

**VARIATION OF MORPHOMETRIC CHARACTERS AND MARKING
PATTERN AMONG THE INDONESIAN POPULATIONS OF THE LESSER
BANDED HORNET, *Vespa affinis* (HYMENOPTERA: VESPIDAE) BASED ON
THE SPECIMENS IN THE COLLECTION OF MUSEUM ZOOLOGICUM
BOGORIENSE (MZB)**

Diah Pusparina¹, I Wayan Suana^{1*}, Raden Pramesa Narakusumo², and Hari Nugroho^{2*}

¹Department of Biology, Faculty of Mathematics and Natural Sciences, University of Mataram, Jl. Majapahit
No.62, Mataram 83125, Indonesia

²Laboratory of Entomology, Museum Zoologicum Bogoriense, Research Center for Biosystematics and Evolution,
National Research and Innovation Agency (BRIN), Widyasatwaloka, Jl. Raya Jakarta-Bogor Km 46, Cibinong,
Bogor 16911, West Java, Indonesia

*Corresponding author: wynsuana@unram.ac.id

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ABSTRACT

Vespa affinis is a hornet with wide geographical distribution, occurring across the Indonesian Archipelago (Sumatra, Java, Kalimantan, Sulawesi, the Moluccas, and Papua) but excluding the Lesser Sunda Islands. Species with wide distribution typically show morphological variations that may differ across their range. This study aims to provide a detailed description of island-to-island diversity in morphometric characters and marking patterns among Indonesian populations of *V. affinis*. A total of 18 morphometric characters and 18 color patterns were analyzed. Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) were employed to distinguish variations in morphometric data. Marking pattern data were analyzed using the hierarchical clustering, to understand the clustering and relationship of marking patterns. The morphometric similarity recorded across the Indonesian archipelago suggests limited morphometric divergence among the populations. The marking patterns of *V. affinis* showed considerable variation across its geographical range, with brighter coloration in populations from eastern Indonesia compared to those from Sundaland.

Key words: geographical distribution, marking pattern, morphometric, *Vespa affinis*

INTRODUCTION

Vespa affinis is a hornet with a wide geographical distribution, spanning continental Asia south of the Himalayas, Taiwan, the Ryukyu Islands, and Malay Archipelago (Nugroho et al., 2011). Insects with broad distributions often exhibit various morphological characteristics, such as body size, wing length, and color patterns, which might vary across their distribution range, usually influenced by environmental and ecological factors (Bai et al., 2016; Pato et al., 2019).

The Indonesian Archipelago, with its diverse environmental conditions, offers a unique opportunity to study intraspecific variation in *V. affinis*. Island populations experience distinct ecological pressures, such as variations in resource availability, habitat types, and climatic conditions, which can influence their morphology and coloration. In some insects, body size

and coloration have been associated with local ecological factors, including altitude and climate. For example, darker coloration in high-altitude populations may provide thermoregulatory advantages, while brighter coloration in lowland populations may serve aposematic or social signaling functions (de Souza et al., 2020; Perrard et al., 2014).

Body size is a key example of variation influenced by geographical traits, such as altitude, climate, and habitat type. Food resource availability is another critical factor that could influence body size, particularly in populations with limited ecological niches (Beerli et al., 2019). Another significant morphological variation in insects with broad distribution could be color pattern, which often is influenced by geographic conditions and potentially related to evolutionary adaptation to environmental conditions (MacDonald & Deyrup, 1989; Smith-Pardo et al., 2020). Such morphological variations could be expected in *V. affinis*, especially its local populations in the Indonesian Archipelago, where the environmental conditions vary significantly across islands, from lowland forests and coastal areas to high altitude mountainous regions, providing a range of ecological contexts for studying such variation in *V. affinis* to understand the diversity and evolutionary dynamics within this species across diverse environmental conditions (Gibert et al., 2019).

Despite its wide distribution, detailed studies on the intraspecific variation of *V. affinis* populations in the Indonesian Archipelago remain limited. The specimens of *V. affinis* collected at various localities in the Indonesian Archipelago and having been deposited in the Museum Zoologicum Bogoriense (MZB) provided us opportunity to make detailed descriptions of island-to-island diversity in morphometric characters and marking patterns among Indonesian populations of *V. affinis*. The present paper presents the results of such study and would provide the basis for further studies that explore the potential ecological and genetical factors driving the diversity having resulted from the unique island distribution in the Indonesian Archipelago.

