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Species and Cladystic of Butterflies (Lepidoptera) in Malonas Village, Dampelas District, Central Sulawesi

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Abstract

Butterflies are a group of insects belonging to the order Lepidoptera, commonly known as scale-winged insects. This study examines the kinship relationships of butterfly species (Lepidoptera) based on morphological and morphometric characters in Malonas Village, Dampelas District, Central Sulawesi, an area that has not been previously documented. The objectives of this study were to identify butterfly characters through morphological and morphometric analyses and to construct kinship patterns that reflect the level of phylogenetic similarity among butterfly species. The research was conducted using a descriptive exploratory method. Sampling was carried out across all areas of Malonas Village, including residential areas, rivers, forests, and plantations, using a roaming survey method with free collection techniques, resulting in 10 butterfly species with a total of 30 individuals. Morphological and morphometric analyses included measurements of wing dimensions and major body parts. Data were analyzed using Principal Component Analysis (PCA) and the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) to determine kinship patterns. The UPGMA analysis showed that all species had a relatively high level of similarity, with a similarity value of approximately 0.78, indicating close relationships among species. PCA results revealed that two principal components (PC1 and PC2) explained 67.0% of the total morphological variation, accounting for 45.3% and 21.7%, respectively. Loading plots indicated that morphometric characters related to wing size and proportions were the main contributors to the formation of the principal components. Biplot graphs demonstrated species grouping based on similarities in morphological and morphometric characters, as well as positive correlations among variables within the same quadrant. The results of this study confirm that wing morphometric characters play an important role in explaining morphological variation and phylogenetic relationships of butterflies in Malonas Village.

Keywords: Butterflies; Central Sulawesi; Cladystic; Lepidoptera; Morphological.

INTRODUCTION

Butterflies are insects belonging to the order *Lepidoptera*, commonly known as scale-winged insects (Surantiwi et al., 2025). They are widely recognized because they can be found in almost all regions and are easily distinguished from other insects due to their unique and attractive colors and the diversity of their wing patterns (Carissa et al., 2024). Butterflies play an important role in natural ecosystems, particularly as pollinators, making their presence essential for environmental sustainability. Within the order *Lepidoptera*, insects are generally classified into two groups, namely butterflies and moths, which can be differentiated based on morphological and behavioral characteristics (Banun, 2021).

Butterflies are an important component of natural ecosystems because they play a role as pollinators in the growth of flowering plants (Ramadani & Akmal, 2023). This ecological function helps maintain ecosystem balance by facilitating plant fertilization, supporting biodiversity structure, and providing food resources for other organisms. Indonesia is home to approximately 2,000 butterfly species, of which about 557 species are distributed across Sulawesi. These species can be distinguished based on their body characteristics, particularly morphometric and morphological traits (Toding et al., 2024).

Morphology describes the body form of living organisms that can be directly observed with the naked eye (Ratnapuri, 2022). Morphometrics is a measurement-based method used to quantify physical characteristics in order to identify differences and variations among species (Ramadhan et al., 2024). In butterflies, morphological traits can be observed in body structures such as the head, wings, and antennae. Morphometric analysis can be conducted through measurements of butterfly wing and body features, including wingspan, body length, forewing length, forewing width, hindwing length, and hindwing width (Warikar et al., 2019).

Studies on butterfly species diversity and their kinship relationships in Central Sulawesi are still limited,

particularly in Malonas Village, Dampelas District. The natural potential of Malonas Village may influence butterfly quality, as butterflies serve as natural bioindicators of environmental conditions. Although butterflies are abundant in the area, their morphological and morphometric kinship relationships have not been clearly identified. Therefore, research on butterflies in Malonas Village is necessary to provide additional information and new scientific records in the field of biology. This study aims to determine the kinship relationships of butterfly species based on morphological and morphometric characters in Malonas Village, Dampelas District.

MATERIALS AND METHODS

Study Area

This study was conducted in September in Malonas Village, Dampelas District, Central Sulawesi (Figure 1). Malonas Village is characterized by a variety of habitats, including residential areas, rivers, forests, and agricultural land, which provide suitable environmental conditions for butterfly diversity and support various stages of their life cycles.

