



Morphological Characterization and Phylogenetic Analysis of Diurnal Lepidoptera in Klangon Hills

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Received: June 2026; Revised: August 2026; Accepted: September 2026; Published: September 2026

Abstract: This study aimed to assess morphological similarity patterns and compare the diversity of diurnal Lepidoptera across four transects with different levels of habitat disturbance in the secondary forest of Bukit Klangon. The main concern in this area is increasing anthropogenic pressure resulting from tourism activities and land conversion, which may reduce the availability of host plants for Lepidoptera. Data collection was conducted from February to March 2026 using purposive sampling along four transects, each measuring 150–300 m in length. Specimens were collected using insect nets, identified based on morphological characteristics, and analyzed using the Sorensen Similarity Index and UPGMA cluster analysis implemented in the Multivariate Statistical Package (MVSP). The study recorded 13 diurnal Lepidoptera species belonging to five families: Nymphalidae (7 species), Pieridae (2 species), Geometridae (2 species), Erebididae (1 species), and Papilionidae (1 species). Species diversity and composition varied among transects, corresponding to differences in habitat disturbance levels at each sampling location. The highest morphological similarity (98%) was observed between *Ypthima huebneri* and *Ypthima philomela*, whereas the lowest similarity (42%) occurred between *Ypthima huebneri* and *Nyctemera adversata*. Cluster analysis based on morphological characters effectively illustrated the degree of morphological similarity among diurnal Lepidoptera species in the secondary forest ecosystem. These findings provide baseline information for future studies investigating Lepidoptera community responses to habitat dynamics in Bukit Klangon.

Keywords: Diurnal Lepidoptera; phenetic analysis; secondary forest; Klangon Hill; morphological characteristics

How to Cite: Ramadhan, K. R., & Astuti, D. S. (2026). Morphological Characterization and Phylogenetic Analysis of Diurnal Lepidoptera in Klangon Hills. *Bioscientist: Jurnal Ilmiah Biologi*, 14(3), 1393–1405. <https://doi.org/10.33394/bioscientist.v14i3.21335>



<https://doi.org/10.33394/bioscientist.v14i3.21335>

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INTRODUCTION

Human-induced habitat modification represents one of the major threats to ecosystem stability and biodiversity worldwide, including in Indonesia. Land-use changes contribute to habitat degradation and fragmentation, which can alter plant communities and subsequently affect insect diversity and abundance (Kurniawan et al., 2020). These environmental changes may influence population dynamics and ecological processes of organisms inhabiting disturbed ecosystems (Azahra, 2021). Among terrestrial insects, Lepidoptera are particularly sensitive to environmental changes because their life cycles depend strongly on the availability of host plants and suitable microhabitat conditions. Butterflies utilize diverse vegetation as larval host plants and adult nectar sources, making them important components of ecosystem functioning (Trovicana & Faizah, 2024). In addition, butterflies serve important ecological roles as pollinators, environmental bioindicators, and prey resources within food webs (Handayani & Rahayuningsih, 2022). Therefore, understanding butterfly community composition and morphological variation in disturbed habitats is essential for supporting biodiversity assessment and ecosystem management.

Based on their activity patterns, Lepidoptera can be categorized into diurnal species, which are active during daylight hours, and nocturnal species, which are active at night (Jumrodah et al., 2023). Indonesia supports high Lepidoptera diversity, including several ecologically important families such as Nymphalidae, Pieridae,

Papilionidae, Lycaenidae, and other groups (Sabran et al., 2021). However, changes in habitat structure may influence species composition, abundance, and community similarity among different locations. Butterfly diversity is affected by multiple environmental factors, including elevation, temperature, humidity, light intensity, rainfall, geographical characteristics, seasonality, and predation pressure (Manurung et al., 2021). Consequently, evaluating Lepidoptera communities across habitats experiencing different levels of disturbance can provide valuable information regarding biodiversity patterns in changing landscapes.