MATERIALS AND METHODS

A total of 274 specimens of the worker caste of *Vespa affinis* deposited in the collection of the Museum Zoologicum Bogoriense (MZB) were examined. These specimens originated from various regions of Indonesia, namely West Sumatera, West and East Kalimantan, West and Central Java, North and Southeast Sulawesi, the Moluccas, and Papua. Morphometric measurements were conducted using L.A.S 4.8.0 software adapted to Leica Z6 AP0 microscope (all from Leica Microsystems, Heerbrugg, Switzerland). Eighteen characters were measured following Rajkhowa et al. (2021): Body Length (BL), as the lengths in lateral view of head, mesosoma and first two metasomal terga combined; Head Length (HL), measured as the distance between dorsal apex of the head and the projection of the apical lobes of clypeus in frontal view; Head Width (HW), measured as the distance between outermost eye margins in frontal view; Clypeus Width (CW), measured as the distance between apexes of the lateral lobes; Clypeus Height (CH), measured as the distance between dorsal and ventral apexes of the clypeus; Mandible Height (MH), measured as the distance between basal part and apical tip along

its outer margin; Mandible Width (MW), measured in view perpendicular at the widest part; Antennal Scape Length (ASL), measured excluding the radicle; Antennal Scape Width (ASW), measured at apical margin; Mesosomal Length in Lateral view (MLL), measured as a projection distance between tip of pronotum and posteriormost of propodeum; Mesosomal Height (MHL), measured in profile perpendicular at the apex of the mesoscutum; Mesosomal Length (MLD) and Mesosomal Width in Dorsal view (MWD), measured in view perpendicular to the mesoscutum; Metasomal Tergum 1 Length (MT1L) and Metasomal Tergum 2 Length (MT2L), measured as the distance between the projection of the outermost part of tergum in dorsal view; Metasomal Tergum 1 Width (MT1W) and Metasomal Tergum 2 Width (MT2W), measured as the distance between outermost arch of the tergum in dorsal view; Forewing Length (FwL), measured as the distance between basal and apical apex. The data were analyzed using Principal Component Analysis (PCA), Linear Discriminant Analysis (LDA) and MANOVA. All statistical analyses were performed using PAST (ver.4.03).

Observation on color marking pattern were made for 18 characters, following Ramadhila et al. (2023): mandible, clypeus, frons, vertex, band along ocular sinus, pronotum, mesoscutum, scutellum, metanotum, propodeum, propodeum spine, tegula, metasomal tergum 1-6 (Fig. 1). Five categories were used to describe the relative size of marking spots against entire surface area of each character ($\leq 25\%$, $>25\%$, $\geq 50\%$, and $>75\%$) (Ramadhila et al., 2023). The data were coded and converted into numerical 0 (spot covering more than 75%), 1 (spot covering between 50% and 75%), 2 (spot covering 25% or more and less than 50%), 3 (spot covering less than 25%), 4 (no spot). Subsequently, the data were analyzed using hierarchy clustering analysis with the “cluster” package (Maechler et al., 2023) in R ver. 4.3.3.

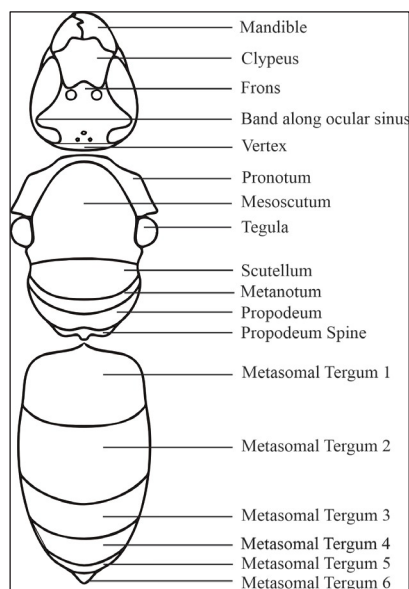


Figure 1. Body parts of *Vespa affinis* for marking pattern analysis.