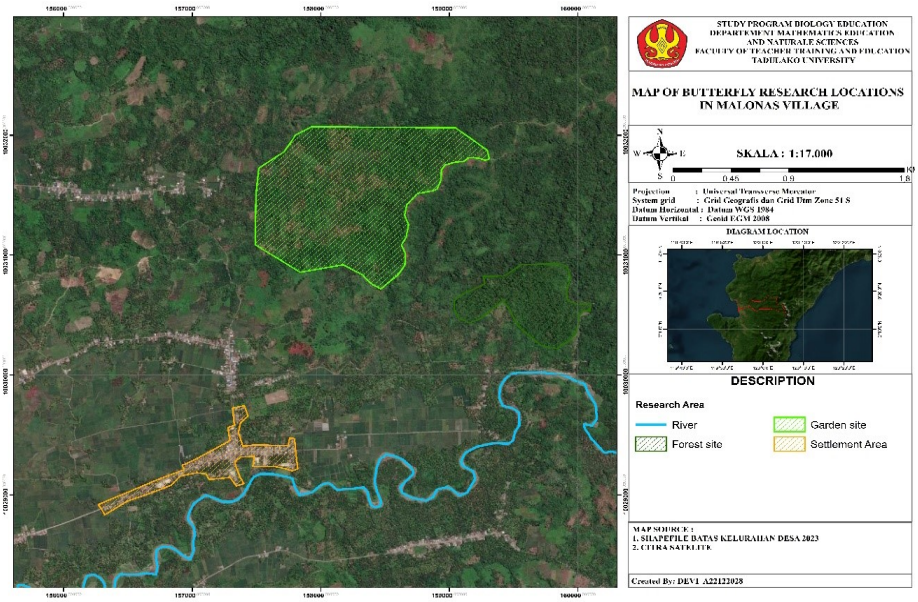

Figure 1. Map of the research location in Malonas Village, Dampelas District, Central Sulawesi, Indonesia.

Procedures

Data Collection Techniques

Data collection in this study began with an initial observation of the research site to assess habitat conditions and determine suitable sampling locations. This was followed by the preparation of the necessary tools and materials prior to fieldwork. Butterfly sampling was conducted using a roaming survey method with free collection techniques, allowing specimens to be collected across various habitat types. Sampling activities were carried out twice daily, in the morning between 07:00–10:00 WITA and in the afternoon between 14:00–17:00 WITA, corresponding to periods of peak butterfly activity.

Butterfly Preservation Technique

Butterfly preservation was performed by injecting alcohol into the thoracic region using a syringe to prevent decomposition and maintain specimen integrity. The preserved specimens were then positioned on a styrofoam board and covered with wax paper to protect the wings and body structures. Insect pins were carefully inserted along the sides of the butterflies to secure their position and maintain the natural shape of the wings for further morphological and morphometric analysis.

Butterfly Species Identification

Butterfly species identification was carried out using standard identification keys and reference literature, particularly Butterfly Bioecology by Rohman et al. (2019). Additional identification support was obtained from relevant scientific journals discussing butterfly taxonomy and kinship relationships. Identification was based on observable morphological characters, including wing coloration, wing patterns, and body structure, to ensure accurate species determination.

Data Analysis

The analysis data were obtained through direct observation and measurement of butterfly body parts. After all data had been collected, they were organized into tables using Microsoft Excel. Data analysis was conducted using PAST version 4.03, which provides clustering methods for data classification. The clustering

analysis employed the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) algorithm to classify taxonomic levels based on a high degree of similarity. The analysis in PAST 4.03 began with the preparation of primary data that had been organized in Microsoft Excel. The primary data were then imported into the PAST 4.03 software. Next, a distance matrix was selected by navigating to the Cluster menu and choosing the UPGMA option. The UPGMA analysis was then executed to analyze the data, and the OK button was clicked to process the dataset. Upon completion of the analysis, PAST generated a phylogenetic tree based on the UPGMA clustering results. Finally, the analysis results were saved by selecting the Save option or exported to the desired file format.