The secondary forest of Bukit Klangon, located on the slope of Mount Merapi, represents an important habitat for Lepidoptera communities undergoing environmental changes. Secondary forests are ecosystems that regenerate after disturbances, either naturally or through anthropogenic activities, such as agricultural expansion, forest degradation, and land conversion (Komul et al., 2022). In Bukit Klangon, increasing tourism activities have resulted in greater anthropogenic pressure through recreational development, including camping areas, trekking routes, and mountain biking trails within forest and plantation landscapes (Belinda et al., 2025; Kurniati et al., 2025). These activities may modify vegetation structure, reduce understory cover, and disturb flowering plants that provide essential resources for butterflies. Since flowering plant availability is closely associated with butterfly diversity through nectar provision (Lestari et al., 2020), habitat modification may influence the composition and distribution patterns of Lepidoptera communities.

Despite increasing interest in biodiversity studies around Mount Merapi, information regarding Lepidoptera communities in Bukit Klangon remains limited. Previous studies in the region have primarily focused on other biological components, including soil macrofauna and vegetation succession. Aminudin et al. (2021), for example, documented soil macrofauna diversity in Kalikuning Park, Mount Merapi, while Afrianto et al. (2016) investigated vegetation composition and succession following the 2010 Mount Merapi eruption. Although several butterfly studies have assessed species richness and abundance in various regions, most have remained descriptive and have not examined morphological similarity patterns among species in relation to habitat variation. Consequently, limited information is available regarding how morphological characteristics and phenetic relationships of diurnal Lepidoptera are distributed across habitats with different levels of disturbance.

Morphological characterization combined with numerical taxonomy provides an effective approach for evaluating similarity patterns among organisms based on observable traits. Phenetic analysis evaluates overall similarity among taxa using measurable morphological characters and differs from molecular phylogenetic approaches that investigate evolutionary relationships based on genetic information. Numerical approaches, including cluster analysis and dendrogram construction, have been widely applied to evaluate relationships among organisms based on morphological variation (Artha et al., 2025). A dendrogram represents similarity relationships among analyzed taxa, where higher similarity coefficients indicate greater resemblance based on the evaluated characters (Astuti, 2019). This approach allows researchers to identify morphological patterns among insect communities and evaluate variation in external characteristics within regenerating ecosystems (Kawahara et al., 2019).

Understanding morphological similarity patterns of Lepidoptera communities is particularly relevant in secondary forests because morphological traits may provide baseline information for biodiversity documentation and ecological monitoring. However, morphological similarity does not necessarily represent evolutionary

relatedness, as phenotypic convergence may occur among unrelated taxa experiencing similar environmental conditions. Therefore, phenetic analysis should be interpreted as a measure of morphological resemblance rather than a direct reconstruction of phylogenetic relationships.

This study aimed to document the diversity of diurnal Lepidoptera and evaluate phenetic relationships based on morphological similarity among species inhabiting secondary forest habitats with different levels of disturbance in Bukit Klangon. The study provides baseline information regarding species composition, morphological variation, and similarity patterns of Lepidoptera communities in a regenerating forest ecosystem. These findings contribute to insect ecology, morphological taxonomy, and biodiversity assessment by improving understanding of Lepidoptera diversity patterns in disturbed habitats and supporting future ecological monitoring and conservation-oriented management strategies.

METHOD

Study Area and Research Period

This study was conducted on 4 February 2026 in the secondary forest area of Bukit Klangon, Cangkringan, Sleman, Yogyakarta, Indonesia (coordinates: 110°27'18.02"E, 7°34'32.918"S), at an elevation ranging from 1,100 to 1,300 m above sea level. During the observation period, weather conditions were generally sunny with occasional cloud cover in the morning and midday. In the afternoon, rainfall occurred with low to moderate intensity, limiting the duration of observations during this period. Environmental variables were measured directly at each observation station. The average air temperature ranged from 25–28 °C, relative humidity ranged from 65–78%, and light intensity varied between 2,200 and 2,700 lux depending on observation time and canopy coverage conditions.

Study Subjects

The primary subjects of this study were diurnal Lepidoptera (butterflies active during daylight hours) inhabiting the secondary forest of Bukit Klangon. Sampling focused on adult individuals observed foraging, resting, or flying within the observation plots and transect areas. Sampling locations were determined using purposive sampling based on habitat representation and variation in environmental disturbance levels. Habitat disturbance levels were assessed based on measurable characteristics, including canopy cover percentage, distance from human activity routes, and degree of land openness.