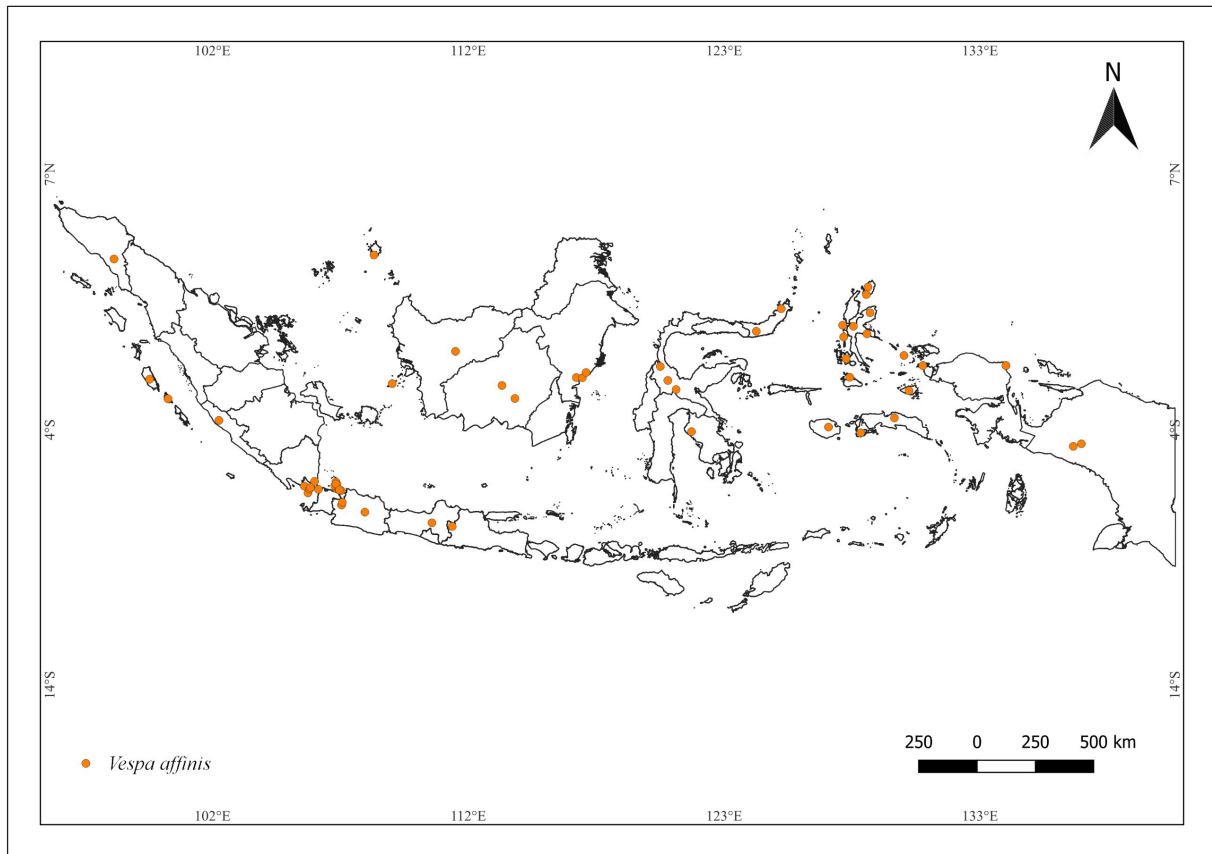


Figure 2. Collection localities of the specimens used in this study (Map created using QGIS version 3.28.3).

RESULTS

Morphometric characteristics

A total of 18 morphometric variables were included in the PCA analysis. The PCA results indicate that the populations from various Indonesian islands were similar in their morphometric characteristics. Most specimens examined clustered centrally in the plot, with a few specimens from the Moluccas and Papua scattered toward the lower right side of the plot. The specimens grouped in the center had an average body length (BL) of 28.73 mm, which were longer than those of the specimens positioned in the lower right side: A 21-25 M (Moluccas); 11-15 P (Papua) had an average body length of 15.99 mm - 17.95 mm, respectively). The first principal component (PC1) accounted for 38.39% of the total variance and the second principal component (PC2) explained 13.73% (Fig. 10). The loadings score showed that variables related mainly to the head contributed significantly to PC 1, that is, they were Antennal Scape Width (ASW); Antennal Scape Length (ASL), Mandible Width (MW), Mandible Height (MH), Clypeus Width (CW), Clypeus Height (CH), Head Width (HW), Head Length (HL), Metasomal Tergum 1 Length (MT1L), Metasomal Tergum 2 Length (MT2L). For PC 2, significant contributing variables including Body Length (BL), Antennal Scape Length (ASL), Antennal scape width

(ASW), Metasomal Tergum 1 Width (MT1W), Metasomal Tergum 2 Width (MT2W), Metasomal Tergum 1 Length (MT1L), Metasomal Tergum 2 Length (MT2L), Mesosomal Width (MWD), Mesosomal Height (MHL), Forewing Length (FwL), and Mandible Height (MH). Body Length showed no correlation with other variables except for Mesosomal Length in Lateral view (MLL), which was positively correlated.