RESULTS AND DISCUSSION

Species of Butterflies

Butterflies are insects belonging to the order *Lepidoptera*, commonly referred to as scale-winged insects. This insect group is widely recognized because it can be found in almost all regions and can be easily distinguished from other insects due to their unique and attractive coloration and the diversity of their wing patterns. The adult butterfly body consists of three main parts: the head, thorax, and abdomen, with three pairs of legs and two pairs of wings attached to the thorax (Nuraini et al., 2020). Based on the results of the field observations, a total of 10 butterfly species comprising 30 individuals were recorded at the study site. Each species exhibited varying numbers of individuals, reflecting differences in species abundance within the research habitat (Figure 2).

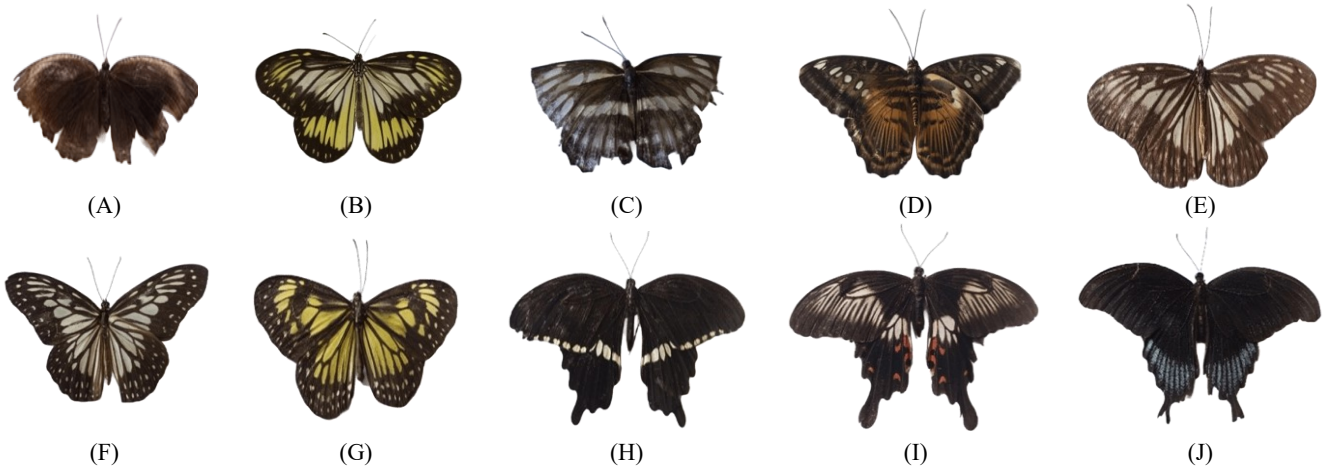

Figure 2. Species of butterflies (Ordo: Lepidoptera). A. *Elymnias panthera*, B. *Ideopsis vitrea*, C. *Common sailor*, D. *Panthenos sylvia*, E. *Ideopsis vulgaris*, F. *Ideopsis juventa*, G. *Parantica cleona*, H. *Papilio theseus*, I. *Papilio polytes*, J. *Papilio ascalaphus.*

Principal Component Analysis (PCA)

Data analysis in this study was performed using Principal Component Analysis (PCA) and visualized in the form of a dendrogram to illustrate the similarity levels among samples based on the observed morphological and morphometric characters. The dendrogram indicates that the samples cluster at relatively high similarity levels, with all samples converging at a similarity value of approximately 0.78. This high similarity suggests a close relationship among the samples, although noticeable variations in certain characteristics are still present between groups. These variations contribute to the formation of distinct clusters while maintaining an overall pattern of relatedness among the samples (Figure 3).