Observation routes were established along predetermined transects selected to represent environmental variation across Bukit Klangon. The study area was selected because it represents a post-eruption secondary forest ecosystem characterized by pioneer vegetation, shrubs, and native flowering plants that provide important resources for insect communities.

Sampling Procedure

Sampling was conducted during three standardized observation periods: morning (08:00–10:00 WIB), midday (11:30–13:30 WIB), and afternoon (15:00–17:00 WIB) to capture variation in diurnal activity patterns. Four observation plots were established, with each plot containing a 200 m transect to standardize sampling effort. The duration and transect length were maintained consistently among plots to ensure comparable sampling intensity.

Plot 1 represented a habitat with dense canopy cover (70–80%), relatively low disturbance intensity, and proximity to water sources. In contrast, Plots 2–4

represented more open habitats with moderate to high disturbance levels, higher sunlight exposure, lower canopy coverage (30–40%), and vegetation dominated by shrubs.

Field data collection was conducted using a 40 cm diameter insect net for active specimen capture. Captured specimens were euthanized by injecting the thorax with a 1 mL syringe containing 70% ethanol solution. This procedure was applied to preserve the structural integrity of the wings and body morphology. Preserved specimens were temporarily stored in paper envelopes and placed in airtight thin-wall plastic containers to prevent mechanical damage during transportation to the laboratory. Ecological field data, including capture time, weather conditions, and perch vegetation type, were recorded directly on field observation sheets.

Morphological Identification and Characterization

To ensure the reliability and validity of species identification, morphological characterization was conducted using internationally recognized identification keys, including identification references by *Bohrer et al.* Taxonomic validation was performed by comparing diagnostic morphological features, including wing venation patterns, coloration patterns, and antennal structures.

Specimen collection was conducted using a standardized time-constrained search method along transects by the same observer to maintain consistency and reliability during sampling. Following identification and documentation, specimens were permanently preserved as voucher specimens in dry collections stored in airtight thin-wall boxes. Voucher specimens were deposited at the Biology Laboratory, Universitas Muhammadiyah Surakarta, for future taxonomic verification.

Phenetic analysis based on morphological characteristics was performed using a binary character matrix (0 and 1), where 1 indicated the presence of a morphological character and 0 indicated its absence. A total of 60 morphological characters were evaluated, covering seven major anatomical structures: caput, thorax, abdomen, wing structures, forewings, hindwings, and legs.

Data Analysis and Phenetic Clustering (UPGMA)

Community structure was analyzed using the Shannon–Wiener diversity index (H') and Simpson dominance index (D) to evaluate species diversity patterns among observation plots. Quantitative data obtained from morphological character coding and species abundance tabulation were analyzed using multivariate statistical approaches. Similarity among observation plots was assessed using the Sorensen Similarity Index according to the following formula (Endang et al., 2024):

$$Cs = \frac{2C}{SA + SB}$$

Note:

C = number of species shared between two areas

SA = number of species in area A

SB = number of species in area B

The Sorensen similarity coefficient ranges from 0 to 1. Values approaching 1 indicate high similarity in species composition between plots, whereas values approaching 0 indicate greater differences in community composition due to ecological segregation or differences in microhabitat characteristics.

The pairwise similarity matrix based on 60 binary morphological characters was further analyzed using the Multivariate Statistical Package (MVSP). Cluster analysis was performed using the Unweighted Pair Group Method with Arithmetic Mean

(UPGMA). The resulting clustering patterns were visualized as a morphological similarity dendrogram.

It should be emphasized that the dendrogram represents morphological similarity patterns among species based on the observed characters and does not represent a phylogenetic tree or evolutionary relationships. Interpretation of the dendrogram was conducted by evaluating branching patterns and similarity coefficients among specimens to determine levels of morphological resemblance. Therefore, this study focuses on describing morphological variation and phenetic relationships of diurnal Lepidoptera communities within the secondary forest ecosystem of Bukit Klangan.