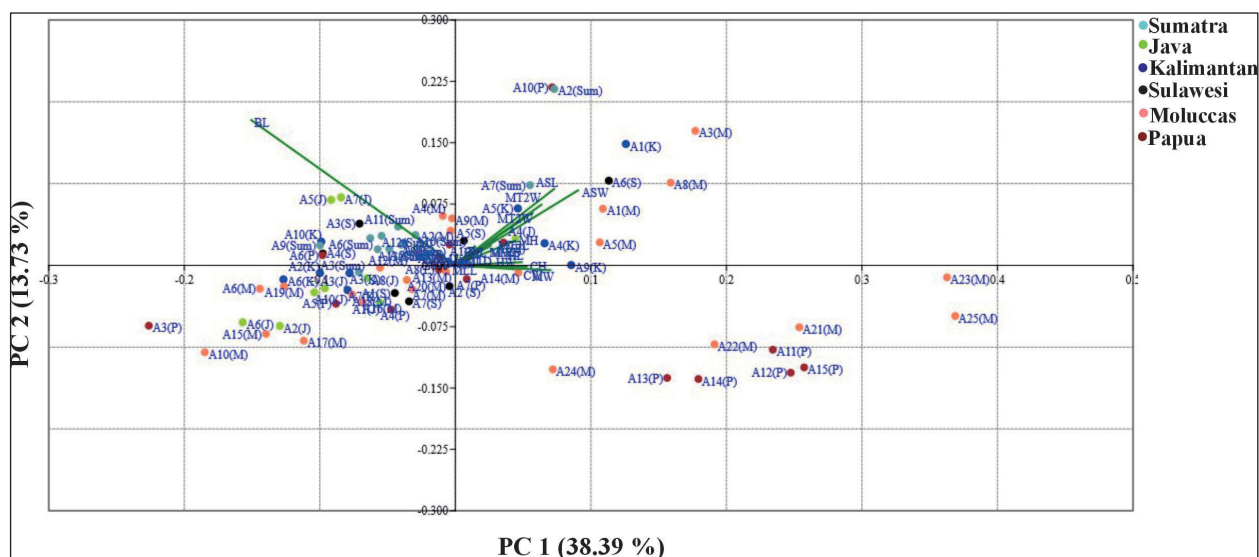


Figure 3. Principal component analysis (PCA) based on morphometry characters of *Vespa affinis*: (PC 1 with 38.39% of the variance, PC 2 with 13.73% of the variance).

Linear Discriminant Analysis (LDA) showed that the local populations in the Indonesian Archipelago (Sumatra, Java, Kalimantan, Sulawesi, the Moluccas, Papua) were grouped together in the central part of the plot, with no distinct separation between populations. Head related variables were positively correlated which included Antennal scape Width (ASW), Antennal scape Length (ASL), Mandible Width (MW), Mandible Height (MH), Clypeus Width (CH), Clypeus Height (CH), Head Length (HL), Head Width (HW). In contrast, the variable related to the mesosoma, metasoma and wings such as Mesosomal Length in Dorsal view (MLD), Mesosomal Width (MWD), Mesosomal Length in Lateral view (MLL), Mesosomal Height (MHL), Metasomal Tergum 1 Length (MT1L), Metasomal Tergum 1 Width (MT1W), Metasomal Tergum 2 Length (MT2L), Metasomal Tergum 2 Width (MT2W), Forewing Length (FwL), and Body Length (BL), were positively correlated with each other but negatively correlated with the head related variables. Several variables influenced axis 1, which were HW, CH, ASL, MHL, MLD, MT1L and MT2L. Variables influenced axis 2 were BL, HL, CW, CH, MW, MT1L, MT2L, MT2W and FwL. Axis 1 and 2 together accounted for most of variations, with Body Length (BL) and Forewing Length (FwL) contributing to the segregation of populations, particularly those from the Moluccas and Papua, which displayed distinct morphometric profiles compared to the populations of other islands.

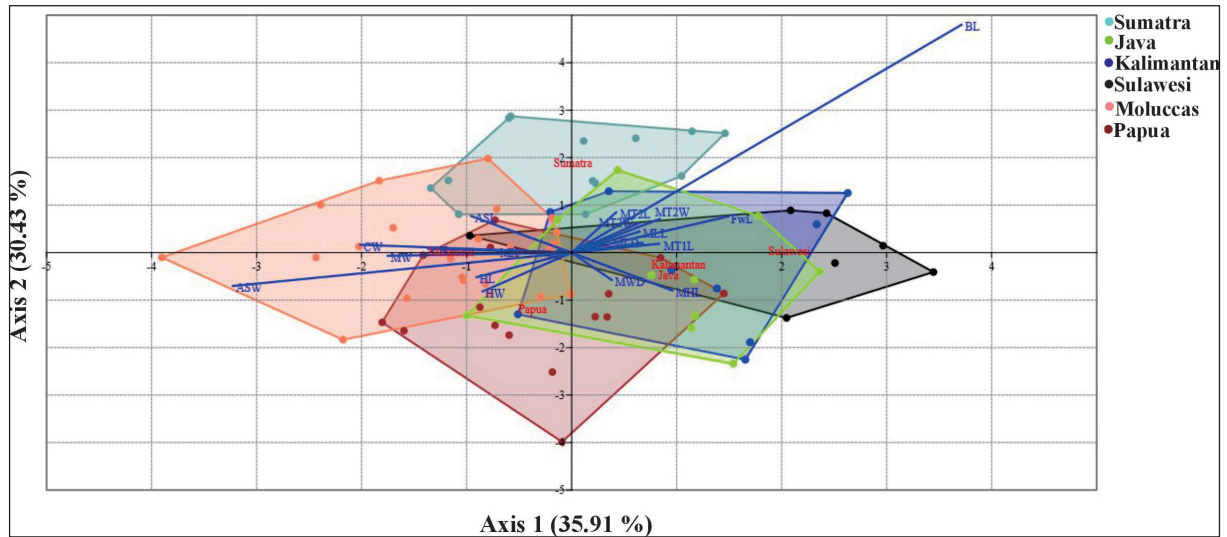


Figure 4. Linear discriminant analysis (LDA) based on morphometry of *Vespa affinis*: (axis with 35.91%; axis 2 with 30.13%).