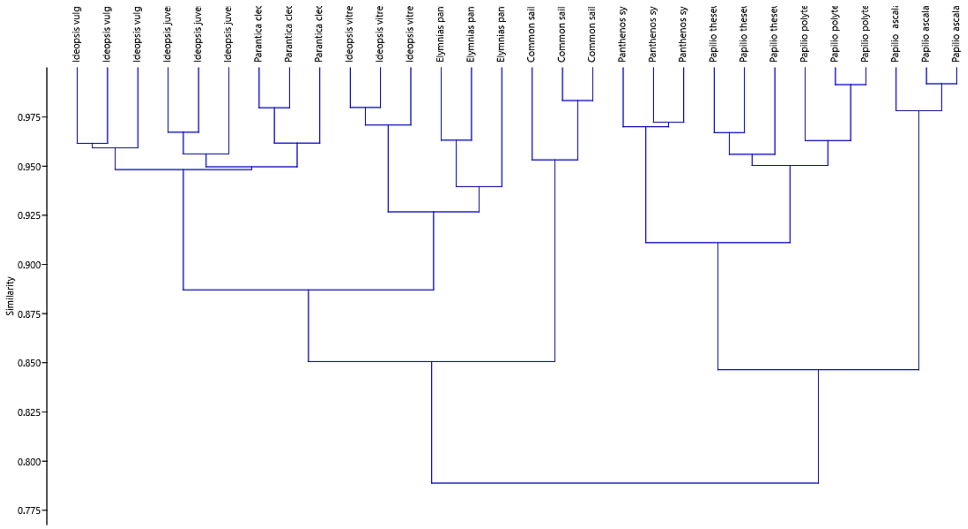

Figure 3. Dendrogram based on Principal Component Analysis (PCA).

Loadings Plot of PCA

The Principal Component Analysis (PCA) presented in the figure illustrates the contribution of each morphological variable in explaining character variation among ten butterfly species (Order: Lepidoptera), comprising 30 individuals, namely *Elymnias panthera*, *Ideopsis vitrea*, *Common sailor*, *Pantheos sylvia*, *Ideopsis vulgaris*, *Ideopsis juventa*, *Parantica cleona*, *Papilio theseus*, *Papilio polytes*, and *Papilio ascalaphus*. PCA was applied to reduce the complexity of multivariate data and to identify the main morphological characters contributing to differences among individuals and species. The displayed graphs represent PCA loading plots, which describe the magnitude of influence of each variable on the formed principal components (Figures 4 and 5).

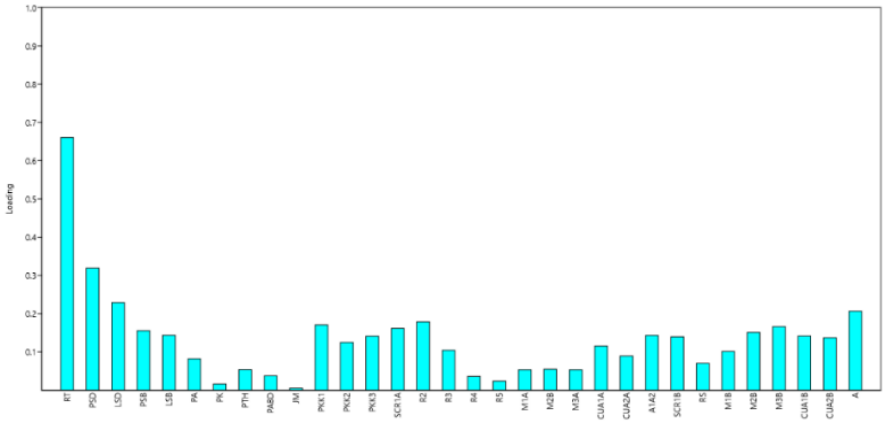

Figure 4. The loadings plot componen 1.

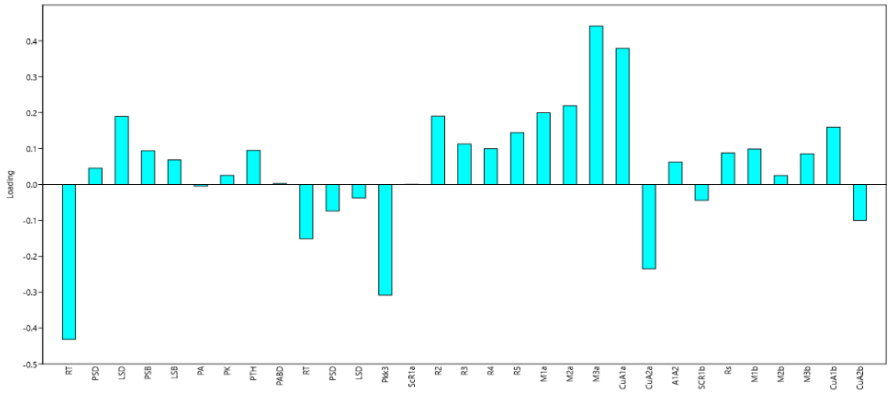

Figure 5. The loadings plot componen 2.