RESULTS AND DISCUSSION

Species Identification

A total of 13 diurnal Lepidoptera species were identified and classified into five families: Nymphalidae, Pieridae, Papilionidae, Geometridae, and Erebidae. Specimens were collected from four observation plots representing different habitat vegetation structures. Each species was recorded based on the characteristics of the vegetation and environmental conditions of the sampling locations. The identified Lepidoptera species are presented in Table 1.

Table 1. Identification of Lepidoptera species recorded in Bukit Klangan secondary forest

No. Species	Family	Genus
1 <i>Ypthima huebneri</i>	Nymphalidae	<i>Ypthima</i>
2 <i>Eurema hecabe</i>	Pieridae	<i>Eurema</i>
3 <i>Delias belisama</i>	Pieridae	<i>Delias</i>
4 <i>Macaria abydata</i>	Geometridae	<i>Macaria</i>
5 <i>Argynnis zenobia</i>	Nymphalidae	<i>Argynnis</i>
6 <i>Argynnis hyperbius</i>	Nymphalidae	<i>Argynnis</i>
7 <i>Ypthima philomela</i>	Nymphalidae	<i>Ypthima</i>
8 <i>Tirumala septentrionis</i>	Nymphalidae	<i>Tirumala</i>
9 <i>Neptis hylas</i>	Nymphalidae	<i>Neptis</i>
10 <i>Argynnis paphia valesina</i>	Nymphalidae	<i>Argynnis</i>
11 <i>Graphium sarpedon</i>	Papilionidae	<i>Graphium</i>
12 <i>Crocota pseudotynctaria</i>	Geometridae	<i>Crocota</i>
13 <i>Nyctemera adversata</i>	Erebidae	<i>Nyctemera</i>

Table 1 shows that 13 Lepidoptera species belonging to different taxonomic groups were successfully identified. The family Nymphalidae was the most dominant group, comprising seven species, while other families, including Pieridae, Geometridae, Papilionidae, and Erebidae, were represented by fewer species.

In transect 1, three species were recorded: *Ypthima huebneri* (4 individuals), *Eurema hecabe* (3 individuals), and *Delias belisama* (1 individual). Transect 2 contained *Macaria abydata*, *Argynnis zenobia*, *Argynnis hyperbius*, and *Ypthima philomela*, with each species represented by 2–3 individuals. In transect 3, *Tirumala septentrionis*, *Neptis hylas*, *Argynnis paphia valesina*, and *Graphium sarpedon* were recorded, with each species represented by 1–2 individuals. The final transect

contained only two species, namely *Crocota pseudotynctaria* (2 individuals) and *Nyctemera adversata* (1 individual).

The morphological characteristics of the identified Lepidoptera species are presented in Table 2.

Table 2. Diagnostic morphological characteristics of identified Lepidoptera species

Species	Figure	Diagnostic morphological characteristics
<i>Ypthima huebneri</i>		<i>Ypthima huebneri</i> has an oval-shaped head with antennae possessing rounded tips. The dorsal wing surface exhibits a light brown to dull gray coloration. The forewing contains an accessory cell, with paired large ocelli surrounded by yellow margins. The hindwing possesses five ocelli (Effendi et al., 2024).
<i>Eurema hecabe</i>		This species has bright yellow wings with black markings along the inner wing margins. Distinctive spots and patterns are present on the outer wing surface, contrasting with the basal wing coloration. Brown markings form characteristic patterns on the wings (Hawa et al., 2025). <i>Eurema hecabe</i> is widely distributed and abundant across Asia, Africa, and Australia (Lee et al., 2023).
<i>Delias belisama</i>		The species exhibits grayish-white dorsal wings with prominent reddish-orange spots at the basal region of the ventral hindwing. Members of Pieridae can also walk using their tarsal claws.
<i>Macaria abydata</i>		This small to medium-sized moth exhibits characteristic golden-yellow coloration. Unlike butterflies, the hindwing possesses a frenulum. The species has tibial spurs and cream-brown wings with faint transverse lines and wavy or angular outer wing margins typical of Geometridae.
<i>Argynnis zenobia</i>		The wings display a fritillary pattern with an orange dorsal background coloration. Black spots form regular rows across the wing surface, accompanied by serrated wing margins. These characteristics distinguish <i>A. zenobia</i> from other fritillary species within the genus.
<i>Argynnis hyperbius</i>		This species exhibits an orange fritillary pattern, with a prominent black dorsal forewing apex and transverse white bands in females. <i>Argynnis hyperbius</i> occurs seasonally and may be sensitive to environmental changes (Ullah et al., 2025).
<i>Ypthima philomela</i>		The species has a dull dark-brown ground coloration, with hindwing ocelli relatively smaller than those of <i>Ypthima huebneri</i> .