Table 1. Morphometric measurements of *Vespa affinis* from Indonesian Archipelago. All specimens were measured, but only specimens with complete 18 morphometric characters were analyzed [Sumatra (n=13); Java (n=10); Kalimantan (n=10); Sulawesi (n=7); Moluccas (n=25); Papua (n=15)]

Parameters (mm)	Sumatra Mean \pm SD	Java Mean \pm SD	Kalimantan Mean \pm SD	Sulawesi Mean \pm SD	Moluccas Mean \pm SD	Papua Mean \pm SD
BL	31.63 \pm 1.16	31.01 \pm 2.22	29.99 \pm 2.41	29.75 \pm 1.69	27.46 \pm 5.02	25.52 \pm 7.04
HL	10.22 \pm 0.48	10.10 \pm 0.73	9.73 \pm 0.60	9.95 \pm 0.58	9.29 \pm 1.28	8.46 \pm 2.33
HW	10.58 \pm 1.37	10.62 \pm 0.44	10.25 \pm 0.55	10.38 \pm 0.49	9.74 \pm 1.42	8.85 \pm 2.41
CW	6.86 \pm 0.32	6.43 \pm 0.31	6.42 \pm 0.27	6.22 \pm 0.16	6.19 \pm 0.89	5.55 \pm 1.49
CH	4.84 \pm 0.16	4.58 \pm 0.35	4.55 \pm 0.33	4.62 \pm 0.22	4.37 \pm 0.60	3.91 \pm 1.03
MH	2.84 \pm 0.30	2.80 \pm 0.23	2.87 \pm 0.54	2.57 \pm 0.32	2.53 \pm 0.43	2.24 \pm 0.59
MW	3.58 \pm 0.19	3.28 \pm 0.28	3.40 \pm 0.42	3.45 \pm 0.12	3.28 \pm 0.56	2.93 \pm 0.71
ASL	3.69 \pm 0.54	3.29 \pm 0.64	3.56 \pm 0.29	3.33 \pm 0.22	3.18 \pm 0.56	2.91 \pm 0.98
ASW	1.04 \pm 0.18	0.97 \pm 0.12	0.96 \pm 0.15	0.96 \pm 0.14	0.98 \pm 0.20	0.88 \pm 0.28
MLL	14.77 \pm 0.77	13.96 \pm 1.24	13.48 \pm 1.24	13.85 \pm 1.00	12.25 \pm 2.27	11.87 \pm 3.53
MHL	11.36 \pm 0.77	11.25 \pm 0.92	11.10 \pm 0.79	11.24 \pm 0.65	9.77 \pm 1.65	9.48 \pm 2.58
MLD	14.84 \pm 0.78	14.24 \pm 0.88	13.54 \pm 1.46	14.38 \pm 0.88	12.61 \pm 2.33	12.12 \pm 3.46
MWD	10.89 \pm 0.39	10.78 \pm 1.21	10.94 \pm 1.27	10.44 \pm 0.55	9.45 \pm 1.65	8.98 \pm 2.38
MT1L	6.83 \pm 0.52	6.97 \pm 0.59	6.84 \pm 0.58	6.40 \pm 0.85	5.93 \pm 1.16	5.36 \pm 1.58
MT2L	7.92 \pm 0.64	7.30 \pm 0.75	7.03 \pm 0.71	7.32 \pm 0.33	6.43 \pm 1.16	6.19 \pm 1.62
MT1W	10.13 \pm 0.82	9.25 \pm 1.15	9.40 \pm 0.90	9.34 \pm 1.24	8.13 \pm 1.53	7.94 \pm 2.15
MT2W	11.00 \pm 0.78	10.04 \pm 1.15	10.07 \pm 1.09	10.39 \pm 1.42	8.95 \pm 1.65	8.68 \pm 2.26
FwL	35.63 \pm 2.27	34.79 \pm 3.40	33.30 \pm 3.11	34.14 \pm 2.21	29.50 \pm 5.95	27.46 \pm 7.27

The MANOVA test showed a Wilks' Lambda staticical of 0.0983, with a *p-value* 0.00003054, indicating no significant difference among the local populations (Table 2).

Table 2. Multivariate analysis of variance (MANOVA) based on morphometry of *Vespa affinis*

Wilks' Lambda				
Statistic	df1	df2	F	p
0.0983	90	281	1.914	0.00003054

Marking Pattern

The markings are commonly observed in the following body parts: mandible, clypeus, frons, vertex, pronotum, mesoscutum, scutellum, metanotum, propodeum, and metasomal tergum 1. The hierarchical cluster analysis (Fig. 5), showed that variation on marking patterns occur between populations in each major island, and even amongst local populations within a given island. Two or three different marking patterns were present within local populations such as Raja Ampat, Manokwari and Kepulauan Seribu. There is no distinctive marking pattern unique to each major island, and multiple patterns are recognized across different regions. In general, metasomal terga 1 and 2 display orange-yellow color with mid and apical brownish spots, except for specimens from Buru Island (2 specimens), Aceh (1 specimen), Bogor (1 specimen), Kepulauan Seribu (3 specimens) and West Java (2 specimens), which have the metasomal tergum 1 completely black. Specimens from Java Island (29 specimens) have the mesosoma black and the head with black vertex but some specimens from West Java (1 specimen) and Kepulauan Seribu (5/23 specimens examined) have reddish-brown vertex.

