and behavioral implications (Chen et al., 2003). Comparable patterns of antennal dimorphism have been reported in other Acrididae, where female variability is often tied to adaptive ecological responses, while male exhibit atabilised morphometrics to optimise mate location efficiency (Chapman, 2013).

Significant differences were also observed in leg length. Male hind legs averaged around 29 mm, while females exceeded 32 mm. These differences are directly associated with locomotor capacity and jumping performance. Males are typically more active in mate searching, where movement efficiency is influenced by flexibility, whereas larger-bodied females rely on stronger hindlegs to support greater body mass and reproductive activity. Such variation aligns with other studies in Acrididae, which emphasize the importance of morphometric differences in shaping survival strategies (Latchininsky et al., 2011). The broader range of female hindleg length observed in the present study may indicate greater plasticity in locomotor strategies, allowing females to balance the dual demands of reproductive weight and predator avoidance, as noted in other Orthoptera populations (Stillwell et al., 2010).

Interestingly, molecular analysis based on sequencing of the cytochrome oxidase I (COI) gene revealed that specimens previously identified morphologically as *V. nigricornis* shared 99.54% similarity with *V. irregularis* (Accession No. HQ969563.1) from Queensland, Australia. This result, confirmed through BLAST searches in GenBank and BOLD Systems, highlights the taxonomic complexity within the genus *Valanga* in Indonesia. The occurrence of *V. irregularis* in Cilacap can be explained through several ecological and evolutionary perspectives. First, both micro- and macroclimatic changes in southern Central Java may have facilitated the range expansion of *Valanga* species previously restricted to certain habitats (Resh & Carde, 2009; Beutel et al., 2014). Second, anthropogenic factors such as human mobility, land-use change, and intensive agroecosystem practices (e.g., reforestation with non-native plant species) may create novel habitats suitable for species that were previously uncommon in the region (Latchininsky et al., 2011). Moreover, the possibility of cryptic species within *Valanga* in Indonesia has not yet been fully explored, making morphology-based identification alone prone to misclassification. The molecular evidence presented here underscores the importance of integrating morphological and molecular approaches in species identification, which has become the standard practice in modern entomology (Hebert et al., 2003).

Conclusion

This study underscores the importance of an integrative approach for identifying *Valanga* spp. in Cilacap, Central Java. Morphometric analysis revealed clear sexual size dimorphism, with females being larger and more variable than males. Phenotypic characters, including the distinctive femoral color pattern, were consistent with the diagnostic features of the genus *Valanga* and supported the initial morphological identification.

However, COI-based DNA barcoding demonstrated that the Cilacap specimens exhibited high genetic similarity to *Valanga irregularis*, in contrast to previous dominant reports that identified them as *Valanga nigricornis*. This finding illustrates that morphology-based identification alone can lead to ambiguity, particularly in genera with broad phenotypic variation.

By combining morphometric data with DNA barcoding, this study achieved a more comprehensive identification while also highlighting the limitations of each method when applied independently. Furthermore, these results contribute to a better understanding of the potential genetic variation and distribution of *Valanga* in Indonesia, carrying important implications for both taxonomic research and the development of agricultural pest management strategies.

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