Species	Figure	Diagnostic morphological characteristics
<i>Tirumala septentrionis</i>		Characterized by distinct white spots extending from the thorax to the head region. The antennae are spindle-shaped with thickened tips. The wings are dark brown with elongated semi-transparent bluish-gray lines and spots.
<i>Neptis hylas</i>		The forewings are blackish, while the hindwings are brownish. A diagnostic characteristic is the presence of contrasting white bands (<i>sailers</i>) across the wings.
<i>Argynnis paphia valesina</i>		This species resembles other fritillary butterflies but differs in coloration, with predominantly brown wings. The ventral hindwing has a greenish background coloration combined with prominent longitudinal white stripes.
<i>Graphium sarpedon</i>		The species has characteristic hindwings with one or more tail-like extensions along the posterior margin. The wings are dark brown with a transverse semi-transparent blue-green band. <i>Graphium sarpedon</i> is associated with Lauraceae plants and belongs to the family Papilionidae (Liao et al., 2024).
<i>Crocota pseudotyncitaria</i>		This moth has comb-like (pectinate) antennae, golden-yellow wings, and hindwings equipped with a frenulum. It is commonly found in shrub and grass habitats.
<i>Nyctemera adversata</i>		The species exhibits black-and-white wing patterns, prominent subcostal and medial veins at the base of the hindwing, and a bright yellow abdomen with transverse black spots. This diurnal moth, commonly known as the marble white moth, is frequently observed resting on flowers of Asteraceae plants such as <i>Bidens pilosa</i> for nectar feeding (Solomon & Venkata, 2020).

Table 2 summarizes the morphological identification of the 13 recorded species, including representative images and diagnostic characteristics. High-resolution images were obtained using a microscope magnification of 10×0.7, and morphological descriptions were provided based on observable external characters.

Morphological Similarity Analysis and Phenetic Clustering

Based on the morphological identification results, the similarity relationships among the recorded Lepidoptera species were analyzed using the Multivariate Statistical Package (MVSP) with the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering approach. The clustering pattern based on morphological characters is presented as a dendrogram in Figure 2.

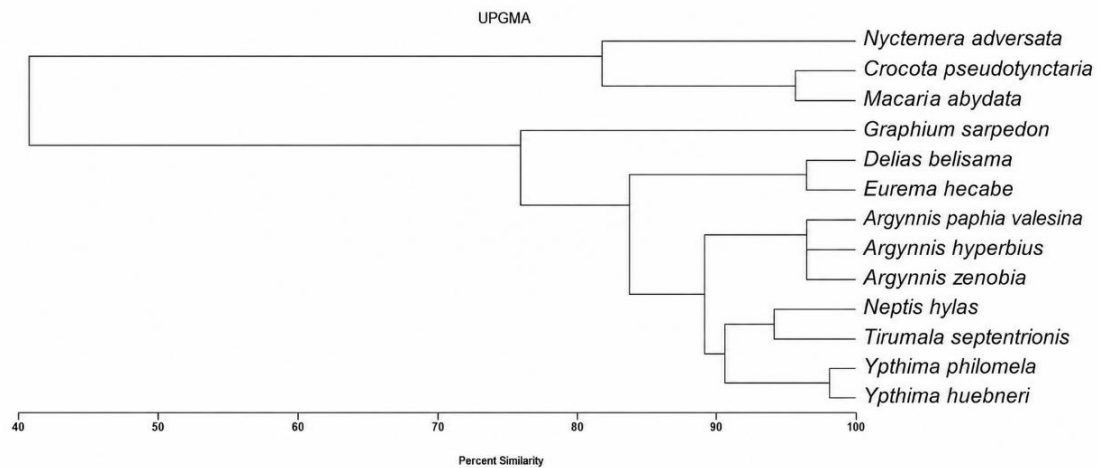


Figure 2. Morphological similarity dendrogram among Lepidoptera species based on UPGMA clustering