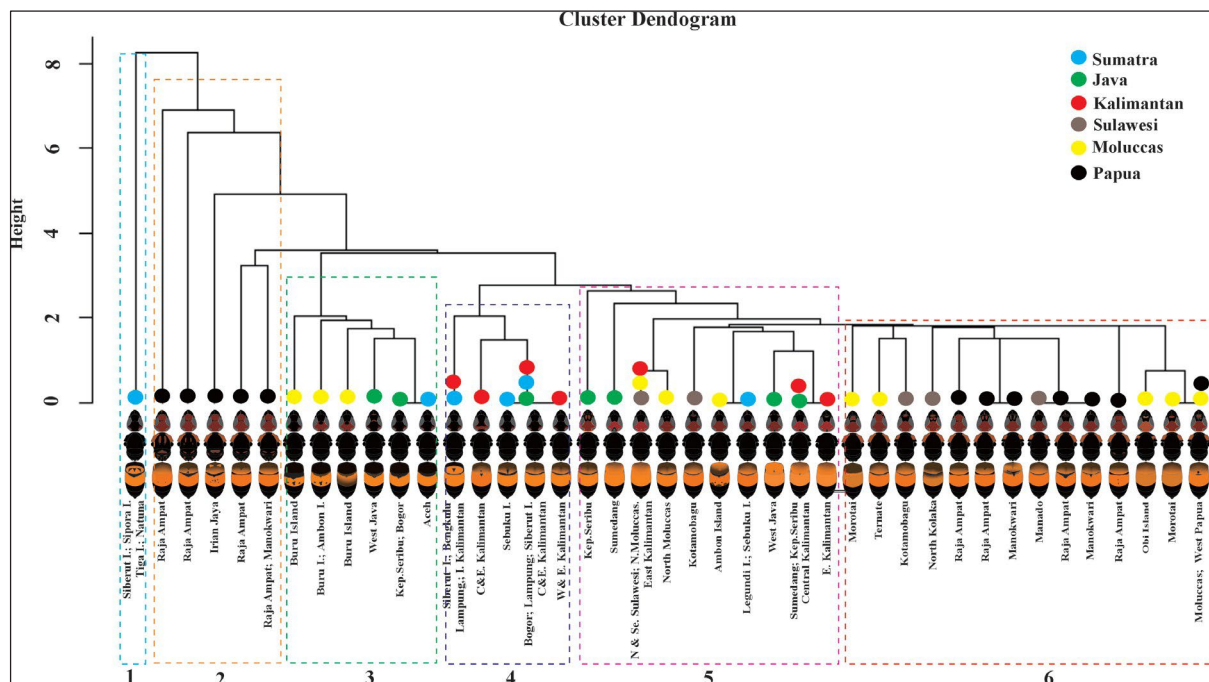


Figure 5. Dendrogram produced by hierarchy cluster analysis represents the consensus of 41 individuals of *Vespa affinis* in several locations.

Distinctive color patterns have been recorded in the specimens from the peripheral islands of Sumatra [Siberut Island (16 specimens), Sipora Island (7 specimens), Tiga Island (1 specimen) and Natuna (1 specimen)], of which metasomal tergum 1 has three triangular patterns spots medially [Fig. 6(c)]. Most specimens from the Moluccas have red vertex, the mandible black and a reddish-brown spot on the apical part of clypeus. In Papua, most specimens examined – have reddish-brown coloration on the vertex and pronotum, as well as reddish-brown markings on the mesoscutum, scutellum, metanotum, and propodeum. Some specimens from Manokwari lack spots on the mesosoma but they have the metasomal tergum 1 covered almost entirely with reddish-brown blotches. Specimens from Kalimantan have reddish-brown vertex and orange-yellow metasomal tergum 1; in some cases, vertex is black with reddish-brown band along the upper part of the ocular sinus. Specimens from Sulawesi (7 specimens) generally display a reddish-brown vertex, reddish-brown spots on the pronotum, but (3 specimens) may lack spots altogether.