Biplot of PCA

The biplot depicts the distribution of morphological characters of ten butterfly species represented by 30 individuals based on the principal components PC1 and PC2. The PCA results indicate that the two main components (PC1 and PC2) explain most of the variation in the morphological data. PC1 serves as the primary axis separating the samples, while PC2 provides additional separation based on variation in specific characters (Figure 6).

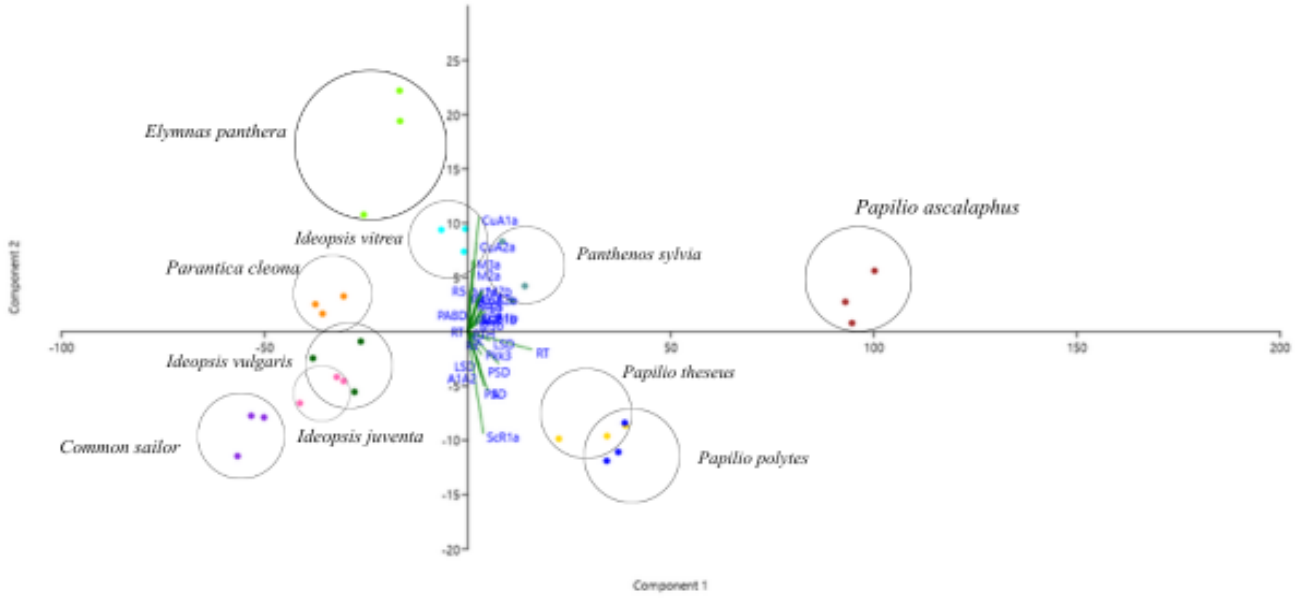

Figure 6. Biplot PCA.