The dendrogram illustrates several clusters formed at different similarity levels based on morphological character comparisons. The morphological identification process involved detailed observations of general external features and diagnostic characters of each species, allowing classification based on overall similarity patterns (Nofisulastri, 2019; Astuti & Nugroho, 2023). The highest morphological similarity coefficient was observed between *Ypthima huebneri* and *Ypthima philomela* (98%), followed by *Eurema hecabe* and *Delias belisama* (96%). Species belonging to the genus *Argynnis* (*A. zenobia*, *A. hyperbius*, and *A. paphia valesina*) were grouped into the same cluster with approximately 95% similarity.

It is important to emphasize that the similarity percentages presented in the dendrogram represent the degree of resemblance based on the evaluated morphological characters and should not be interpreted as direct evidence of evolutionary relatedness or phylogenetic relationships. Phenetic analysis evaluates overall morphological similarity and may be influenced by both shared ancestral traits and convergent morphological characteristics resulting from similar environmental pressures.

The family Nymphalidae was the dominant group in the study area, comprising seven of the 13 recorded species. This dominance may be associated with the ecological flexibility and broad dietary range of many Nymphalidae members, particularly species belonging to Satyrinae and Limenitidinae. Their polyphagous feeding behavior enables them to utilize various host plants and persist under changing environmental conditions, even when specific host plants become unavailable (Sabran et al., 2021). The understory vegetation in Bukit Klangon, which was dominated by Poaceae, Cyperaceae, and Asteraceae shrubs, likely provided suitable resources for larval development and adult nectar feeding. Such ecological flexibility may allow Nymphalidae species to persist more effectively in disturbed habitats compared with more specialized butterfly groups. A characteristic feature of Nymphalidae is the reduction of the forelegs, which are not primarily used for walking. In males, the forelegs are modified into brush-like structures, giving rise to the common name “brush-footed butterflies” (Bhimasha et al., 2018).

The high morphological similarity among Nymphalidae species was also reflected in the clustering pattern. *Ypthima huebneri* and *Ypthima philomela* formed the closest cluster, sharing numerous morphological characters, including head structure, proboscis and labial palps, ocelli patterns, antennae, thoracic structure, abdomen

morphology, forewing and hindwing characteristics, accessory cells, and leg structures. The primary differences between these two species were observed in wing coloration and ocelli patterns.

Similarly, three species within the genus *Argynnis*, namely *Argynnis zenobia*, *Argynnis hyperbius*, and *Argynnis paphia valesina*, formed a highly similar morphological cluster. Their similarities were associated with shared fritillary wing patterns, orange-brown coloration, and bilateral symmetry of wing markings. However, differences among these species were observed in specific wing patterns and coloration characteristics. In addition, *Tirumala septentrionis* and *Neptis hylas* were grouped within the same cluster, although they exhibited distinct diagnostic traits. *Tirumala septentrionis* is characterized by white spots extending from the thorax to the head region, whereas *Neptis hylas* possesses distinctive black wing coloration with contrasting white bands (*sailers*). Several species in this study also exhibited intraspecific morphological variation, consistent with previous observations in Amazonian satyrine butterflies, where variation in wing patterns and external markings contributed to species-level differentiation (Nakahara et al., 2020).

Graphium sarpedon was the only representative of the family Papilionidae recorded in this study. This species was clustered with Nymphalidae species at approximately 75% similarity. Despite this clustering position, *G. sarpedon* possessed several distinct morphological features characteristic of Papilionidae, particularly the presence of one or more tail-like extensions on the posterior margin of the hindwing and specific wing venation patterns. These diagnostic traits distinguish Papilionidae from other butterfly families.

Two Pieridae species, *Eurema hecabe* and *Delias belisama*, were recorded from different sampling locations but clustered together based on morphological similarity. Both species share several characteristics typical of Pieridae, including wing structural features associated with the family. However, clear differences were observed in their coloration patterns. *Eurema hecabe* exhibits yellow wings with brown markings and characteristic spot patterns (Hawa et al., 2025), whereas *Delias belisama* is distinguished by prominent orange markings at the basal region of the wings. The high phenotypic similarity despite belonging to different genera highlights the challenges of morphology-based identification in groups with overlapping external characteristics. Similar phenotypic patterns may complicate taxonomic interpretation, and additional evidence such as molecular phylogenetic approaches may be required to clarify evolutionary relationships among closely related taxa (Leong et al., 2025).