The hierarchical cluster analysis (Fig. 5) identified six main color marking patterns across Indonesian Archipelago (Fig. 6). The color variations of this polymorphic and widely distributed species exhibit mosaic pattern on their distribution across archipelago (Fig. 7). Color pattern (a) is found in Sumatra, Java (including Kepulauan Seribu) and the Moluccas, in which the head and thorax are black with a reddish spot along ocular sinus, and the metasomal tergum 1 is black, while the metasomal tergum 2 is orange. Color pattern (b) is found in Sumatra (including Siberut and Sipora Island), Java and Kalimantan, in which the metasomal terga 1 and 2 are orange, with dark brown blotches in the metasomal tergum 1. Color pattern (c) is observed in Mentawai and Natuna Islands, in which the metasomal tergum 1 is orange with three dorsal triangular patterns in the middle and metasomal tergum 2 is orange. Color pattern (d) is found in Sumatra (including Legundi and Sebuk Island), Java (including Kepulauan Seribu) and Kalimantan, in which the mesosoma is entirely black, the vertex is red, and the clypeus and mandibles are black with a reddish-brown spot (less than 25%) and metasomal terga 1 and 2 are orange. Color pattern (e) is recorded in Sulawesi, the Moluccas and Papua (including Raja Ampat Island), in which the vertex is red, the mandible and clypeus are black with three patterns in the middle of clypeus, and the mesosoma is black with ferruginous markings on the pronotum and the metasomal terga 1 and 2 are orange with dark brown blotches. Color pattern (f) is found in Papua (including Raja Ampat Island), in which the head is red, the mandibles are black, and reddish-brown markings are present on the scutellum and propodeum, and the metasomal terga 1 and 2 are orange with dark brown blotches.

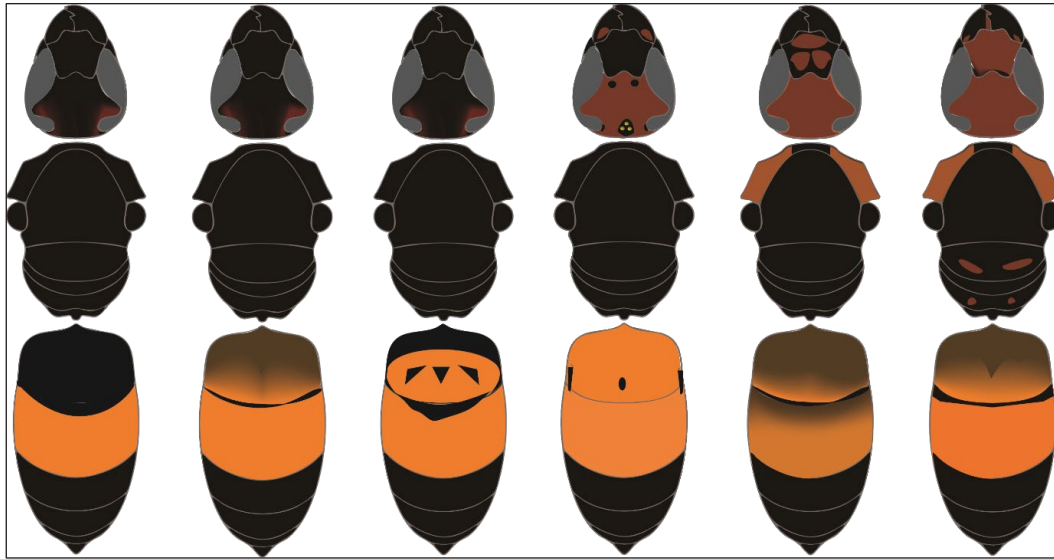


Figure 6. Main color pattern of *Vespa affinis* distributed in Indonesian Archipelago. (a) Sumatra, Java (including Kep. Seribu), Moluccas; (b) Sumatra (including Siberut and Sebuk I.), Java, Kalimantan; (c) Mentawai I. Natuna I; (d) Sumatra (Legundi and Sebuk I.), Java (including Kep. Seribu); Kalimantan, Sulawesi, Moluccas; (e) Sulawesi, Moluccas, Papua (including Raja Ampat I.); (f) Papua (including Raja Ampat I.).