DISCUSSION

This study investigated the kinship relationships of butterfly species based on morphological and morphometric characters in Malonas Village, Dampelas District, Central Sulawesi. Sampling was conducted in the morning between 08:00–10:00 and in the afternoon between 14:00–17:00 WIB using a roaming survey method with butterfly nets. Relatively stable environmental conditions at the study site supported butterfly survival and diversity. The results recorded 10 butterfly species, namely *Elymnias panthera*, *Ideopsis vitrea*, Common sailor, *Pantheos sylvia*, *Ideopsis vulgaris*, *Ideopsis juventa*, *Parantica cleona*, *Papilio theseus*, *Papilio polytes*, and *Papilio ascalaphus*. A total of 30 individuals were observed with varying distributions among species, indicating that the area provides adequate ecological resources such as host plants, nectar sources, and suitable microclimatic conditions. Butterflies are known to be sensitive to environmental changes; therefore, high species presence and diversity are commonly used as indicators of well-maintained habitat quality (Ramadhani et al., 2025). Differences in species abundance also reflect variation in adaptive capacity and ecological tolerance among species to local environmental conditions (Ramadhana et al., 2025).

Kinship relationship analysis using the UPGMA hierarchical clustering method produced a dendrogram showing clear grouping patterns based on morphological and morphometric similarities (Wangiyani, 2019). The dendrogram revealed that most species formed subgroups at high similarity levels, exceeding 0.90, indicating strong morphological resemblance, particularly in wing size and proportions (Imran, 2019). Such similarity is likely associated with comparable ecological functions, including flight ability, foraging strategies, and adaptation to similar habitat conditions. At slightly lower similarity levels, ranging from 0.85 to 0.88, several subgroups began to merge into larger clusters (Pangestu et al., 2024), reflecting more distinct intergroup differences while still indicating relatively close kinship relationships (Efendi et al., 2024). The convergence of all samples at a similarity value of approximately 0.78 suggests that, despite observable differences among groups, all butterfly species recorded in this study maintain relatively close kinship relationships (Sabran et al., 2021). This similarity reflects shared fundamental characteristics at a higher taxonomic level, as all species belong to the same order (*Lepidoptera*) (Jannah et al., 2022).

The PCA loading plot indicates that the contribution of each morphological and morphometric character to the formation of the principal components varied (Hikmah et al., 2023). Wingspan (WS) showed the highest loading value, indicating that it is the most dominant factor in explaining morphological variation among butterfly species (Makzhuni, 2013). The strong contribution of wingspan suggests that overall wing size plays a crucial role in species differentiation, closely related to flight performance, movement efficiency, and ecological

adaptation. In addition, forewing length (FWL) and forewing width (FWW) contributed significantly, emphasizing the importance of forewing dimensions in species separation. Hindwing length (HWL) and hindwing width (HWW) showed moderate contributions, while antenna length, head length, and thorax length exhibited relatively low loading values, indicating a tendency toward homogeneity in these body traits. Overall, these findings confirm that wing-related morphometric characters are key indicators for explaining variation and kinship relationships among butterfly species (Warikar et al., 2019).

PCA results presented in the form of a biplot for the 10 butterfly species comprising 30 individuals demonstrated that the first two principal components explained most of the morphological variation in the dataset (Bibas et al., 2025). Principal Component 1 (PC1) had the highest eigenvalue and accounted for 45.3% of the total variation, while Principal Component 2 (PC2) explained 21.7%. Together, PC1 and PC2 cumulatively explained 67.0% of the total morphological variation, indicating that dimensional reduction through PCA was effective and representative of the original data structure (Purnama & Sihombing, 2021). The loading plot revealed that several wing vein parameters, particularly CuA1, CuA2, M2, and M3, had high loading values on PC1 and PC2, contributing significantly to the formation of these principal components (Aryasatya et al., 2024). Variables located farther from the coordinate center indicate a dominant role in explaining morphological variation, whereas those closer to the center contribute less (Winaya et al., 2018). Variables positioned within the same quadrant show positive correlations, while those in opposite directions indicate negative relationships among morphological parameters (Awanni & Saputra, 2024).

CONCLUSIONS

A total of 10 butterfly species comprising 30 individuals were recorded in Malonas Village, Dampelas District, Central Sulawesi, indicating that the area provides suitable habitat conditions for butterfly diversity. Analysis based on morphological and morphometric characters using UPGMA and PCA revealed relatively close kinship relationships among species, with all taxa converging at a similarity value of approximately 0.78. The first two principal components explained 67.0% of the total morphological variation, with PC1 and PC2 accounting for 45.3% and 21.7%, respectively.

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Competing Interests: The authors declare that there are no competing interests.

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