The two Geometridae species, *Macaria abydata* and *Crocota pseudotynctaria*, also exhibited high morphological similarity and were grouped within the same cluster. The high morphological resemblance among Geometridae species, combined with limited taxonomic exploration in tropical regions, suggests that the diversity of this moth family remains incompletely documented. Global species richness estimates indicate that the number of valid Geometridae species may substantially increase beyond currently described taxa, highlighting the presence of potentially undiscovered diversity (Rajaei et al., 2022). Furthermore, Geometridae has been recognized as a species-rich moth family with potential value as an indicator group for environmental changes (Enkhtur et al., 2020).

The final species, *Nyctemera adversata*, belongs to the family Erebididae and showed distinct morphological characteristics compared with other recorded taxa. Previous studies have reported that *N. adversata* is widely distributed across the Indian subcontinent, occurring across a broad elevational range from approximately 400 to 1,500 m above sea level and reaching up to 1,600 m in Nepal (Smetacek & Aghinotri,

2021). This broad distribution suggests ecological tolerance across different environmental conditions. Diagnostic morphological features of this species include distinct wing patterns and characteristic venation structures, including four-branched cubital veins on the forewing.

The lowest morphological similarity was observed between *Ypthima huebneri* and *Nyctemera adversata*, with a similarity coefficient of 42%. This low similarity value reflects substantial differences in external morphological characteristics between the two species. The distinct clustering pattern is also consistent with their taxonomic differences, as *Y. huebneri* belongs to the family Nymphalidae, whereas *N. adversata* belongs to the family Erebidae.

CONCLUSION

This study documented 13 diurnal Lepidoptera species belonging to five families, namely Nymphalidae, Pieridae, Papilionidae, Geometridae, and Erebidae, in the secondary forest ecosystem of Bukit Klangon. The family Nymphalidae exhibited the highest species richness, accounting for seven of the recorded species. Morphological characterization and phenetic analysis based on 60 morphological characters revealed distinct similarity patterns among the recorded Lepidoptera species. The UPGMA clustering analysis showed the highest morphological similarity between *Ypthima huebneri* and *Ypthima philomela* (98%), followed by *Eurema hecabe* and *Delias belisama* (96%), whereas the lowest similarity was observed between *Ypthima huebneri* and *Nyctemera adversata* (42%). These findings demonstrate that morphological characterization can effectively describe phenetic similarity patterns among diurnal Lepidoptera in secondary forest habitats. However, the obtained similarity patterns represent morphological resemblance based on observable characters and should not be interpreted as evidence of evolutionary relationships or phylogenetic relatedness. This study provides baseline information on diurnal Lepidoptera diversity and morphological variation in Bukit Klangon, which may support future biodiversity assessments, ecological monitoring, and conservation-oriented management strategies.

RECOMMENDATION

Future studies should incorporate seasonal sampling and long-term monitoring to provide a more comprehensive understanding of Lepidoptera diversity, abundance patterns, and community dynamics. Standardized transect methods combined with host plant surveys and environmental assessments are recommended to improve understanding of species–habitat relationships. Furthermore, integrating DNA barcoding with morphological characterization is encouraged to confirm taxonomic identities, resolve morphologically similar species, and provide more accurate assessments of relationships among Lepidoptera taxa. These integrative approaches will support improved biodiversity documentation and conservation management of secondary forest ecosystems.

ACKNOWLEDGMENT

The authors would like to express their gratitude to the management of Klangon Hill tourism area for granting research permission and providing assistance during field activities. The authors also thank the Biology Laboratory of Universitas Muhammadiyah Surakarta for providing facilities and technical support throughout the research process. Appreciation is also extended to all individuals who contributed to the successful completion of this study.

The authors used AI-assisted technologies solely to improve the readability and language quality of the manuscript. The authors reviewed and edited the final content and take full responsibility for the manuscript.

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