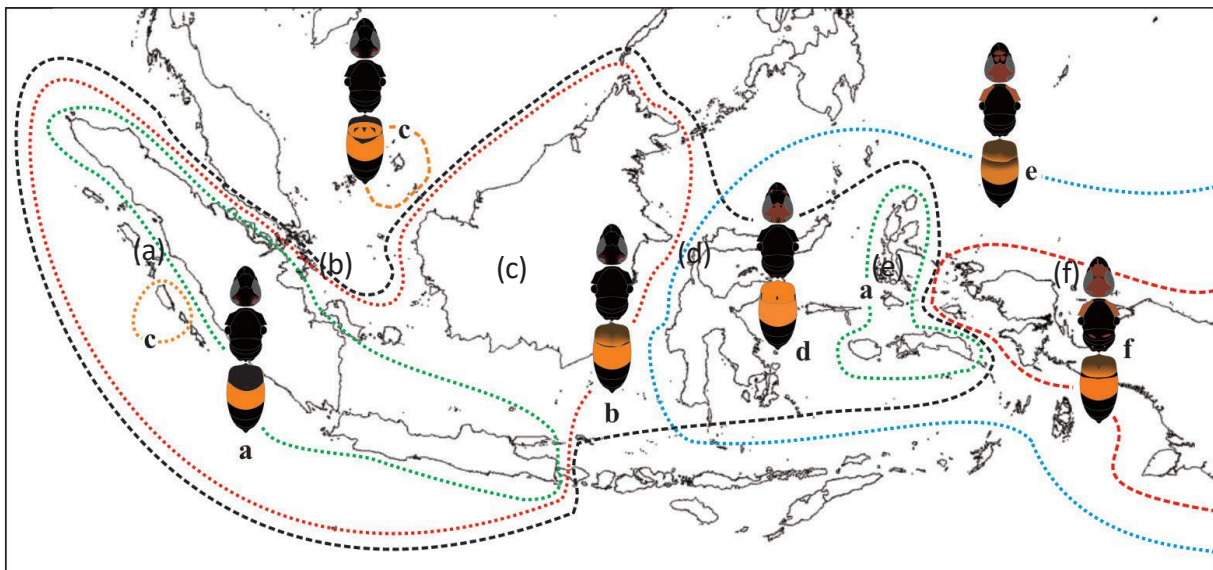


Figure 7. Map showing distribution of the main color patterns of *Vespa affinis* in Indonesian Archipelago. (a) Su- matra, Java (including Kep. Seribu), Moluccas; (b) Sumatra (including Siberut and Sebuk I.), Java, Kalimantan; (c) Mentawai I. Natuna I; (d) Sumatra (Legundi and Sebuk I.), Java (including Kep. Seribu); Kalimantan, Sulawesi, Moluccas; (e) Sulawesi, Moluccas, Papua (including Raja Ampat I.); (f) Papua (including Raja Ampat I.).

DISCUSSION

The morphometric analysis reveals limited variation in body size and shape among local populations, as demonstrated by the overlapping groupings in the PCA and LDA plots (Figs. 3 & 4). This indicates that the populations share broadly similar morphometric traits, likely due to comparable ecological conditions across their habitats or a shared evolutionary history. However, populations from Sumatra and Java exhibit larger average body sizes compared to those from smaller islands in the Moluccas and small island(s) adjacent to Papua (Table 1), suggesting geographic differences influenced by island size and ecological diversity. Smaller islands often impose ecological constraints, including reduced food availability and limited genetic diversity, which can result in smaller individuals (Spengler et al., 2011).

These findings align with previous studies in other insect taxa, such as *Polistes* wasps (Miller & Sheehan, 2021) and Sphingid moths (Beerli et al., 2019), where geographic constraints and ecological differences are shown to shape morphometric traits. This suggests that both environmental factors and evolutionary processes, such as genetic drift in isolated populations, contribute to the observed variation in *Vespa affinis* populations across the archipelago.

The marking patterns of *V. affinis* exhibit substantial geographic variation across the Indonesian Archipelago, though no distinct island-specific patterns were evident. Populations from eastern regions (Sulawesi, the Moluccas, and Papua) displaying brighter coloration on the head and mesosoma compared to populations from Sundaland (Sumatra, Java, and Kalimantan) (Figs. 5–7). For example, most specimens from Papua had a reddish-brown marking pattern on mesosoma, while Java populations showed darker form (Fig. 5). This variation is likely a product of founder effects and genetic drift, especially in small, isolated populations from the Moluccas and Papua.

The mosaic distribution of marking patterns, where multiple patterns coexist within local populations, supports the idea that random genetic events, rather than adaptation or natural selection, drive the observed variation. For instance, populations from Raja Ampat show diverse marking patterns, which may reflect historical bottlenecks or limited gene flow in this region. Similar findings in other Hymenopterans highlight the role of genetic drift in shaping traits in isolated populations (Perrard et al., 2014; Nugroho et al., 2020). Variation in marking patterns and coloration may also result from a combination of ecological and evolutionary pressures. Founder effect and genetic drift likely contribute to the distinctive coloration observed in smaller or isolated populations, such as those in the Moluccas and Papua. Predator-prey interactions, which can drive aposematism, may further amplify this variation.

CONCLUSION

The morphometric analysis of *Vespa affinis* populations across the Indonesian Archipelago indicates that island size and associated ecological constraints influence body size, with larger individuals observed in populations from large island, i.e., Java and Sumatra, and smaller individuals from small island(s), i.e., Obi and Misool. These differences are likely shaped by resource availability, genetic drift, and founder effects rather than broad stabilizing selection.

Marking patterns show significant geographic variation, with brighter coloration in eastern populations and darker coloration in Sundaland. This variation is primarily a product of genetic drift and founder effects, highlighting the role of historical processes in shaping phenotypic diversity in *V. affinis*. This study emphasizes the importance of integrating ecological, genetic, and historical perspectives to understand the diversity of *V. affinis*. Future research should focus on incorporating genetic analyses and detailed environmental data to further elucidate the evolutionary dynamics driving the observed patterns.

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